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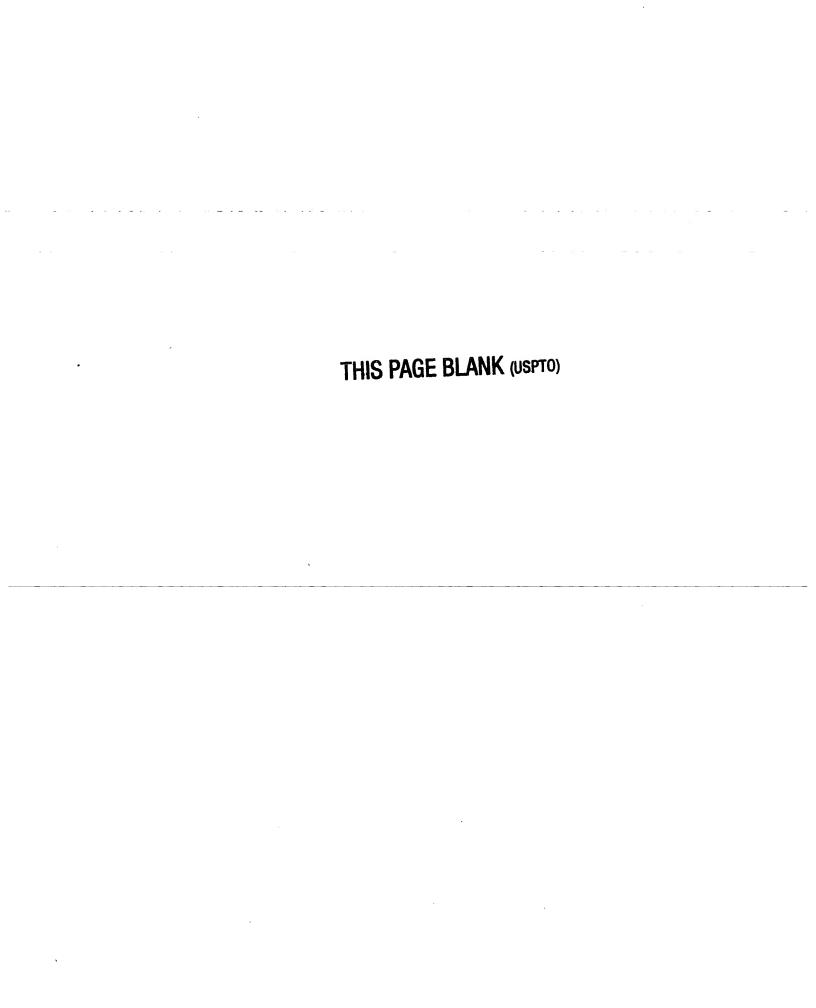
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PTO-1590 (1-2000)

# 43804 SEARCH REQUEST FORM

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Art Unit: /6 Y / Phone N Mail Box and Bldg/Room Location	umber 30 <u>8 - 6 9 70</u>	Its Format Preferred (circle): PAPER DISK E-MAIL
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Title of Invention:		·
Inventors (please provide full names): _		
Earliest Priority Filing Date: 92-		<u> </u>
*For Sequence Searches Only* Please include appropriate serial number.	de all pertinent information (j	parent, child, divisional, or issued patent numbers) along with the
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of tumors, see	claims 1,	diagnosis + treatment
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	Patent Family	
Online Time:	Other	Other (specify) CGN

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FILE 'REGISTRY' ENTERED AT 11:09:26 ON 11 JUN 2001 E CONDUCTINE/CN

FILE 'CAPLUS' ENTERED AT 11:09:46 ON 11 JUN 2001 L1 0 S CONDUCTINE

FILE 'MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, JAPIO, CANCERLIT' ENTERED AT 11:10:14 ON 11 JUN 2001

L2 6 S L1

L3 6 DUP REM L2 (0 DUPLICATES REMOVED)

L3 ANSWER 1 OF 6 JAPIO COPYRIGHT 2001 JPO

ACCESSION NUMBER:

1996-024402

**JAPIO** GAME BALL PASSING SENSOR

TITLE: INVENTOR:

YOSHIKAWA TOSHISUKE

PATENT ASSIGNEE(S):

KYOWA GIKEN KK, (CO)

PATENT INFORMATION:

PATENT NO KIND DATE MAIN IPC JP 08024402 A 19960130 Heisei (6) A63F007-02

JP

APPLICATION INFORMATION

ST19N FORMAT:

JP1994-169178

19940721

ORIGINAL:

JP06169178

Heisei.

SOURCE:

PATENT ABSTRACTS OF JAPAN (CD-ROM), Unexamined

Applications, Vol. 96, No. 1

AN 1996-024402 **JAPIO** 

AΒ PURPOSE: To prevent an erroneous operation by electromagnetic wave or exter nal light, and precisely detect the passing of game ball by making an operating piece pushed into a switch housing part when the ball passes the through-hole of a switch case, thereby a switch is brought into non-conductine stake and the passing of the ball is detected.

CONSTITUTION: When no game ball passes a through-hole 30, one end of an operating piece 70 supported in the inner part of a switch housing part 40 is in the state capable of protruding into the through-hole 30, and the energizing force of a torsion spring 60 acts on the free end part on the other end to energize the operating piece 70 in the protruding direction. Both ends of the torsion spring 60 come into contact with a fixed pin 54 and a contact pin 53 in this state to hold the conductive state between the connecting terminals 51, 52 of a base 50. When a game ball passes the through-hole 30, the operating piece 70 is pushed against the energizing force of the torsion spring 60. Thus, one end of the torsion spring 60 is pushed in and separated from the contact pin 53 to bring the connecting terminals 51, 52 into the non-conductive

state, thereby the passing of the game ball can be detected.

ANSWER 2 OF 6 MEDLINE

ACCESSION NUMBER: 90181913

MEDLINE

DOCUMENT NUMBER:

90181913 PubMed ID: 2560672

TITLE:

[Sodium conductin of the human brain: purification

and functional characterization].

La conductine au sodium du cerveau humain: purification et caracterisation fonctionnelle.

AUTHOR:

Materne-De Rycker C

SOURCE:

BULLETIN ET MEMOIRES DE L ACADEMIE ROYALE DE MEDECINE

DE BELGIQUE, (1989) 144 (8-9) 426-33.

Journal code: BOX; 7608462. ISSN: 0377-8231.

PUB. COUNTRY:

Belgium

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE:

French

FILE SEGMENT:

Priority Journals

ENTRY MONTH:

199004

ENTRY DATE:

Entered STN: 19900601

Last Updated on STN: 19900601

Entered Medline: 19900426

A sodium channel enriched preparation was obtained from human brain. AB Human sodium channel appeared as a heterocomplex peptide alpha beta 1 beta 2. Functional properties of the protein were maintained since, after reconstitution into liposomes, ion fluxes were sensitive to sodium channel specific toxins and to membrane potential. Moreover, the reconstituted protein showed a well defined ionic selectivity.

ANSWER 3 OF 6 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD

ACCESSION NUMBER:

1988-347509 [49]

DOC. NO. NON-CPI:

N1988-263366

TITLE:

Semiconductor shift register in memory output state - has two conductive type transistor connected in

series between power supply terminal and node.

DERWENT CLASS:

U14

INVENTOR(S):

NAKAGAWA, K; TAKEUCHI, Y

PATENT ASSIGNEE (S):

(TOKE) TOSHIBA KK

COUNTRY COUNT:

PATENT INFORMATION:

PA	TENT NO	KIND	DATE	WEEK	LA	PG
EP	293808 R: DE FI		19881207	(198849)*	EN	15
JP	63304494	A	19881212	(198904)		
US	4856034	A	19890808	(198939)		14
EP	293808	B1	19930929	(199339)	EN	16

R: DE FR GB

DE 3884460 G 19931104 (199345)

#### APPLICATION DETAILS:

PA'	TENT NO	KIND	AP	PLICATION	DATE
EP	293808	A	EP	1988-108632	19880530
JP	63304494	A	JP	1987-139405	19870603
US	4856034	A	US	1988-199914	19880527
EP	293808	B1	EP	1988-108632	19880530
DE	3884460	G	DE	1988-3884460	19880530
			EP	1988-108632	19880530

#### FILING DETAILS:

PATENT NO	KIND	PATENT NO
		<del>.</del>
DE 3884460	G Based on	EP 293808

PRIORITY APPLN. INFO: JP 1987-139405 19870603

AN 1988-347509 [49] WPIDS

AB EP 293808 A UPAB: 19930923

The circuit has a logic circuit (12) with two inputs connected to receive a control clock signal (Phi G) and an input signal (Vin) a two conductine type transistors (P11 P12) are connected in series between a power supply terminal and a node. The first transistor (P11) has a gate connected to receive an output signal of the logic circuit. The other transistor (P12) has a gate connected to receive the control clock signal.

A third transistor (N11) of a different conductive type connects the first node and the second power supply terminal together.

The transistor gate is connected to receive the output signal of the logic circuit.

USE/ADVANTAGE - Latch circuit or swift register in the output stage of the memory.

#### ABEQ US 4856034 A UPAB: 19930923

The semiconductor integrated circuit consists of a three-valued logic circuit connected to receive an output signal of a logic circuit to receive at one input a control clock signal and at the other input an input signal. A flip-flop circuit is composed of a clocked inverter to receive the output signal of the three-valued logic circuit, and another inverter.

ABEQ EP 293808 B UPAB: 19931123

A semiconductor integrated circuit, comprising: a logic circuit (12) consisting of a NOR gate (72) or a NAND gate (82) and having a first

and a second input connected to receive a control clock signal ( G) and an input signal (Vin), respectively; first and second transistors (P11, P12) of a first conductivity type connected in series between a first power supply terminal (Vcc) and a first node (1), said first transistor (P11) having a gate connected to receive an output signal of said logic circuit, and said second transistor (P12) having a gate connected to receive the control clock signal; a third transistor (N11) of a second conductivity type connected between said first node and a second power supply terminal (Vss) and having a gate connected to receive the output signal of said logic circuit; fourth and fifth transistors (P13, P14) of the first conductivity type connected in series between said first power supply terminal and a second node (2) connected to said first node, said fourth transistor (P14) having a gate connected to receive the output signal of said logic circuit, and said fifth transistor (P13) having a gate connected to a third node (3); sixth and seventh transistors (N14, N13) of the second conductivity type connected in series between said second power supply terminal and said second node, said sixth transistor (N14) having a gate connected to receive the clock signal, and said seventh transistor (N13) having a gate connected to said third node; an eighth transistor (P15) of the first conductivity type connected between said third node and said first power supply terminal and having a gate connected to said second node; and a ninth transistor (N15) of the second conductivity type connected between said third node and said second power supply terminal, and having a gate connected to said second node; an output signal (Vout) of said semiconductor integrated circuit being taken from at least one of said second node and said third node. Dwg.1/10

L3 ANSWER 4 OF 6 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD ACCESSION NUMBER: 1978-A8315A [04] WPIDS

TITLE:

Insulated splice and terminal - is made from crimped composite strip of non-conductive and

electrically conducting materials.

DERWENT CLASS:

V04

INVENTOR (S):

FISCHER, E M; MEISINGER, W R; ZAHN, I

PATENT ASSIGNEE(S):

(GEST-N) GEN STAPLE CO

COUNTRY COUNT:

Т

PATENT INFORMATION:

PRIORITY APPLN. INFO: US 1973-335417 19730223; US 1974-537532

19741230; US 1976-711604 19760804

AN 1978-A8315A [04] WPIDS

US 4067105 A UPAB: 19930901 AB

> An elongated layer of non-conductive materials is adhered to an elongated layer of electrically conductive material so as to form a composite supply strip. A predetermined length is severed and crimped about the elements to be joined until the electrically conductive material is in electrical contact with the elements and so that the non-conductine material forms an outer insulated layer enclosing the splice or at least a portion of the terminal.

> In a pref. method there is further step of causing the non-conductive material of the splice to "flow" whereby a resultant sealed splice is produced which is impervious to moisture and other contaminants. PRef. the non-conductive material is a thermoplastic resin and the conductive material is brass.

ANSWER 5 OF 6 JAPIO COPYRIGHT 2001 JPO L3

ACCESSION NUMBER:

1977-115854 **JAPIO** 

TITLE:

ELECTRICALLY CONDUCTINE RESIN AND

INTERMEDIATES AND ELECTRICALLY CONDUCTIVE COATED

PAPERS

INVENTOR:

JIYOSEFU RII GAANAA

PATENT ASSIGNEE(S):

DOW CHEM CO: THE, US (CO 000723)

PATENT INFORMATION:

PATENT NO KIND DATE ERA MAIN IPC \_\_\_\_\_ JP 52115854 A 19770928 Showa (2) C08L025-06

APPLICATION INFORMATION

ST19N FORMAT: JP1977-29130

19770316

ORIGINAL:

JP52029130

Showa

PRIORITY APPLN. INFO.: US1976 668335

19760319

AN 1977-115854 JAPIO

ANSWER 6 OF 6 JAPIO COPYRIGHT 2001 JPO

ACCESSION NUMBER: 1977-019984

**JAPIO** 

TITLE:

MANUFACTURE PROCESS FOR A ISOLATION LAYER USED

INVENTOR:

PATENT ASSIGNEE(S):

TO MAKE A SEMICONDUCTOR ELEMENT KOMATSU RYOSAKU; HARUHARA YOSHIO NIPPON TELEGR & TELEPH CORP <NTT>, JP (CO

000422)

PATENT INFORMATION:

PATENT NO KIND DATE ERA MAIN IPC

JP 52019984 A 19770215 Showa (2) H01L021-76

JP

APPLICATION INFORMATION

ST19N FORMAT:

JP1975-96053

19750807

ORIGINAL:

JP50096053

Showa

SOURCE:

PATENT ABSTRACTS OF JAPAN, Unexamined

Applications, Section: E, Sect. No. 34, Vol. 1,

No. 851, P. 1733 (19770809)

AN 1977-019984 **JAPIO** 

PURPOSE: To pour p type ion to the N type semiconductor substrate an AB order to make a p type conductine area as a isolation layer. In this way, we make plural isolation layers at the same time with a desired size and high precision, saving the manufacture work.

FILE 'REGISTRY' ENTERED AT 11:14:12 ON 11 JUN 2001

E CONDUCTIN/CN L4

2 SEA ABB=ON PLU=ON ("CONDUCTIN (HUMAN FETAL BRAIN REDUCED) "/CN OR "CONDUCTIN (HUMAN) "/CN)

FILE 'CAPLUS' ENTERED AT 11:14:41 ON 11 JUN 2001

L5 25 SEA ABB=ON PLU=ON L4 OR CONDUCTIN

15 SEA ABB=ON PLU=ON L5 AND (TUMOUR OR TUMOR OR NEOPLAS? OR CANCER? OR CARCIN?)

ANSWER 1 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER:

2001:208094 CAPLUS

DOCUMENT NUMBER:

134:247261

TITLE:

L6

Agents for treating human diseases, especially

for treating tumors such as colon

cancers and melanomas or for

regenerating tissue and promoting hair growth

INVENTOR (S): PATENT ASSIGNEE(S):

Birchmeier, Walter; Von Kries, Jens-peter Max-Delbruck-Centrum fur Molekulare Medizin,

Germany

SOURCE:

PCT Int. Appl., 28 pp.

CODEN: PIXXD2

DOCUMENT TYPE:

Patent

LANGUAGE:

German

FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

PATENT NO. KIND DATE APPLICATION NO. DATE ----

WO 2001019353 **A2** 20010322 WO 2000-DE3104 20000.907

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH,

GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK,

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LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ,
PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ,
UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU,
TJ. TM
```

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

DE 1999-19944404 19990916 A1 20010322 DE 19944404

PRIORITY APPLN. INFO.:

DE 1999-19944404 A 19990916

The invention relates to agents for treating human diseases which are based on substances that specifically influence the binding of .beta.-catenin with LEF-1/TCF transcription factors, APC or conductin/axin. The invention particularly relates to the identification and use of hydrophobic pockets on the mol. surface in the proximity of the essential binding points for the binding partners of .beta.-catenin with the aim of optimizing these substances. The invention also relates to the use of the substances, preferably for treating tumors, e.g. colon cancers and melanomas, or for regenerating tissue and promoting hair growth.

ANSWER 2 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER:

2000:735507 CAPLUS

DOCUMENT NUMBER:

134:28066

TITLE:

Mutations in AXIN2 cause colorectal

cancer with defective mismatch repair by

activating .beta.-catenin/TCF signaling

Liu, Wanguo; Dong, Xiangyang; Mai, Ming; Seelan, AUTHOR (S):

Ratnam S.; Taniguchi, Ken; Krishnadath, Kausilia K.; Halling, Kevin C.; Cunningham, Julie M.;

Qian, Chiping; Christensen, Eric; Roche, Patrick

C.; Smith, David I.; Thibodeau, Stephen N.

CORPORATE SOURCE:

Div. of Experimental Pathol., Dep. of Lab. Med.

and Pathol., Mayo Clinic and Mayo Med. Sch.,

Rochester, MN, USA

SOURCE:

Nat. Genet. (2000), 26(2), 146-147

CODEN: NGENEC; ISSN: 1061-4036

PUBLISHER:

Nature America Inc.

DOCUMENT TYPE:

Journal: General Review

LANGUAGE:

English

Colorectal cancer (CRC) with defective DNA mismatch repair AB (MMR) is assocd. with alterations in one of several DNA MMR genes. Here we show that AXIN2 encoding a Wnt signaling component, is mutated in 11 of 45 CRC with defective MMR. We tested the functional importance of AXIN2 mutations in the development of CRCwith defective MMR in a TCF reporter assay. Our findings now provide a link between defective MMR and the activation of TCF-dependent transcription, as mutations in AXIN2 alter the APC

pathway.

REFERENCE COUNT:

REFERENCE(S):

14

- (1) Behrens, J; Science 1998, V280, P596 CAPLUS
- (2) Boland, C; Cancer Res 1998, V58, P5248 CAPLUS
- (3) Chan, E; Nature Genet 1999, V21, P410 CAPLUS
- (4) Ganguly, A; Proc Natl Acad Sci USA 1993, V90, P10325 CAPLUS
- (5) Ishitani, T; Nature 1999, V399, P798 CAPLUS
- ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 3 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER:

2000:651706 CAPLUS

DOCUMENT NUMBER:

134:1816

TITLE:

Hot spots in .beta.-catenin for interactions

with LEF-1, conductin and APC

AUTHOR (S):

Von Kries, Jens Peter; Winbeck, Georgia; Asbrand, Christian; Schwarz-Romond, Thomas; Sochnikova, Natalia; Dell'Oro, Andrea; Behrens,

Jurgen; Birchmeier, Walter

CORPORATE SOURCE:

Max-Delbruck-Center for Molecular Medicine,

Berlin, 13093, Germany

SOURCE:

Nat. Struct. Biol. (2000), 7(9), 800-807

CODEN: NSBIEW; ISSN: 1072-8368

PUBLISHER:

Nature America Inc.

DOCUMENT TYPE:

Journal

LANGUAGE:

English

Interactions between .beta.-catenin and LEF-1/TCF, APC and conductin/axin are essential for wnt-controlled stabilization of .beta.-catenin and transcriptional activation. wnt signal transduction pathway is important in both embryonic development and tumor progression. We identify here amino acid residues in .beta.-catenin that distinctly affect its binding to LEF-1/TCF, APC and conductin. These residues form sep. surface clusters, termed hot spots, along the armadillo superhelix of .beta.-catenin. We also show that complementary charged and hydrophobic amino acids are required for formation of the bipartite .beta.-catenin-LEF-1 transcription factor. Moreover, we demonstrate that conductin/axin binding to .beta.-catenin is essential for .beta.-catenin degrdn., and that APC acts as a cofactor of conductin/axin in this process. Binding of APC to conductin/axin activates the latter and occurs between their SAMP and RGS domains, resp.

REFERENCE COUNT:

50

REFERENCE(S):

- (1) Aberle, H; EMBO J 1997, V16, P3797 CAPLUS
- (2) Aberle, H; J Cell Sci 1994, V107, P3655 CAPLUS
- (3) Behrens, J; Nature 1996, V382, P638 CAPLUS

(4) Behrens, J; Science 1998, V280, P596 CAPLUS(5) Brunner, E; Nature 1997, V385, P829 CAPLUS

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 4 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER:

2000:547045 CAPLUS

DOCUMENT NUMBER:

134:27977

TITLE:

Control of .beta.-catenin signaling in

tumor development .

AUTHOR (S):

Behrens, Jurgen

CORPORATE SOURCE:

Max-Delbruck-Center for Molecular Medicine,

Berlin, 13122, Germany

SOURCE:

Ann. N. Y. Acad. Sci. (2000), 910 (Colorectal

Cancer), 21-35

CODEN: ANYAA9; ISSN: 0077-8923 New York Academy of Sciences

DOCUMENT TYPE:

Journal; General Review

LANGUAGE:

PUBLISHER:

English

The wnt signal transduction pathway is A review, with 72 refs. AB involved in various differentiation events during embryonic development and leads to tumor formation when aberrantly activated. The wnt signal is transmitted to the nucleus by the cytoplasmic component .beta.-catenin: in the absence of wnts, .beta.-catenin is constitutively degraded in proteasomes, whereas in the presence of wnts .beta.-catenin is stabilized and can assoc. with HMG box transcription factors of the LEF/TCF family. LEF/TCF/.beta.-catenin complexes activate specific wnt target genes. In tumors, .beta.-catenin degrdn. is blocked by mutations of .beta.-catenin or of the tumor suppressor gene product APC. As a consequence, .beta.-catenin is stabilized, constitutive complexes with LEF/TCF factors are formed, and oncogenic target genes, such as c-myc, cyclin D1, and c-jun, are activated. control of .beta.-catenin is a major regulatory event in normal wnt signaling and during tumor formation. It has been found that a multiprotein complex assembled by the cytoplasmic component conductin induces degrdn. of cytoplasmic .beta.-catenin. The complex includes APC, the serine/threonine kinase GSK3.beta., and .beta.-catenin, which bind to conductin at distinct domains. In colon carcinoma cells, forced expression of conductin down-regulates .beta.-catenin, whereas in normal cells mutants of conductin that are deficient in complex formation stabilize .beta.-catenin. Fragments of APC that contain a c nductin-binding domain also block .beta.-catenin degrdn. In Xenopus embryos, conductin inhibits the wnt pathway. In situ hybridization anal. shows that conductin is expressed in various embryonal tissues known to be regulated by wnts, such as the developing brain, mesenchyme below the epidermis, lung mesenchyme, and kidney. It is suggested that conductin

controls wnt signaling by assembling the essential components of the .beta.-catenin degrdn. pathway. Alterations of conductin function may lead to tumor formation.

REFERENCE COUNT:

REFERENCE (S):

- (1) Aberle, H; EMBO J 1997, V16, P3797 CAPLUS
- (2) Ahmed, Y; Cell 1998, V93, P1171 CAPLUS
- (3) Aoki, M; Proc Natl Acad Sci 1999, V96, P139 CAPLUS
- (4) Bauer, A; Proc Natl Acad Sci 1998, V95, P14787 CAPLUS
- (5) Behrens, J; Cancer Metastasis Rev 1999, V18, P15 CAPLUS

ALL CITATIONS AVAILABLE IN THE RE FORMAT

ANSWER 5 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER:

2000:275313 CAPLUS

DOCUMENT NUMBER:

132:313670

TITLE:

Coated substrates for blood, plasma, or tissue

washing and columns equipped with these

substrates

INVENTOR(S):

Dunzendorfer, Udo; Will, Gottfried

PATENT ASSIGNEE(S):

Germany

SOURCE:

Ger. Offen., 30 pp.

CODEN: GWXXBX

DOCUMENT TYPE:

LANGUAGE:

Patent

German FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO. DATE
==			
DE 19845286	A1	20000427	DE 1998-19845286 19981001
EP 1004598	A2	20000531	EP 1999-118541 19990918
EP 1004598	<b>A</b> 3	20000607	

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO

PRIORITY APPLN. INFO.:

DE 1998-19845286

Columns, filters, cannulas, etc. contg. substrates coated with specific antibodies can be used during plasmapheresis to remove pathogenic cytokines such as tumor necrosis factor (TNF), anti-TNF, fragments of TNF or anti-TNF, or TNF transport proteins from blood, plasma, or tissues. The substrates may addnl. be coated with antibodies to microbial or viral pathogens or mixts. of pathogens as well as to polysaccharide antigens, viral capsids, microbial antigens, reverse transcriptase, endothelin, protein A, etc. Selective removal of these pathogens, antigens, proteins, etc. leaves all normal plasma components unchanged and obviates the need for supplementation of the plasma with these components. Suitable

substrates include polymers, polymer-coated metals, cellulose derivs., starch, and Sepharose; these may be derivatized for covalent binding of the pathogens or pathogenic mols. Thus, Escherichia coli pyelonephritis was successfully treated by plasmapheresis coupled with columns loaded with anti-TNF-.alpha. for 14 days, 4 h/day, as detd. by decreases in plasma TNF-.alpha. levels and colony counts in urine cultures.

L6 ANSWER 6 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 2000:94336 CAPLUS

DOCUMENT NUMBER: 133:56735

TITLE: The regulation of .beta.-catenin degradation and

cancer

AUTHOR(S): Kishida, Shosei; Kikuchi, Akira

CORPORATE SOURCE: Sch. Med., Hiroshima Univ., Hiroshima, 734-8551,

Japan

SOURCE: Mol. Med. (Tokyo) (2000), 37(2), 166-175

CODEN: MOLMEL; ISSN: 0918-6557

PUBLISHER: Nakayama Shoten

DOCUMENT TYPE: Journal; General Review

LANGUAGE: Japanese

AB A review with 37 refs. The structure of .beta.-catenin is described. .beta.-Catenin accumulates in colon cancer and malignant melanoma. .beta.-Catenin is degraded by the ubiquitin/proteasome system. Axin (conductin) possesses regulators of G protein signaling (RGS) for binding APC at N-terminus, GSK-3.beta. and .beta.-catenin binding domains at central region, and DIX region at C-terminus. Wnt protein releases .beta.-catenin from the Axin complex.

L6 ANSWER 7 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 2000:53973 CAPLUS

DOCUMENT NUMBER: 132:303902

TITLE: The yin-yang of TCF/.beta.-catenin signaling
AUTHOR(S): Barker, Nick; Morin, Patrice J.; Clevers, Hans
CORPORATE SOURCE: Department of Immunology, University Hospital,

Utrecht, 85500, Neth.

SOURCE: Adv. Cancer Res. (2000), 77, 1-24

CODEN: ACRSAJ; ISSN: 0065-230X

PUBLISHER: Academic Press

DOCUMENT TYPE: Journal; General Review

LANGUAGE: English

AB A review with 90 refs. Wingless/Wnt signaling directs cell-fate choices during embryonic development. In Drosophila, Wingless signaling mediates endoderm induction and the establishment of segment polarity in the developing embryo. The fly Wingless cascade is strikingly similar to the vertebrate Wnt signaling pathway, which controls a no. of key developmental decisions such as dorsal-ventral

patterning in Xenopus. Factors of the TCF/LEF HMG domain family (Tcfs) have recently been established as the downstream effectors of the Wingless/Wnt signal transduction pathways. Upon Wingless/Wnt signaling, a cascade is initiated that results in the accumulation of cytoplasmic .beta.-catenin (or its fly homolog, Armadillo). There is also a concomitant translocation of .beta.catenin/Armadillo to the nucleus, where it interacts with a specific sequence motif at the N terminus of Tcfs to generate a transcriptionally active complex. This bipartite transcription factor is targeted to the upstream regulatory regions of Tcf target genes including Siamois and Nodal related gene-3 in Xenopus, engrailed and Ultrabithorax in Drosophila via the sequence-specific HMG box, and mediates their transcriptional activation by virtue of transactivation domains contributed by .beta.-catenin/Armadillo. the absence of Wingless/Wnt signals, a key neg. regulator of the pathway, GSK3.beta., is activated, which mediates the downregulation of cytoplasmic .beta.-catenin/Armadillo via the ubiquitin-proteasome pathway. In the absence of nuclear .beta.-catenin, the Tcfs recruit the corepressor protein Groucho to the target gene enhancers and actively repress their transcription. An addnl. corepressor protein, CREB-binding protein (CBP), may also be involved in this repression of Tcf target gene activity. Several other proteins, including adenomatous polyposis coli (APC), GSK3.beta., and Axin/ Conductin, are instrumental in the regulation of .beta.-catenin/Armadillo. In APC-deficient colon carcinoma cell lines, .beta.-catenin accumulates and is constitutively complexed with nuclear Tcf-4. A proportion of APC wild-type colon carcinomas and melanomas also contains constitutive nuclear Tcf-4/.beta.-catenin complexes as a result of dominant mutations in the N terminus of .beta.-catenin that render it insensitive to downregulation by APC, GSK3.beta., and Axin/Conductin. This results in the unregulated expression of Tcf-4 target genes such as c-myc. Based on the established role for Tcf-4 in maintaining intestinal stem cells it is likely that deregulation of c-myc expression as a result of constitutive Tcf-4/.beta.-catenin activity promotes uncontrolled intestinal cell proliferation. This would readily explain the formation of intestinal polyps during colon carcinogenesis. Similar mechanisms leading to deregulation of Tcf target gene activity are likely to be involved in melanoma and other forms of cancer. (c) 2000 Academic Press.

REFERENCE COUNT:

90

REFERENCE(S):

- (2) Barker, N; Am J Pathol 1999, V154, P29 CAPLUS
- (3) Behrens, J; Nature (London) 1996, V382, P638 CAPLUS
- (4) Behrens, J; Science 1998, V280, P596 CAPLUS
- (5) Bhanot, P; Nature (London) 1996, V382, P225

CAPLUS

(6) Bienz, M; Trends Genet 1994, V10, P22 CAPLUS ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 8 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER:

1999:737696 CAPLUS

DOCUMENT NUMBER:

132:90977

TITLE:

Identification and characterization of E-APC, a

novel Drosophila homolog of the tumor

suppressor APC

AUTHOR (S):

Hamada, Fumihiko; Murata, Yoji; Nishida, Ayumu; Fujita, Fumitaka; Tomoyasu, Yoshinori; Nakamura, Makoto; Toyoshima, Kumao; Tabata, Tetsuya; Ueno,

Naoto; Akiyama, Tetsu

CORPORATE SOURCE:

Department of Oncogene Research, Research

Institute for Microbial Diseases, Osaka

University, Suita, 565-0871, Japan Genes Cells (1999), 4(8), 465-474

CODEN: GECEFL; ISSN: 1356-9597

SOURCE:
PUBLISHER:

Blackwell Science Ltd.

DOCUMENT TYPE:

Journal English

LANGUAGE:

We have identified a novel Drosophila homolog of APC, E-APC, which is similar to but differs in several respects from D-APC. The E-APC cDNA encodes a protein of predicted 1067 amino acids, with 7 armadillo repeats, 2 copies of the 15-amino acid repeat, 5 copies of the 20-amino acid repeat, and 1 Axin/conductin binding site. E-APC directly interacts with D-Axin and Armadillo (Arm, the Drosophila homolog of .beta.-catenin) in vitro, destabilizes intracellular .beta.-catenin, and suppresses .beta.-catenin/TCF-regulated transcription in APC-/- colon cancer cells. The E-APC mRNA is ubiquitously expressed throughout all developmental stages in Drosophila. Our findings suggest that E-APC may be universally involved in the regulation of the Wingless signaling

REFERENCE COUNT:

35

REFERENCE(S):

- (1) Ahmed, Y; Cell 1998, V93, P1171 CAPLUS
- (2) Baeg, G; EMBO J 1995, V14, P5618 CAPLUS
- (3) Behrens, J; Science 1998, V280, P596 CAPLUS
- (4) Cadigan, K; Genes Dev 1997, V11, P3286 CAPLUS
- (5) Hamada, F; Science 1999, V283, P1739 CAPLUS

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 9 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER:

1999:733931 CAPLUS

pathway by down-regulating the level of Arm in Drosophila.

DOCUMENT NUMBER:

131:333485

TITLE:

Signaling through .beta.-catenin and Lef/Tcf

AUTHOR (S):

CORPORATE SOURCE:

Novak, A.; Dedhar, S.

Sunnybrook Health Science Center, Toronto, ON,

M4N 3M5, Can.

SOURCE:

Cell. Mol. Life Sci. (1999), 56(5/6), 523-537

CODEN: CMLSFI; ISSN: 1420-682X

PUBLISHER:

Birkhaeuser Verlag

DOCUMENT TYPE: Journal; General Review

LANGUAGE:

English

A review with 167 refs. is given. .beta.-Catenin plays a structural role in cell adhesion by binding to cadherins at the intracellular surface of the plasma membrane and a signaling role in the cytoplasm as the penultimate downstream mediator of the wnt signaling pathway. The ultimate mediator of this pathway is a nuclear complex of .beta.-catenin acting as a coactivator with lymphoid enhancer factor/T cell factor (Lef/Tcf) transcription factors to stimulate transcription of a variety of target genes. Signaling through .beta.-catenin is regulated by modulating its degrdn. and nuclear translocation. In the absence of an activating signal, phosphorylation of .beta.-catenin by glycogen synthase kinase 3 (GSK3) acting in conjunction with adenomatous polyposis coli and axin/ conductin causes .beta.-catenin to interact with the .beta.-transducin repeat-contg. protein which results in its ubiquitination and degrdn. Signaling from the wnt pathway activates dishevelled which, in an as yet undefined manner, inhibits the activity of GSK3 resulting in an increase in the cytoplasmic free pool of .beta.-catenin, and translocation into the nucleus. The integrin-linked kinase (ILK) pathway also activates .beta.-catenin-Lef/Tcf signaling. ILK phosphorylates CiSK3 to inhibit its activity and translocates .beta.-catenin into the In addn., ILK downregulates the expression of E-cadherin and upregulates Lef-1 expression. In the final step of the .beta.-catenin-Lef/Tcf signaling pathway, nuclear .beta.-catenin binds pontin52-TATA binding protein and displaces Groucho-related gene or CREB-binding protein corepressors from Lef/ Tcf resulting in stimulation of transcription. During development, .beta.-catenin-Lef/Tcf signaling is involved in the formation of dorsal mesoderm and dorsal axis. Furthermore, defects in the .beta.-catenin-Lef/Tcf pathway are involved in the development of several types of cancers.

REFERENCE COUNT:

REFERENCE(S):

167

- (1) Aberle, H; EMBO J 1997, V16, P3797 CAPLUS
- (2) Aberle, H; J Cell Biochem 1996, V61, P514 CAPLUS
- (4) Ahmed, Y; Cell 1998, V93, P1171 CAPLUS
- (5) Aoki, M; Proc Natl Acad Sci USA 1999, V96, P139 CAPLUS
- (7) Axelrod, J; Science 1996, V271, P1826 CAPLUS ALL CITATIONS AVAILABLE IN THE RE FORMAT

308-4994

Searcher : Shears

L6 ANSWER 10 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1999:549289 CAPLUS

DOCUMENT NUMBER: 131:194280

TITLE: Agents for treating cancer and other

human illnesses based on .beta.-catenin

INVENTOR(S): Birchmeier, Walter; Von Kries, Jens-Peter

PATENT ASSIGNEE(S): Max-Delbrueck-Centrum fuer Molekulare Medizin,

Germany

SOURCE: PCT Int. Appl., 26 pp.

CODEN: PIXXD2

DOCUMENT TYPE:

FAMILY ACC. NUM. COUNT:

Patent

LANGUAGE: German

PATENT INFORMATION:

PATENT NO.	KIND DATE	APPLICATION NO.	DATE
WO 9942481	A2 19990826	WO 1999-DE554	19990222
WO 9942481	A3 20000210		
W: CA, JP	, ŪS		
RW: AT, BE	, CH, CY, DE, DK, ES	, FI, FR, GB, GR, IE	, IT, LU, MC,
NL, PT	, SE	·	
DE 19909251	A1 19990826	DE 1999-19909251	19990222

EP 1054899 A2 20001129 EP 1999-913097 19990222

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, NL, SE, PT, IE, FI

PRIORITY APPLN. INFO.:

DE 1998-19807390 A 19980221 WO 1999-DE554 W 19990222

C.beta.-catenin is a central mol. of the Wnt signal path. AB Increasing .beta.-catenin in the cell leads to its translocation into the cell nucleus and to its interaction with transcription factors of the LEF-1/TCF family. This can lead to colonic cancers and melanomas (oncogenic signal path). However, .beta.-catenin also interacts with the tumor-suppressor genes APC, conductin, and E-cadherin, which have a contrary effect on the cell (antioncogenic effect). derived from LEF-1-/TCF-4 transcription factors and analogous mols. can be used in the treatment of tumors, esp. colonic cancers and melanomas. These peptides and analogous mols. influence the interaction between .beta.-catenin and LEF-1/TCF. peptides comprise parts of the LEF-1/TCF-4 transcription factors and variants and mutations thereof, preferably the 10-40 N-terminal amino acids of LEF-1 or TCF-4, as well as peptides derived from the armadillo region of .beta.-catenin which were identified as interaction domains with LEF-1/TCF, APC, conductin, and E-cadherin. The peptides constituting interaction domains with APC or conductin can increase the concn. of .beta.-catenin in

the cell. These last mols. can be used to influence the formation of tissues and organs, e.g. to promote hair growth.

IT 221220-50-4, Conductin (human)

RL: BPR (Biological process); BIOL (Biological study); PROC (Process)

(interaction with .beta.-catenin, modulators of; agents for treating cancer and other human illnesses based on .beta.-catenin)

L6 ANSWER 11 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER:

1999:189197 CAPLUS

DOCUMENT NUMBER:

130:232471

TITLE:

The protein conductin and its

application for diagnosis and gene therapy of

colon cancer

INVENTOR (S):

Behrens, Jurgen; Birchmeier, Walter

PATENT ASSIGNEE(S):

Max-Delbruck-Centrum fur Molekulare Medizin,

Germany

SOURCE:

PCT Int. Appl., 22 pp.

CODEN: PIXXD2

DOCUMENT TYPE:

Patent

LANGUAGE:

German

FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

PATENT NO.	KIND DAT	E .	APPLICATION NO.	DATE
WO 9911780	A2 199	90311	WO 1998-DE2621	19980901
WO 9911780	A3 199	90527		
W: CA, JP,	US			
RW: AT, BE,	CH, CY, DE	, DK, ES, F	I, FR, GB, GR, I	E, IT, LU, MC.
NL, PT,				
DE 19840875	A1 199	90512	DE 1998-1984087	5 19980901
EP 1029047	A2 200	00823	EP 1998-954120	19980901
R: AT, BE,	CH, DE, DK	, FR, GB, I	T, LI, NL, SE, F	r
PRIORITY APPLN. INFO	.:		1997-19738205 A	
		WO	1998-DE2621 W	19980901

AB The invention concerns the novel protein conductin that is able to regulate the .beta.-catenin function and interacts with the tumor suppressor adenomatous polyposis coli (APC); and its application in the gene therapy of colon cancer. The 840 amino acid contg. protein contains domains with various activities: 78-200 is the RGS (Regulator of G-Protein Signalling) binding sequence; 343-396 is the GSK 3.beta. (glycogen synthase kinase 3.beta.) binding sequence; 397-465 is the .beta.-catenin binding sequence; 783-833 is the Dishevelled homol. region. Mutations, variants and fragments of conductin with the corresponding coding genes and mRNA sequences are also included. Antibodies and

nucleic acid probes for the detection of c nductin are part of the diagnosis tools. For therapeutic purposes a vector contg. the conductin gene is constructed; substances that activate and reactivate conductin in the body are co-administered, e.g. a substance that activates the c nductin promoter or stabilizes mRNA. The effect of conductin was proved using SW480 cells with APC mutation and thus increased .beta.-catenin level. Introduction of conductin resulted in the decrease of .beta.-catenin to the same concn. as in non APC mutated SW480 cells. In an expt. with Xenopus embryos it was shown that conductin inhibits the Wnt/Wingless signaling pathway via its interaction with .beta.-catenin.

IT 221220-50-4, Conductin (human)

RL: BAC (Biological activity or effector, except adverse); PRP (Properties); BIOL (Biological study)

(amino acid sequence; protein conductin and application for diagnosis and gene therapy of colon cancer)

L6 ANSWER 12 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER:

1999:179719 CAPLUS

DOCUMENT NUMBER:

131:16667

TITLE:

APC protein: protein interactions and cellular

functions

AUTHOR(S):

Jais, Philippe; Laurent-Puig, Pierre; Olschwang,

Sylviane

CORPORATE SOURCE:

Unite des Marqueurs Genetiques des Cancers (UMGC), Institut Gustave-Roussy, Villejuif,

94805, Fr.

SOURCE:

Gastroenterol. Clin. Biol. (1998), 22(12),

1071-1080

CODEN: GCBIDC; ISSN: 0399-8320

PUBLISHER:

Masson Editeur

DOCUMENT TYPE:

Journal; General Review

LANGUAGE:

French

AB A review with 112 refs., discussing structures of APC gene and protein; functions of APC protein in epithelial cell homeostasis and cell adhesion; assocn. of APC protein with .beta.-catenin, conductin, and GSK3.beta. in normal and transformed cells and other proteins-assocns.

REFERENCE COUNT:

112

REFERENCE(S):

- (1) Aberle, H; EMBO J 1997, V16, P3797 CAPLUS
- (3) Behrens, J; Nature 1996, V382, P638 CAPLUS
- (4) Behrens, J; Science 1998, V280, P596 CAPLUS
- (5) Beinhauer, J; J Cell Biol 1997, V139, P717 CAPLUS
- (6) Beroud, C; Nucleic Acids Res 1996, V24, P121 CAPLUS

#### ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 13 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER:

1999:134134 CAPLUS

DOCUMENT NUMBER:

131:14675

TITLE:

Cloning of the Human Homolog of Conduction

(AXIN2), a Gene Mapping to Chromosome 17q23-q24

AUTHOR (S):

Mai, Ming; Qian, Chiping; Yokomizo, Akira;

Smith, David I.; Liu, Wanguo

CORPORATE SOURCE:

Division of Experimental Pathology, Mayo

Clinic/Foundation, Rochester, MN, 55905, USA

SOURCE:

Genomics (1999), 55(3), 341-344 CODEN: GNMCEP; ISSN: 0888-7543

PUBLISHER:

Academic Press

DOCUMENT TYPE:

Journal

LANGUAGE:

English

AΒ Conduction or Axil, an Axin homolog, plays an important role in the regulation of .beta.-catenin stability in the Wnt signaling pathway. To facilitate the mol. anal. of the human gene, we isolated the human homolog, AXIN2. The cDNA contains a 2529-bp open reading frame and encodes a putative protein of 843 amino acids. Compared with rat and mouse homologs, AXIN2 shows an overall 89% amino acid identity. Several functional domains in this protein are highly conserved including the GRS (95.9%), GSK-3.beta. (96.3%), Dsh (98%), and .beta.-catenin (89.9%) domains. Radiation hybrid mapping localized the AXIN2 gene to human chromosome 17q23-q24, a region that shows frequent loss of heterozygosity in breast cancer , neuroblastoma, and other tumors. Human AXIN2 is thus a very strong candidate involved in multiple tumor types. (c) 1999 Academic Press.

226387-63-9, Conduction (human fetal brain reduced) IT RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(amino acid sequence; cloning of the human homolog of conductin (AXIN2), a gene mapping to chromosome 17q23-q24)

REFERENCE COUNT:

REFERENCE (S):

- (1) Aberle, H; EMBO J 1997, V16, P3797 CAPLUS
- (2) Aberle, H; J Cell Sci 1994, V107, P3655 **CAPLUS**
- (3) Barlund, M; Genes Chromosomes Cancer 1997, V20, P372 CAPLUS
- (4) Behrens, J; Nature 1996, V382, P638 CAPLUS
- (5) Behrens, J; Science 1998, V280, P596 CAPLUS
- ALL CITATIONS AVAILABLE IN THE RE FORMAT

ANSWER 14 OF 15 CAPLUS COPYRIGHT 2001 ACS ACCESSION NUMBER: 1999:106086 CAPLUS

DOCUMENT NUMBER:

130:323365

TITLE:

Identification of APC2, a homolog of the

adenomatous polyposis coli tum r

suppressor

AUTHOR (S):

Van Es, J. H.; Kirkpatrick, C.; Van de Wetering,

M.; Molenaar, M.; Miles, A.; Kuipers, J.;

Destree, O.; Peifer, M.; Clevers, H.

CORPORATE SOURCE:

Department of Immunology, University Hospital,

Utrecht, 3508 GA, Neth.

SOURCE:

Curr. Biol. (1999), 9(2), 105-108

CODEN: CUBLE2; ISSN: 0960-9822

PUBLISHER:

Current Biology Publications

DOCUMENT TYPE:

Journal

LANGUAGE: English

We report the identification and genomic structure of APC homologs. Mammalian APC2, which closely resembles APC in overall domain structure, was functionally analyzed and shown to contain 2 SAMP domains, both of which are required for binding to conductin

. Like APC, APC2 regulates the formation of active .beta.-catenin-Tcf complexes, as demonstrated using transient transcriptional activation assays in APC-/- colon carcinoma cells. Human APC2 maps to chromosome 19p13.3. APC and APC2 may therefore have comparable functions in development and cancer.

REFERENCE COUNT:

23

REFERENCE(S):

- (1) Aberle, H; EMBO J 1997, V16, P3797 CAPLUS
- (2) Behrens, J; Nature 1996, V382, P638 CAPLUS
- (3) Behrens, J; Science 1998, V280, P596 CAPLUS
- (4) Brunner, E; Nature 1997, V385, P829 CAPLUS
- (5) Cadigan, K; Genes Dev 1997, V11, P3286 CAPLUS

ALL CITATIONS AVAILABLE IN THE RE FORMAT

ANSWER 15 OF 15 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER:

1998:302214 CAPLUS

TITLE:

Functional interaction of an axin homolog, conductin, with .beta.-catenin, APC and

GSK3.beta.

AUTHOR (S):

Behrens, Jurgens; Jerchow, Boris-Alexander; Wurtele, Martin; Grimm, Jan; Asbrand, Christian; Wirtz, Ralph; Kuhl, Michael; Wedlich, Doris;

Birchmeier, Walter

CORPORATE SOURCE:

Max Delbruck Cent. Molecular Med., Berlin,

13122, Germany

SOURCE:

Science (Washington, D. C.) (1998), 280 (5363),

596-599

CODEN: SCIEAS; ISSN: 0036-8075

PUBLISHER:

American Association for the Advancement of

Science

DOCUMENT TYPE:

Journal

LANGUAGE:

English

AB Control of stability of .beta.-catenin is central in the wnt signaling pathway. Here, the protein conductin was found to form a complex with both .beta.-catenin and the tumor suppressor gene product adenomatous polyposis coli (APC). Conductin induced .beta.-catenin degrdn., whereas mutants of conductin that were deficient in complex formation stabilized .beta.-catenin. Fragments of APC that contained a conductin-binding domain also blocked .beta.-catenin degrdn. Thus, conductin is a component of the multiprotein complex that directs .beta.-catenin to degrdn. and is located downstream of APC. In Xenopus embryos, conductin interfered with wnt-induced axis formation.

(FILE 'MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, JAPIO, CANCERLIT' ENTERED AT 11:17:14 ON 11 JUN 2001)

L7

57 S L6

L8

22 DUP REM L7 (35 DUPLICATES REMOVED)

ACCESSION NUMBER:

ANSWER 1 OF 22 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD

2001-246094 [26] WPIDS

DOC. NO. CPI:

C2001-074206

TITLE:

Agent for tumor therapy, tissue

regeneration or stimulation of hair growth,

comprising inhibitor of binding of beta-catenin to

LEF-1/TCF-transcription factors, APC or conductin, obtained by specific screening

method.

DERWENT CLASS:

B04 D16

INVENTOR (S):

BIRCHMEIER, W; VON KRIES, J

PATENT ASSIGNEE (S):

(DELB-N) DELBRUECK CENT MOLEKULARE MEDIZIN MAX

COUNTRY COUNT:

94

PATENT INFORMATION:

PATENT	ИО	KIND	DATE	WEEK	LA	₽G

A1 20010322 (200126) \* DE 19944404 WO 2001019353 A2 20010322 (200126) GE

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TZ UG ZW

W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW

#### APPLICATION DETAILS:

	IND		LICATION	DATE
	A1		1999-19944404	
WO 2001019353	A2	WO	2000-DE3104	20000907

PRIORITY APPLN. INFO: DE 1999-19944404 19990916

2001-246094 [26] WPIDS

DE 19944404 A UPAB: 20010515 AΒ

> NOVELTY - An agent (I) for therapy of human disorders, comprising an inhibitor of the binding of beta -catenin to LEF-1/TCF-transcription factors, APC (undefined) or conductin, is new.

DETAILED DESCRIPTION - An INDEPENDENT CLAIM is included for identifying agents (I), comprising identifying hydrophobic pockets in the vicinity of essential binding sites in the beta -catenin molecule, and synthesizing compounds which fit in these pockets.

ACTIVITY - Cytostatic.

No biological data is given.

MECHANISM OF ACTION - Inhibition of binding of beta -catenin to LEF-1/TCF-transcription factors, APC or conductin.

USE - For therapy of tumors (e.g. colon carcinoma or melanoma), for tissue regeneration or for stimulation of hair growth (claimed). Dwg.0/3

ANSWER 2 OF 22 EMBASE COPYRIGHT 2001 ELSEVIER SCI. B.V.

ACCESSION NUMBER:

2001083138 EMBASE

Oncogenic targets of .beta.-catenin-mediated TITLE:

transcription in molecular pathogenesis of intestinal

polyposis.

Watson S.A. AUTHOR:

S.A. Watson, Academic Unit of Cancer Studies, CORPORATE SOURCE:

University of Nottingham, Nottingham NG7 2UH, United

Kingdom. sue.watson@nottingham.ac.uk

Lancet, (24 Feb 2001) 357/9256 (572-573). SOURCE:

Refs: 14

ISSN: 0140-6736 CODEN: LANCAO

United Kingdom COUNTRY: DOCUMENT TYPE: Journal; Note

FILE SEGMENT: 016 Cancer

> 022 Human Genetics

Clinical Biochemistry 029

048 Gastroenterology

LANGUAGE: English

ANSWER 3 OF 22 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD L8

ACCESSION NUMBER:

2000-293152 [25] WPIDS

DOC. NO. NON-CPI:

N2000-219772 C2000-088675

DOC. NO. CPI: TITLE:

Novel human tumor suppressor gene,

adenomatous polyposis coli (APC)-2, used in the

diagnosis, prevention, and treatment of

cancer.

DERWENT CLASS:

B04 C06 D16 P14 S03

INVENTOR (S):

CLEVERS, J C; PELFER, M A; VAN ES, J H

PATENT ASSIGNEE(S):

(UYUT-N) RIJKSUNIV UTRECHT

COUNTRY COUNT:

89

PATENT INFORMATION:

PATENT NO KIND DATE WEEK LA PG

WO 2000018913 A1 20000406 (200025)\* EN 42

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ TZ UG ZW

W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM
 EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ
 LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD
 SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW

AU 9960106 A 20000417 (200035)

#### APPLICATION DETAILS:

PATENT NO KIND	APPLICATION	DATE
WO 2000018913 A1	WO 1999-NL595	19990924
AU 9960106 A	AU 1999-60106	19990924

#### FILING DETAILS:

PATENT NO	KIND	PATENT NO	
			_
AU 9960106	A Base	d on wo annagara	

PRIORITY APPLN. INFO: EP 1998-203237 19980925

AN 2000-293152 [25] WPIDS

AB WO 200018913 A UPAB: 20000524

NOVELTY - Isolated and/or recombinant nucleic acid (NA) or a specific fragment, homolog or derivative thereof (I), corresponding to a gene located at position 19p13.3 in humans and comprising the 2397 base pair (bp) sequence given in the specification (adenomatous polyposis coli (APC)-2), is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

an expression vector comprising (I);

- (2) a cell comprising (I) or the expression vector of (1);
- (3) an animal comprising the cell of (2);
- (4) a protein, derivative, or fragment encoded by (I) or produced by the cell of (2);
  - (5) an antibody directed against the protein of (4);
- (6) identifying a candidate drug (especially a drug for use in a cancer patient), by using of the cell of (2), animal of (3), protein of (4), or antibody of (5); and
- (7) diagnosing cancer by using (I), the cell of (2), animal of (3), protein of (4), or antibody of (5).

ACTIVITY - Cytostatic.

MECHANISM OF ACTION - The adenomatous polyposis coli (APC) -2 tumor suppressor gene controls the Wnt pathway by the formation of a complex with GSK-3b, axin/conductin and beta -catenin, inducing the rapid degradation of the latter.

USE - The adenomatous polyposis coli (APC) -2 polynucleotides are used for the diagnosis (claimed), prevention and treatment of cancer. They are also used for the recombinant production of APC-2 proteins. The methods are used to identify candidate drugs (claimed), especially for use in the treatment of cancers, preferably a fetal cancer, cancers with a stem cell phenotype, brain, lung, kidney or intestinal cancer (all claimed).

ADVANTAGE - None given.

DESCRIPTION OF DRAWING(S) - The figure shows the comparison of adenomatous polyposis coli (APC) and APC-2. Domain structures conserved between these APC relatives are indicated in various boxes.

Dwg. 1A/4

L8 ANSWER 4 OF 22 SCISEARCH COPYRIGHT 2001 ISI (R)

ACCESSION NUMBER: 2000:808103 SCISEARCH

THE GENUINE ARTICLE: 366KD

TITLE: Differential regulation of glycogen synthase kinase

3 beta by insulin and Wnt signaling

AUTHOR: Ding V W; Chen R H; McCormick F (Reprint)

CORPORATE SOURCE: UNIV CALIF SAN FRANCISCO, CANC RES INST, 2340 SUTTER

ST, BOX 0128, SAN FRANCISCO, CA 94115 (Reprint); UNIV CALIF SAN FRANCISCO, CANC RES INST, SAN

FRANCISCO, CA 94143

COUNTRY OF AUTHOR: USA

SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (20 OCT 2000) Vol.

275, No. 42, pp. 32475-32481.

Publisher: AMER SOC BIOCHEMISTRY MOLECULAR BIOLOGY

INC, 9650 ROCKVILLE PIKE, BETHESDA, MD 20814.

ISSN: 0021-9258.

DOCUMENT TYPE: Article; Journal

FILE SEGMENT: LIFE

LANGUAGE:

English

REFERENCE COUNT:

53

\*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\*

Glycogen synthase kinase 3 beta (GSK3 beta) is a key component in many biological processes including insulin and Wnt signaling. Since the activation of each signaling pathway results in a decrease in GSK3 beta activity, we examined the specificity of their downstream effects in the same cell type. Insulin induces an increased activity of glycogen synthase but has no influence on the protein level of beta -catenin. In contrast, Wnt increases the cytosolic pool of beta -catenin but not glycogen synthase activity. We found that, unlike insulin, neither the phosphorylation status of the serine9 residue of GSK3 beta nor the activity of protein kinase B is regulated by Wnt. Although the decrease in GSK3 beta activity is required, GSK3 beta may not be the limiting component for Wnt signaling in the cells that we examined. Our results suggest that the axinconductin complexed GSK3 beta may be dedicated to Wnt rather than insulin signaling. Insulin and Wnt pathways regulate GSK3 beta through different mechanisms, and therefore lead to distinct downstream events.

L8 ANSWER 5 OF 22 MEDLINE

DUPLICATE 1

ACCESSION NUMBER:

2000455676 MEDLINE

DOCUMENT NUMBER:

20423090 PubMed ID: 10966653

TITLE:

Hot spots in beta-catenin for interactions with

LEF-1, conductin and APC.

AUTHOR:

von Kries J P; Winbeck G; Asbrand C; Schwarz-Romond T; Sochnikova N; Dell'Oro A; Behrens J; Birchmeier W

CORPORATE SOURCE:

Max-Delbruck-Center for Molecular Medicine,

Robert-Rossle-Strasse 10, 13093 Berlin, Germany.

SOURCE:

NATURE STRUCTURAL BIOLOGY, (2000 Sep) 7 (9) 800-7.

Journal code: B98; 9421566. ISSN: 1072-8368.

PUB. COUNTRY:

United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE:

English

FILE SEGMENT:

Priority Journals

ENTRY MONTH:

200009

ENTRY DATE:

Entered STN: 20001005

Last Updated on STN: 20001005

Entered Medline: 20000928

AB Interactions between beta-catenin and LEF-1/TCF, APC and conductin/axin are essential for wnt-controlled stabilization of beta-catenin and transcriptional activation. The wnt signal transduction pathway is important in both embryonic development and tumor progression. We identify here amino acid residues in beta-catenin that distinctly affect its binding to LEF-1/TCF, APC and conductin. These residues form separate surface clusters, termed hot spots, along the armadillo superhelix

of beta-catenin. We also show that complementary charged and hydrophobic amino acids are required for formation of the bipartite beta-catenin-LEF-1 transcription factor. Moreover, we demonstrate that conductin/axin binding to beta-catenin is essential for beta-catenin degradation, and that APC acts as a cofactor of conductin/axin in this process. Binding of APC to conductin/axin activates the latter and occurs between their SAMP and RGS domains, respectively.

ANSWER 6 OF 22 BIOSIS COPYRIGHT 2001 BIOSIS L8

ACCESSION NUMBER: 2000:275471 BIOSIS PREV200000275471 DOCUMENT NUMBER:

Human conductin (Axin2), like its mouse TITLE:

counterpart, binds to APC, GSK3betaand beta-catenin. Dong, Xiangyang (1); Mai, Ming (1); Seelan, Ratnam AUTHOR (S):

(1); Qian, Chiping (1); Smith, David I. (1); Liu,

Wanguo (1)

(1) Mayo Clin, Rochester, MN USA CORPORATE SOURCE:

Proceedings of the American Association for Cancer SOURCE:

Research Annual Meeting, (March, 2000) No. 41, pp.

745. print..

Meeting Info.: 91st Annual Meeting of the American Association for Cancer Research. San Francisco,

California, USA April 01-05, 2000

ISSN: 0197-016X.

Conference DOCUMENT TYPE:

English LANGUAGE: SUMMARY LANGUAGE: English

**DUPLICATE 2** ANSWER 7 OF 22 MEDLINE

ACCESSION NUMBER: 2000123741 MEDLINE

20123741 PubMed ID: 10656974 DOCUMENT NUMBER:

Biochemical interactions in the wnt pathway. TITLE:

Seidensticker M J; Behrens J AUTHOR:

Max-Delbruck-Center for Molecular Medicine, CORPORATE SOURCE:

Robert-Rossle-Strasse 10, 13122, Berlin, Germany.

BIOCHIMICA ET BIOPHYSICA ACTA, (2000 Feb 2) 1495 (2) SOURCE:

168-82. Ref: 143

Journal code: AOW; 0217513. ISSN: 0006-3002.

Netherlands PUB. COUNTRY:

Journal; Article; (JOURNAL ARTICLE)

General Review; (REVIEW)

(REVIEW, TUTORIAL)

LANGUAGE: English

Priority Journals FILE SEGMENT:

200005 ENTRY MONTH:

ENTRY DATE: Entered STN: 20000512

Last Updated on STN: 20000512

Entered Medline: 20000502

AB The wnt signal transduction pathway is involved in many differentiation events during embryonic development and can lead to tumor formation after aberrant activation of its components. The cytoplasmic component beta-catenin is central to the transmission of wnt signals to the nucleus: in the absence of wnts beta-catenin is constitutively degraded in proteasomes, whereas in the presence of wnts beta-catenin is stabilized and associates with HMG box transcription factors of the LEF/TCF family. In tumors, beta-catenin degradation is blocked by mutations of the tumor suppressor gene APC (adenomatous polyposis coli), or of beta-catenin itself. As a consequence, constitutive TCF/beta-catenin complexes are formed and activate oncogenic target genes. This review discusses the mechanisms that silence the pathway in cells that do not receive a wnt signal and goes on to describe the regulatory steps involved in the activation of the pathway.

L8 ANSWER 8 OF 22 MEDLINE

DUPLICATE 3

ACCESSION NUMBER:

2001019501

MEDLINE

DOCUMENT NUMBER:

20472311 PubMed ID: 11017067

TITLE:

Mutations in AXIN2 cause colorectal cancer with defective mismatch repair by activating

beta-catenin/TCF signalling.

AUTHOR:

Liu W; Dong X; Mai M; Seelan R S; Taniguchi K;

Krishnadath K K; Halling K C; Cunningham J M; Qian C;

Christensen E; Roche P C; Smith D I; Thibodeau S N

CORPORATE SOURCE:

Division of Experimental Pathology, Department of Laboratory Medicine and Pathology, Mayo Clinic and Mayo Medical School, Rochester, Minnesota, USA..

liu.wanguo@mayo.edu

CONTRACT NUMBER:

CA 48031 (NCI)

CA 60117 (NCI)

SOURCE:

NATURE GENETICS, (2000 Oct) 26 (2) 146-7.

Journal code: BRO. ISSN: 1061-4036.

PUB. COUNTRY:

United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE:

English

FILE SEGMENT:

Priority Journals

ENTRY MONTH:

200011

ENTRY DATE:

Entered STN: 20010322

Last Updated on STN: 20010322 Entered Medline: 20001108

L8 ANSWER 9 OF 22 MEDLINE

DUPLICATE 4

ACCESSION NUMBER:

2000400028

MEDLINE

DOCUMENT NUMBER:

20369556 PubMed ID: 10911903

TITLE:

Control of beta-catenin signaling in tumor

development.

Searcher

Shears

308-4994

AUTHOR: Behrens J

CORPORATE SOURCE: Max-Delbruck-Center for Molecular Medicine, Berlin,

Germany.. jbehren@mdc-berlin.de

SOURCE: ANNALS OF THE NEW YORK ACADEMY OF SCIENCES, (2000

Jun) 910 21-33; discussion 33-5. Ref: 72 Journal code: 5NM; 7506858. ISSN: 0077-8923.

Journal code: 5NM; 7506858. ISSN: 0077-8923

PUB. COUNTRY: United States

Journal; Article; (JOURNAL ARTICLE)

General Review; (REVIEW)

(REVIEW, TUTORIAL)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200008

ENTRY DATE: Entered STN: 20000824

Last Updated on STN: 20000824 Entered Medline: 20000817

The wnt signal transduction pathway is involved in various AB differentiation events during embryonic development and leads to tumor formation when aberrantly activated. The wnt signal is transmitted to the nucleus by the cytoplasmic component beta-catenin: in the absence of wnts, beta-catenin is constitutively degraded in proteasomes, whereas in the presence of wnts beta-catenin is stabilized and can associate with HMG box transcription factors of the LEF/TCF family. The LEF/TCF/beta-catenin complexes activate specific wnt target genes. In tumors, beta-catenin degradation is blocked by mutations of beta-catenin or of the tumor suppressor gene product APC. As a consequence, beta-catenin is stabilized, constitutive complexes with LEF/TCF factors are formed, and oncogenic target genes, such as c-myc, cyclin D1, and c-jun, are activated. Thus, control of beta-catenin is a major regulatory event in normal wnt signaling and during tumor formation. It has been found that a multiprotein complex assembled by the cytoplasmic component conductin induces degradation of cytoplasmic beta-catenin. The complex includes APC, the serine/threonine kinase GSK3 beta, and beta-catenin, which bind to conductin at distinct domains. In colon carcinoma cells, forced expression of conductin downregulates beta-catenin, whereas in normal cells mutants of conductin that are deficient in complex formation stabilize beta-catenin. Fragments of APC that contain a conductin-binding domain also block beta-catenin degradation. In Xenopus embryos, conductin inhibits the wnt pathway. In situ hybridization analysis shows that conductin is expressed in various embryonal tissues known to be regulated by wnts, such as the developing brain, mesenchyme below the epidermis, lung mesenchyme, and kidney. It is suggested that conductin controls wnt signaling by assembling the essential components of the beta-catenin degradation pathway. Alterations of

conductin function may lead to tumor formation.

L8 ANSWER 10 OF 22 MEDLINE

DUPLICATE 5

ACCESSION NUMBER:

2000017120

MEDLINE

DOCUMENT NUMBER:

20017120 PubMed ID: 10549354

TITLE:

The Yin-Yang of TCF/beta-catenin signaling.

AUTHOR:

Barker N; Morin P J; Clevers H

CORPORATE SOURCE:

Department of Immunology, University Hospital,

Utrecht, The Netherlands.

SOURCE:

ADVANCES IN CANCER RESEARCH, (2000) 77 1-24. Ref:

100

100

Journal code: 2J6; 0370416. ISSN: 0065-230X.

PUB. COUNTRY:

United States

Journal; Article; (JOURNAL ARTICLE)

General Review; (REVIEW)

(REVIEW, ACADEMIC)

LANGUAGE:

English

FILE SEGMENT:

Priority Journals

ENTRY MONTH:

199911

ENTRY DATE:

Entered STN: 20000111

Last Updated on STN: 20000111

Entered Medline: 19991123

Wingless/Wnt signaling directs cell-fate choices during embryonic AB development. In Drosophila, Wingless signaling mediates endoderm induction and the establishment of segment polarity in the developing embryo. The fly Wingless cascade is strikingly similar to the vertebrate Wnt signaling pathway, which controls a number of key developmental decisions such as dorsal-ventral patterning in Xenopus. Factors of the TCF/LEF HMG domain family (Tcfs) have recently been established as the downstream effectors of the Wingless/Wnt signal transduction pathways. Upon Wingless/Wnt signaling, a cascade is initiated that results in the accumulation of cytoplasmic beta-catenin (or its fly homolog, Armadillo). There is also a concomitant translocation of beta-catenin/Armadillo to the nucleus, where it interacts with a specific sequence motif at the  ${\tt N}$ terminus of Tcfs to generate a transcriptionally active complex. This bipartite transcription factor is targeted to the upstream regulatory regions of Tcf target genes including Siamois and Nodal related gene-3 in Xenopus, engrailed and Ultrabithorax in Drosophila via the sequence-specific HMG box, and mediates their transcriptional activation by virtue of transactivation domains contributed by beta-catenin/Armadillo. In the absence of Wingless/Wnt signals, a key negative regulator of the pathway, GSK3 beta, is activated, which mediates the downregulation of cytoplasmic beta-catenin/Armadillo via the ubiquitin-proteasome pathway. In the absence of nuclear beta-catenin, the Tcfs recruit the corepressor protein Groucho to the target gene enhancers and actively repress their transcription. An additional corepressor protein, CREB-binding

protein (CBP), may also be involved in this repression of Tcf target gene activity. Several other proteins, including adenomatous polyposis coli (APC), GSK3 beta, and Axin/Conductin, are instrumental in the regulation of beta-catenin/Armadillo. In APC-deficient colon carcinoma cell lines, beta-catenin accumulates and is constitutively complexed with nuclear Tcf-4. A proportion of APC wild-type colon carcinomas and melanomas also contains constitutive nuclear Tcf-4/beta-catenin complexes as a result of dominant mutations in the N terminus of beta-catenin that render it insensitive to downregulation by APC, GSK3 beta, and Axin/ C nductin. This results in the unregulated expression of Tcf-4 target genes such as c-myc. Based on the established role for Tcf-4 in maintaining intestinal stem cells it is likely that deregulation of c-myc expression as a result of constitutive Tcf-4/beta-catenin activity promotes uncontrolled intestinal cell proliferation. This would readily explain the formation of intestinal polyps during colon carcinogenesis. Similar mechanisms leading to deregulation of Tcf target gene activity are likely to be involved in melanoma and other forms of cancer

L8 ANSWER 11 OF 22 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD

ACCESSION NUMBER:

1999-214706 [18] WPIDS

DOC. NO. NON-CPI:

N1999-158020

DOC. NO. CPI:

C1999-063258

TITLE:

Tumor-suppressing protein

conductin - used for treatment and

diagnosis of tumors.

DERWENT CLASS:

B04 D16 S03

INVENTOR (S):

BEHRENS, J; BIRCHMEIER, W

PATENT ASSIGNEE(S):

(DELB-N) DELBRUECK CENT MOLEKULARE MEDIZIN MAX

COUNTRY COUNT:

22

PATENT INFORMATION:

PATENT	NO	KIND	DATE	WEEK	LA	PG

WO 9911780 A2 19990311 (199918) \* GE 2

RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE

W: CA JP US

DE 19840875 A1 19990512 (199925)

EP 1029047 A2 20000823 (200041) GE

R: AT BE CH DE DK FI FR GB IT LI NL SE

#### APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
		<del>-</del>	
WO 9911780	A2	WO 1998-DE2621	19980901

DE 19840875 **A1** EP 1029047 **A2** 

DE 1998-19840875 19980901 EP 1998-954120 19980901 WO 1998-DE2621 19980901

FILING DETAILS:

PATENT NO KIND

PATENT NO

EP 1029047

A2 Based on

WO 9911780

PRIORITY APPLN. INFO: DE 1997-19738205 19970902

AN 1999-214706 [18] WPIDS

AB 9911780 A UPAB: 19990511

> NOVELTY - The protein conductin (I) and its variants, mutants and fragments are new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following: (1) composition for diagnosing tumors comprising an agent that detects (I), the (I)-encoding gene (II) or derived mRNA; (2) composition for treating tumors containing an agent that activates or reactivates (I) in vivo; (3) cDNA (III) that encodes (I), its variants, mutants or fragments; (4) use of (II) for gene therapy of tumors; and (5) partial sequences of the adenomatosis polyposis coli (APC) protein comprising amino acids (aa) 1464-1604, 1516-1595, 1690-1778 or 1995-2083 as RGS-domain interaction sites (RGS = regulator of G-protein signaling).

USE - Detecting presence or amount of (I), at protein or nucleic acid levels, is used to diagnose tumors, while agents that (re)activate (I) are used for tumor therapy. Antitumor. (I) binds to beta -catenin and induces its cytoplasmic degradation, resulting in blockade of the Wnt/Wingless signaling pathway in vertebrates. (I) also binds to APC fragments and, in conjunction with APC, acts as a tumor suppressor. In SW840 cells APC is mutated, leading to increased levels of beta -catenin in cytoplasm and the nucleus. When (I) was introduced into these cells, beta -catenin was depleted in both cell compartments, with the effect being as strong as that for wild-type APC. Dwg. 0/4

T.8

ANSWER 12 OF 22 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD

ACCESSION NUMBER:

1999-470389 [40] WPIDS

DOC. NO. CPI:

C1999-138212

TITLE:

Agents for treating human diseases, particularly

cancer, modulate interaction of

beta-catenin with transcription factors or

tumor suppressor gene products.

DERWENT CLASS:

B04 D16

INVENTOR(S):

BIRCHMEIER, W; VON KRIES, J

Searcher

Shears 308-4994

PATENT ASSIGNEE(S):

(DELB-N) DELBRUECK CENT MOLEKULARE MEDIZIN MAX

COUNTRY COUNT:

22

PATENT INFORMATION:

PATENT NO KIND DATE WEEK LA PG

DE 19909251 A1 19990826 (199940)\* 15

WO 9942481 A2 19990826 (199942) GE

RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE

W: CA JP US

EP 1054899 A2 20001129 (200063) GE

R: AT BE CH DE DK ES FI FR GB GR IE IT LI NL PT SE

#### APPLICATION DETAILS:

PAT	ENT NO	KIND		PLICATION	DATE
DE	19909251	A1		1999-19909251	
WO	9942481	A2	WO	1999-DE554	19990222
EP	1054899	A2	ΕP	1999-913097	19990222
			WO	1999-DE554	19990222

#### FILING DETAILS:

PATENT NO	KIND	PATENT NO
EP 1054899	A2 Based on	WO 9942481

PRIORITY APPLN. INFO: DE 1998-19807390 19980221

AN 1999-470389 [40] WPIDS

AB DE 19909251 A UPAB: 19991004

NOVELTY - Agent (A) for treating human disease is based on substances (I) that modulate (inhibit or promote) the interaction of beta -catenin (bC) with transcription factors or products of tumor suppressor genes.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following: (a) peptide (II) comprising part of the LEF-1/TCF-4 transcription factors, or their variants and mutants; (b) peptide and related molecules (III) from the armadillo domain (arm units 3-8) of bC, and mutants of the complete bC molecule, that include at least one of the specific interaction domains for LEF-1, TCF-4, APC, conductin or E-cadherin; and (c) enzyme-linked immunosorbent assay (ELISA) for screening substance libraries for compounds that modulate interaction of bC with LEF-1/TCF, APC, conductin or E-cadherin.

ACTIVITY - Antitumor.

MECHANISM OF ACTION - bC is a key compound in the Wnt signaling pathway and is involved in development of tumors.

Generally its interaction with LEF-1 or TCF-4 is oncogenic but interaction with APC, conductin or E-cadherin is anti-oncogenic.

USE - (A) which inhibit interaction are particularly used to treat tumors, especially carcinoma of the colon and melanoma, but also, where they promote interaction, to stimulate regeneration of organs and tissues, specifically hair growth. Dwg.0/6

L8 ANSWER 13 OF 22 MEDLINE

DUPLICATE 6

ACCESSION NUMBER:

2000047719 MEDLINE

DOCUMENT NUMBER:

20047719 PubMed ID: 10580987

TITLE:

beta-catenin signaling and cancer.

AUTHOR:

Morin P J

CORPORATE SOURCE:

Laboratory of Biological Chemistry, Gerontology Research Center, National Institute on Aging, 5600

Nathan Shock Drive, Baltimore, MD 21224, USA..

MorinP@grc.nia.nih.gov

SOURCE:

BIOESSAYS, (1999 Dec) 21 (12) 1021-30. Ref: 88

Journal code: 9YY; 8510851. ISSN: 0265-9247.

PUB. COUNTRY:

ENGLAND: United Kingdom

Journal; Article; (JOURNAL ARTICLE)

General Review; (REVIEW)

(REVIEW, TUTORIAL)

LANGUAGE:

English

FILE SEGMENT:

Priority Journals

ENTRY MONTH:

200002

ENTRY DATE:

Entered STN: 20000209

Last Updated on STN: 20000209 Entered Medline: 20000203

Since its discovery as a protein associated with the cytoplasmic AB region of E-cadherin, beta-catenin has been shown to perform two apparently unrelated functions: it has a crucial role in cell-cell adhesion in addition to a signaling role as a component of the Wnt/wg pathway. Wnt/wg signaling results in beta-catenin accumulation and transcriptional activation of specific target genes during development. It is now apparent that deregulation of beta-catenin signaling is an important event in the genesis of a number of malignancies, such as colon cancer, melanoma, hepatocellular carcinoma, ovarian cancer, endometrial cancer, medulloblastoma pilomatricomas, and prostate cancer. beta-catenin mutations appear to be a crucial step in the progression of a subset of these cancers , suggesting an important role in the control of cellular proliferation or cell death. The APC/beta-catenin pathway is highly regulated and includes players such as GSK3-beta, CBP, Groucho, Axin, Conductin, and TCF. c-MYC and cyclin D1 were recently identified as a key transcriptional targets of this pathway

#### 09/587574

and additional targets are likely to emerge. Published 1999 John Wiley & Sons, Inc.

L8 ANSWER 14 OF 22 MEDLINE

DUPLICATE 7

ACCESSION NUMBER:

2001120045

MEDLINE

DOCUMENT NUMBER:

21079826 PubMed ID: 11212302

TITLE:

Signaling through beta-catenin and Lef/Tcf.

AUTHOR:

Novak A; Dedhar S

CORPORATE SOURCE:

Cancer Research, S-218, Sunnybrook Health Science

Centre, Toronto, Ontario, Canada.

SOURCE:

CELLULAR AND MOLECULAR LIFE SCIENCES, (1999 Oct 30)

\_56\_(5-6)\_523-37. Ref: 167\_\_\_\_\_

Journal code: CLE. ISSN: 1420-682X.

PUB. COUNTRY:

Switzerland

Journal; Article; (JOURNAL ARTICLE)

General Review; (REVIEW)

(REVIEW, ACADEMIC)

LANGUAGE:

English

FILE SEGMENT:

Priority Journals

ENTRY MONTH:

200102

ENTRY DATE:

Entered STN: 20010322

Last Updated on STN: 20010322 Entered PubMed: 20010209 Entered Medline: 20010215

Beta-catenin plays a structural role in cell adhesion by binding to AB cadherins at the intracellular surface of the plasma membrane and a signaling role in the cytoplasm as the penultimate downstream mediator of the wnt signaling pathway. The ultimate mediator of this pathway is a nuclear complex of beta-catenin acting as a coactivtor with lymphoid enhancer factor/T cell factor (Lef/Tcf) transcription factors to stimulate transcription of a variety of target genes. Signaling through beta-catenin is regulated by modulating its degradation and nuclear translocation. In the absence of an activating signal, phosphorylation of beta-catenin by glycogen synthase kinase 3 (GSK3) acting in conjunction with adenomatous polyposis coli and axin/conductin causes beta-catenin to interact with the beta-transducin repeat-containing protein which results in its ubiquitination and degradation. Signaling from the wnt pathway activates dishevelled which, in an as yet undefined manner, inhibits the activity of GSK3 resulting in an increase in the cytoplasmic free pool of beta-catenin, and translocation into the nucleus. The integrin-linked kinase (ILK) pathway also activates beta-catenin-Lef/Tcf signaling. ILK phosphorylates GSK3 to inhibit its activity and translocates beta-catenin into the nucleus. In addition, ILK downregulates the expression of E-cadherin and upregulates Lef-1 expression. In the final step of the beta-catenin-Lef/Tcf signaling pathway, nuclear beta-catenin binds pontin52-TATA binding protein and displaces Groucho-related gene or

#### 09/587574

CREB-binding protein corepressors from Lef/Tcf resulting in stimulation of transcription. During development, beta-catenin-Lef/Tcf signaling is involved in the formation of dorsal mesoderm and dorsal axis. Furthermore, defects in the beta-catenin-Lef/Tcf pathway are involved in the development of several types of cancers.

L8 ANSWER 15 OF 22 MEDLINE

**DUPLICATE 8** 

ACCESSION NUMBER:

1999457298

MEDLINE

DOCUMENT NUMBER:

99457298 PubMed ID: 10526234

TITLE:

Identification and characterization of E-APC, a novel

Drosophila homologue of the tumour

suppressor APC.

**AUTHOR:** 

SOURCE:

Hamada F; Murata Y; Nishida A; Fujita F; Tomoyasu Y;

Nakamura M; Toyoshima K; Tabata T; Ueno N; Akiyama T

CORPORATE SOURCE:

Department of Oncogene Research, Research Institute

for Microbial Diseases, Osaka University, 3-1

Yamadaoka, Suita 565-0871, Japan. and. GENES TO CELLS, (1999 Aug) 4 (8) 465-74.

Journal code: CUF; 9607379. ISSN: 1356-9597.

PUB. COUNTRY:

ENGLAND: United Kingdom

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE:

English

FILE SEGMENT:

Priority Journals

ENTRY MONTH:

199912

ENTRY DATE:

Entered STN: 20000113

Last Updated on STN: 20000915 Entered Medline: 19991223

AB BACKGROUND: Mutations in the adenomatous polyposis coli (APC) tumour suppressor gene are implicated in the genesis of colorectal cancers. The product of the APC gene forms a complex with beta-catenin, glycogen synthase kinase 3beta (GSK-3beta) and Axin/conductin, and induces the degradation of beta-catenin. RESULTS: We have identified a novel Drosophila homologue of APC, E-APC, which is similar to but differs in several respects from D-APC. The E-APC cDNA encodes a protein of predicted 1067 amino acids, with seven armadillo repeats, two copies of the 15-amino acid repeat, five copies of the 20-amino acid repeat, and one Axin/conductin binding site. E-APC directly interacts with D-Axin and Armadillo (Arm, the Drosophila homologue of beta-catenin) in vitro, destabilizes intracellular beta-catenin, and suppresses beta-catenin/TCF-regulated transcription in APC-/- colon cancer cells. The E-APC mRNA is ubiquitously expressed throughout all developmental stages in Drosophila. CONCLUSION: Our findings suggest that E-APC may be universally involved in the regulation of the Wingless signalling pathway by down-regulating the level of Arm in Drosophila.

L8 ANSWER 16 OF 22 MEDLINE

**DUPLICATE 9** 

ACCESSION NUMBER:

1999168905

MEDLINE

DOCUMENT NUMBER:

99168905 PubMed ID: 10049590

TITLE:

Cloning of the human homolog of conductin

(AXIN2), a gene mapping to chromosome 17q23-q24.

AUTHOR:

Mai M; Qian C; Yokomizo A; Smith D I; Liu W

CORPORATE SOURCE:

Department of Laboratory Medicine and Pathology, Mayo

Clinic/Foundation, Rochester, Minnesota 55905, USA.

CONTRACT NUMBER:

CA48031 (NCI)

SOURCE:

GENOMICS, (1999 Feb 1) 55 (3) 341-4.

Journal code: GEN; 8800135. ISSN: 0888-7543.

PUB. COUNTRY:

United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE:

English

FILE SEGMENT:

Priority Journals GENBANK-AF078165

OTHER SOURCE: ENTRY MONTH:

199905

ENTRY DATE:

Entered STN: 19990607

Last Updated on STN: 19990607 Entered Medline: 19990524

Conductin or Axil, an Axin homolog, plays an important role in the regulation of beta-catenin stability in the Wnt signaling pathway. To facilitate the molecular analysis of the human gene, we isolated the human homolog, AXIN2. The cDNA contains a 2529-bp open reading frame and encodes a putative protein of 843 amino acids. Compared with rat and mouse homologs, AXIN2 shows an overall 89% amino acid identity. Several functional domains in this protein are highly conserved including the GRS (95.9%), GSK-3beta (96.3%), Dsh (98%), and beta-catenin (89.9%) domains. Radiation hybrid mapping localized the AXIN2 gene to human chromosome 17q23-q24, a region that shows frequent loss of heterozygosity in breast cancer, neuroblastoma, and other tumors.

Human AXIN2 is thus a very strong candidate involved in multiple tumor types.

L8 ANSWER 17 OF 22 SCISEARCH COPYRIGHT 2001 ISI (R)

ACCESSION NUMBER:

2000:63768 SCISEARCH

THE GENUINE ARTICLE: 274MZ

TITLE:

Modulation of Wnt signaling by Axin and Axil

AUTHOR:

Kikuchi A (Reprint)

CORPORATE SOURCE:

HIROSHIMA UNIV, SCH MED, DEPT BIOCHEM, MINAMI KU,

1-2-3 KASUMI, HIROSHIMA 7348551, JAPAN (Reprint)

COUNTRY OF AUTHOR:

JAPAN

SOURCE:

CYTOKINE & GROWTH FACTOR REVIEWS, (SEP-DEC 1999)

Vol. 10, No. 3-4, pp. 255-265.

Publisher: ELSEVIER SCI LTD, THE BOULEVARD, LANGFORD LANE, KIDLINGTON, OXFORD OX5 1GB, OXON, ENGLAND.

ISSN: 1359-6101.

DOCUMENT TYPE:

Article; Journal

LANGUAGE:

English

REFERENCE COUNT:

97

\*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\* AΒ The Wnt signaling pathway is conserved in various species from worms to mammals, and, plays important roles in development, cellular proliferation, and differentiation. The molecular mechanisms by which the Wnt signal regulates cellular functions are becoming increasingly well understood. Wnt stabilizes cytoplasmic beta-catenin, which stimulates the expression of genes including c-myc, c-jun, fra-1, and cyclin D1. Axin and its homolog Axil, newly recognized as components of the Wnt signaling pathway, negatively regulate this pathway. Other components of the Wnt signaling pathway, including DvI, glycogen synthase kinase-3 beta (GSK-3). beta), beta-catenin, and adenomatous polyposis coli (APC), interact with Axin, and the phosphorylation and stability of beta-catenin are regulated in the Axin complex. Axil has similar functions to Axin. Thus, Axin and Axil act as scaffold proteins in the Wnt signaling pathway, thereby modulating the Wnt-dependent cellular functions. (C) 2000 Elsevier Science Ltd. All rights reserved.

L8 ANSWER 18 OF 22 MEDLINE

DUPLICATE 10

ACCESSION NUMBER:

1999147086 MEDLINE

DOCUMENT NUMBER:

99147086 PubMed ID: 10021369

TITLE:

Identification of APC2, a homologue of the

adenomatous polyposis coli tumour

suppressor.

**AUTHOR:** 

van Es J H; Kirkpatrick C; van de Wetering M;

Molenaar M; Miles A; Kuipers J; Destree O; Peifer M;

Clevers H

CORPORATE SOURCE:

Department of Immunology, University Hospital, P.O.

Box 85500, 3508 GA, Utrecht, The Netherlands.

SOURCE:

CURRENT BIOLOGY, (1999 Jan 28) 9 (2) 105-8. Journal code: B44; 9107782. ISSN: 0960-9822.

PUB. COUNTRY: ENGLAND: United Kingdom

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE:

English

FILE SEGMENT:

Priority Journals

OTHER SOURCE:

GENBANK-AF091430; GENBANK-AJ012652; GENBANK-AJ130783; GENBANK-AJ130784; GENBANK-AJ130785; GENBANK-AJ130786; GENBANK-AJ130787; GENBANK-AJ130788; GENBANK-AJ130799; GENBANK-AJ130791; GENBANK-AJ130792; GENBANK-AJ130793; GENBANK-AJ130794; GENBANK-AJ130795;

GENBANK-AJ130796; GENBANK-AJ131187

ENTRY MONTH:

199903

ENTRY DATE:

Entered STN: 19990402

Last Updated on STN: 20000303 Entered Medline: 19990323

Searcher

Shears

308-4994

The adenomatous polyposis coli (APC) tumour-suppressor AB protein controls the Wnt signalling pathway by forming a complex with glycogen synthase kinase 3beta (GSK-3beta), axin/ conductin and betacatenin. Complex formation induces the rapid degradation of betacatenin. In colon carcinoma cells, loss of APC leads to the accumulation of betacatenin in the nucleus, where it binds to and activates the Tcf-4 transcription factor (reviewed in [1] [2]). Here, we report the identification and genomic structure of APC homologues. Mammalian APC2, which closely resembles APC in overall domain structure, was functionally analyzed and shown to contain two SAMP domains, both of which are required for binding to conductin. Like APC, APC2 regulates the formation of active betacatenin-Tcf complexes, as demonstrated using transient transcriptional activation assays in APC -/- colon carcinoma cells. Human APC2 maps to chromosome 19p13.3. APC and APC2 may therefore have comparable functions in development and cancer.

L8 ANSWER 19 OF 22 JICST-EPlus COPYRIGHT 2001 JST

ACCESSION NUMBER:

990756513 JICST-EPlus

TITLE:
AUTHOR:

Arthroscopic treatment for dorsal wrist ganglion. NISHIKAWA SHINJI; ARAI KOICHI; TAKEUCHI KAZUNARI;

FUKUDA AKIRA; WADA KAN'ICHIRO

CORPORATE SOURCE:

Mutsu Gen. Hosp.

SOURCE:

Kansetsukyo (Arthroscopy), (1999) vol. 24, no. 1, pp.

85-90. Journal Code: L0107A (Fig. 7, Ref. 9)

ISSN: 0910-223X

PUB. COUNTRY:

Japan

DOCUMENT TYPE:

Conference; Article

LANGUAGE:

Japanese

STATUS:

New

In excising a ganglion located at the dorsum of the wrist joint, one AB may lose sight of the base of the ganglion, which may result in a recurrence of the condition; or the surgical procedure may leave a large, unsightly surgical cicatrix on the dorsum of the hand due to the size of the lesion. To eliminate these problems, we have been conductin surgery on ganglions of the dorsal wrist joint under arthroscopy. The details are reported below. A total of 16 joints(10 right and 6 left) in 16 patients(7 males and 9 females, ages ranging from 12 to 83 years, with a mean of 42 years) have undergone the arthroscopic procedure. A nodule was palpated at the center of the dorsum of the wrist in each patients and all reported pain that was associated with movement. Six had experienced repeated recurrences for six months or more; the condition had developed for the first time in eight (among whom, two had been subjected to repeated aspiration therapy); and the condition had returned in one following surgical therapy. MRI was conducted prior to surgery to confirm that there was communication between the ganglion and the

scapholunate joint(SL joint). Arthroscopy was conducted at portals I-II and a probe and a shaver were inserted through portals IV-V. The position of the base of the ganglion that was palpated at the dorsum of the scapholunate ligament(SL ligament) was confirmed under arthroscopy and excised with the shaver. No recurrence was noted and the postoperative course was satisfactory for a follow-up period that lasted from 2 to 15 months (mean, 6.4). The method introduced above applies to all ganglions that originate at the SL joint: but it is particularly suitable for large growths that are likely to leave prominent surgical scars or for radical treatment of those that return repeatedly after aspiration and cause pain associated with wrist movement. (author abst.)

L8 ANSWER 20 OF 22 BIOSIS COPYRIGHT 2001 BIOSIS

ACCESSION NUMBER:

1999:174930 BIOSIS

DOCUMENT NUMBER:

PREV199900174930

TITLE:

Cloning of the human homolog of conduction (AXIN2), a

gene mapping to chromosome 17q23-24.

AUTHOR (S):

Mai, M. (1); Qian, C.; Yokomizo, A.; Smith, D. I.;

Liu, W.

CORPORATE SOURCE:

(1) Div. Exp. Pathol., Dep. Lab. Med. Pathol.,

Rochester, MN 55905 USA

SOURCE:

Proceedings of the American Association for Cancer Research Annual Meeting, (March, 1999) Vol. 40, pp.

Meeting Info.: 90th Annual Meeting of the American

Association for Cancer Research Philadelphia, Pennsylvania, USA April 10-14, 1999 American

Association for Cancer Research

. ISSN: 0197-016X.

DOCUMENT TYPE:

Conference

LANGUAGE:

English

ACCESSION NUMBER:

ANSWER 21 OF 22 BIOSIS COPYRIGHT 2001 BIOSIS DUPLICATE 11

1999:165640 BIOSIS

DOCUMENT NUMBER:

PREV199900165640

TITLE:

APC protein: Protein interactions and cellular

functions.

AUTHOR (S):

Jais, Philippe (1); Laurent-Puig, Pierre; Olschwang,

Sylviane

CORPORATE SOURCE:

(1) Unite Marqueurs Genet. Cancers, Inst.

Gustave-Roussy, 39 rue Camille-Desmoulins, 94805

Villejuif Cedex France

SOURCE:

Gastroenterologie Clinique et Biologique, (Dec.,

1998) Vol. 22, No. 12, pp. 1071-1080.

ISSN: 0399-8320.

DOCUMENT TYPE:

General Review

LANGUAGE:

French

Searcher Shears L8 ANSWER 22 OF 22 MEDLINE

DUPLICATE 12

ACCESSION NUMBER: 1998221239

998221239 MEDLINE

DOCUMENT NUMBER:

98221239 PubMed ID: 9554852

TITLE:

Functional interaction of an axin homolog, conductin, with beta-catenin, APC, and

GSK3beta.

**AUTHOR:** 

Behrens J; Jerchow B A; Wurtele M; Grimm J; Asbrand

C; Wirtz R; Kuhl M; Wedlich D; Birchmeier W

CORPORATE SOURCE:

Max Delbruck Center for Molecular Medicine,

Robert-Rossle-Strasse 10, 13122 Berlin, Germany.

SOURCE:

SCIENCE, (1998 Apr 24) 280 (5363) 596-9.

Journal code: UJ7; 0404511. ISSN: 0036-8075.

PUB. COUNTRY:

United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE:

English

FILE SEGMENT: OTHER SOURCE: Priority Journals GENBANK-AF073788

ENTRY MONTH:

199805

ENTRY DATE:

Entered STN: 19980514

Last Updated on STN: 20000303 Entered Medline: 19980507

AB Control of stability of beta-catenin is central in the wnt signaling pathway. Here, the protein conductin was found to form a complex with both beta-catenin and the tumor suppressor gene product adenomatous polyposis coli (APC). Conductin induced beta-catenin degradation, whereas mutants of conductin that were deficient in complex formation stabilized beta-catenin. Fragments of APC that contained a conductin-binding domain also blocked beta-catenin degradation. Thus, conductin is a component of the multiprotein complex that directs beta-catenin to degradation and is located downstream of APC. In Xenopus embryos, conductin interfered with wnt-induced axis formation.

(FILE 'CAPLUS' ENTERED AT 11:20:11 ON 11 JUN 2001)

L9 150 SEA FILE=CAPLUS ABB=ON PLU=ON CONDUCTING(3A) (PROTEIN

OR PEPTIDE)

L10 3 SEA FILE=CAPLUS ABB=ON PLU=ON L9 AND (TUMOUR OR TUMOR

OR NEOPLAS? OR CANCER? OR CARCIN?)

L11 3 S L10 NOT L6

L11 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER:

1996:427508 CAPLUS

DOCUMENT NUMBER:

125:135608

TITLE:

Co-translational effects of temperature on

Searcher :

Shears

308-4994

#### 09/587574

membrane insertion and orientation of

P-glycoprotein sequences

AUTHOR (S):

Zhang, Jian-Ting; Chong, Crispina H.

CORPORATE SOURCE:

Dep. Physiol. Biophys., Univ. Texas Med. Branch,

Galveston, TX, 77555-0641, USA

SOURCE:

Mol. Cell. Biochem. (1996), 159(1), 25-31

CODEN: MCBIB8; ISSN: 0300-8177

DOCUMENT TYPE:

Journal

LANGUAGE:

English

AB P-glycoprotein (pgp) is a membrane transport protein that causes multidrug resistance (MDR) by actively extruding a wide variety of cytotoxic agents out of cells. In may also function as a peptide transporter, a vol.-regulated chloride channel, and an ATP channel. Previously, it has been shown that hamster pgp1 Pgp is expressed in more than one topol. form and that the generation of these structures is modulated by charged amino acids flanking the predicted transmembrane (TM) segments 3 and 4 and by sol. cytoplasmic factors. Different topol. structures of Pgp may be related to its different functions. This study examd. the effects of translation temp. on the membrane insertion process and the topologies of Pgp. The rabbit reticulocyte lysate expression system was used to show that translation at different temps. affects the membrane insertion and orientation of the putative TM3 and TM4 of hamster pgpl Pgp in a co-translational manner. This observation suggests that the membrane insertion process of TM3 and TM4 of Pgp mols. may involve a protein conducting channel and/or the interaction between TM3 and TM4, which act in a temp. sensitive manner. Manipulating temp. may provide a way to understand the structure-function relationship of Pgp and help overcome Pgp-related multidrug resistance of cancer cells.

L11 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER:

1982:400304 CAPLUS

DOCUMENT NUMBER:

97:304

TITLE:

Antitumor agents. XLVIII: structure-activity relationships of quassinoids as in vitro protein

synthesis inhibitors of P-388 lymphocytic

leukemia tumor cell metabolism

AUTHOR (S):

Liou, Y. F.; Hall, I. H.; Okano, M.; Lee, K. H.;

Chaney, S. G.

CORPORATE SOURCE:

Sch. Med., Univ. North Carolina, Chapel Hill,

NC, 27514, USA

SOURCE:

J. Pharm. Sci. (1982), 71(4), 430-5

CODEN: JPMSAE; ISSN: 0022-3549

DOCUMENT TYPE:

Journal

LANGUAGE:

English

GI

I,  $R=CHMe_2$ , Z=H, n=1

II, R=Me, Z=H, n=1

III, R=Me, Z=COCH2CO, n=2

AB A series of brusatol, bisbrusatol, and bruceantin esters were examd. for their ability to inhibit protein synthesis in P-388 lymphocytic leukemia cells. Compds. which produced high antileukemic activities resulted in ID50 of 5.4-15.5 .mu.M for inhibition of whole cell protein synthesis, ID50 of 1.3-13 .mu.M for inhibition of endogenous protein synthesis in cell homogenates, and ID50 of 1.9-6 .mu.M for inhibition of polyuridine directed polyphenylalanine synthesis using runoff ribosomes and a pH 5 enzyme prepn. The polyuridine directed polyphenylalanine synthesis requires neither initiation nor termination factors, suggesting that quassinoids are exclusively elongation inhibitors. bruceantin (I) [41451-75-6], brusatol (II) [14907-98-3], and bisbrusatolyl malonate (III) [80096-78-2] allowed a runoff of the polyribosomes to 80-S free ribosomes. However, formation of the ternary complex and 80-S initiation complex were not inhibited by the quassinoids. Thus, these agents do not affect the individual steps leading to the formation of a stable 80-S initiation complex in P-388 cells. Brusatol, bruceantin, and bisbrusatolyl malonate inhibited the formation of the first peptide bond between puromycin and [3H] methionyl-transfer RNA bound to the initiation complex, indicating peptidyl transferase activity is inhibited by the quassinoids in P-388 cells. Apparently, the free 80-S ribosome is the site of binding by the quassinoid. Ribosomes actively conducting protein synthesis will continue protein synthesis and terminate before the quassinoids bind. Thus, quassinoids are elongation inhibitors of tumor cells. A strong correlation was obsd. between potent antileukemic activity and the ability to inhibit protein synthesis in P-388 lymphocytic leukemia cells.

L11 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER:

1960:24381 CAPLUS

DOCUMENT NUMBER: ORIGINAL REFERENCE NO.: 54:4860c-d

54:24381

TITLE:

The nature of the interaction of biologically

active agents with tissue constituents

AUTHOR (S):

Mason, R.

CORPORATE SOURCE:

Univ. Coll., London

SOURCE:

Acta Unio Intern. contra Cancrum (1959), 15,

650-1

DOCUMENT TYPE:

Journal

LANGUAGE: Unavailable

The electronic structure of carcinogen-protein mol. complexes was examd. theoretically and the possibility of charge transfer in the complex discussed. A banded-electronic model of a protein suggests that electron transfer within such a mol. complex will take place only when the energy levels of the mols. of the complex are closely matched. Aromatic carcinogens satisfy a precise criterion for such matching of levels, and carcinogenesis is to be assocd. with the induction of conducting properties in the protein.

(FILE 'MEDLINE, BIOSIS, EMBASE, WPIDS, CONFSCI, SCISEARCH, JICST-EPLUS, JAPIO, CANCERLIT' ENTERED AT 11:22:50 ON 11 JUN 2001)

L12

18 S L10

L13

18 S L12 NOT (L2 OR L7)

L14

9 DUP REM L13 (9 DUPLICATES REMOVED)

L14 ANSWER 1 OF 9 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD

ACCESSION NUMBER:

2001-266373 [27] WPIDS

DOC. NO. NON-CPI: DOC. NO. CPI:

N2001-190479 C2001-080736

TITLE:

Detection of proteins by using a protein

fingerprinting system which comprises linearizing the protein, labeling a first amino acid residue type and detecting first and second residue types,

useful in the diagnosis of cancer.

DERWENT CLASS:

B04 D16 S03

INVENTOR(S):

BRENT, R; BURBULIS, I E; CARLSON, R H

PATENT ASSIGNEE(S):

(MOLE-N) MOLECULAR SCI INST INC

COUNTRY COUNT:

93

PATENT INFORMATION:

PATENT NO KIND DATE

WO 2001025794 A2 20010412 (200127) \* EN

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TZ UG ZW

> Searcher Shears

W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG UZ VN YU ZA ZW

#### APPLICATION DETAILS:

PATENT NO KIND APPLICATION DATE

WO 2001025794 A2 WO 2000-US26958 20000929

PRIORITY APPLN. INFO: US 1999-412732 19991005

AN 2001-266373 [27] WPIDS

AB WO 200125794 A UPAB: 20010518

NOVELTY - A new method (M1) for detecting proteins having at least two different types of residues comprises giving a detectable set of distinguishing ancillary properties (a 'fingerprint') to the proteins and then detecting the fingerprint by linearizing the protein, labeling the first type of residue and detecting first and second amino acid residues.

DETAILED DESCRIPTION - A new method (M1) for detecting proteins having at least two different types of residues comprises giving a detectable set of distinguishing ancillary properties (a 'fingerprint') to the proteins and then detecting the fingerprint by linearizing the protein, labeling the first type of residue and detecting first and second amino acid residues.

In detail, M1 comprises:

- (a) linearizing the protein molecule with a denaturation means;
- (b) labeling each of the first type of amino acid residue with a tag;
- (c) detecting the fingerprint of the protein with a detection means, by detecting a first fingerprint constituent imparted by the tag and a second fingerprint constituent imparted by the second type of amino acid residue.

INDEPENDENT CLAIMS are also included for the following:

- (1) identifying a protein molecule having at least two different amino acid residue types in a sample containing several proteins, by linearizing each protein as in M1 step (a), isolating the **protein**, **conducting** steps (b) and (c) of M1, and comparing the fingerprint obtained (optionally using a computer receiving signals from the detection means) to a library of fingerprints of known protein molecules;
- (2) a library of fingerprint values of known proteins, listing the identity of the proteins and first and second (and optionally third) fingerprint constituents of each protein, being representative of the number and sequence of the first and second

(and optionally third) types of amino acid residues respectively;

- (3) characterizing protein molecules, by isolating the protein and using M1 which is modified such that first and second types of amino acid types are both labeled with different tags;
- (4) protein molecules having an identifiable fingerprint, comprising two amino acid residue types each separately tagged, or three amino acid types (optionally including tryptophan), imparting up to six fingerprint constituents by using combinations of excitation and emitted radiations; and
- (5) identifying a protein in a sample containing several proteins, following the method of (1) which is modified such that first and second residue types are both labeled with different tags.

USE - The method is useful to enable rapid identification of protein molecules, especially in biological samples e.g. plant, microorganism or animal (especially human) tissues or cells e.g. in clinical or research applications to identify aberrant or mutant forms of proteins involved in diseases such as cancers or inherited disorders such as cystic fibrosis and hemophilia. It also enables the production of a library of known proteins and their corresponding fingerprints, useful to identify unknown proteins in a sample.

Dwg.0/33

L14 ANSWER 2 OF 9 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD

ACCESSION NUMBER:

2001-050022 [06] WPIDS

DOC. NO. NON-CPI:

N2001-038339

DOC. NO. CPI:

C2001-013790

TITLE:

Assessing translocation of proteins such as glucose transporter GLUT4, cystic fibrosis transmembrane conductance regulator by using modified protein of interest comprising the protein and detectable

tags.

DERWENT CLASS:

B04 D16 S03

INVENTOR (S):

BOGAN, J S; LODISH, H

PATENT ASSIGNEE(S):

(GEHO) GEN HOSPITAL CORP; (WHED) WHITEHEAD INST

BIOMEDICAL RES

COUNTRY COUNT:

93

PATENT INFORMATION:

PATENT NO KIND DATE WEEK LA PG

WO 2000075188 A1 20001214 (200106) \* EN 75

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC

MW MZ NL OA PT SD SE SL SZ TZ UG ZW

W: AE AG AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP

KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL

PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU

# ZA ZW AU 2000054775 A 20001228 (200119)

#### APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 20000751		WO 2000-US15904	
AU 20000547	75 A	AU 2000-54775	20000609

#### FILING DETAILS:

PATENT	NO KIND		PATENT NO
AU 2000	054775 A	Based on	WO 200075188

PRIORITY APPLN. INFO: US 1999-154078 19990915; US 1999-138237 19990609

AN 2001-050022 [06] WPIDS

AB WO 200075188 A UPAB: 20010126

NOVELTY - Translocation of a protein of interest from an intracellular location to the plasma membrane in mammalian cells, when the cells are exposed to a condition or a stimulus, is assessed by using a modified protein of interest (MP) comprising the protein of interest and an epitope tag in an extracellular domain and a fluorescent tag in an intracellular domain.

DETAILED DESCRIPTION - Translocation of a protein of interest from an intracellular location to the plasma membrane in mammalian cells, when the cells are exposed to a condition or a stimulus, is assessed by using a modified protein of interest (MP) comprising the protein of interest and an epitope tag in an extracellular domain and a fluorescent tag in an intracellular domain.

The method (I) comprises:

- (a) culturing mammalian cells (test cells) expressing MP, under a condition or a stimulus to be assessed for its effects on translocation of the protein of interest;
- (b) determining a value corresponding to proportion of MP at the cell membrane to total MP in the test cells that produces a test value; and
- (c) comparing the test value with a control value, where the control value corresponds to the proportion of MP at the cell membrane to MP in control cells, where the control cells are the same cells as are cultured in (a), except that the control cells are not cultured under the condition or stimulus to be assessed, where the test value greater than the control value indicates that translocation of MP has occurred.

INDEPENDENT CLAIMS are also included for the following:

(1) determining (II) whether a protein of interest undergoes

translocation from an intracellular location to the plasma membrane in mammalian cells in the presence of a condition or stimulator, comprising:

- (a) culturing cells that express MP in the absence of the stimulator producing cultured cells;
- (b) determining the relative proportion of MP at the plasma membrane of cultured cells to total MP in the cultured cells, by producing a control value;
- (c) culturing cells that express MP under the same conditions as in (a) and in the presence of the stimulator, by producing test cells;
- (d) determining the relative proportion of MP at the plasma membrane of test cells to total MP in the test cells, by producing a test value; and
- (e) comparing the control value and the test value, where a test value that is greater than the control value indicates that protein of interest undergoes translocation following stimulation of the cells by the stimulator;
- (2) identifying (III) a drug which enhances translocation of a protein of interest from an intracellular location to the plasma membrane in mammalian cells by:
- (a) culturing cells which express RT in the presence of a candidate drug;
- (b) determining the relative proportion of MP at the plasma membrane of cultured cells to total MP in the cultured cells, producing a test value; and
- (c) comparing the test value with the control value, which is the relative proportion of the protein of interest at the plasma membrane to MP in cells cultured under same conditions in the absence of drug, where the test value greater than the control value indicates that the candidate drug enhances translocation of the protein of interest; and
- (3) eukaryotic cells (IV) expressing MP comprising a protein of interest and a detectable tag in an extracellular domain and at least 1 detectable tag in an intracellular domain, where the tags are different from each other and the protein of interest undergoes translocation in the eukaryotic cells upon contact with or exposure to a condition.
- USE The method is useful for determining translocation of a protein of interest such as aquaporin-2, cystic fibrosis transmembrane conductance regulator, gastric H+/K+ATPase, in particular GLUT4 from an intracellular location to the plasma membrane in mammalian cells in the presence of a condition or a stimulator. (III) is useful for assessing the effect of a drug on translocation of a protein such as GLUT4. Such drugs are useful in treating insulin resistance such as in adult-onset diabetes, obesity and polycystic ovary syndrome.

ADVANTAGE - Translocation of the protein of interest can be

# 09/587574

easily assessed using the tags. The tags can be detected individually, quantified and the addition of tags does not alter trafficking of the protein of interest.

Dwg.0/7

L14 ANSWER 3 OF 9 WPIDS COPYRIGHT 2001 DERWENT INFORMATION LTD

ACCESSION NUMBER: 1999-571821 [48] WPIDS

DOC. NO. CPI: C1999-166854

TITLE: New isolated RGS-GEF polypeptides, used to develop

products for modulating, e.g. cell proliferation

and integrin-mediated interactions.

DERWENT CLASS: B04 D16

INVENTOR(S): BOLLAG, G; HART, M J; JIANG, X; KOZASA, T; POLAKIS,

P; ROSCOE, W; STERNWEIS, P

PATENT ASSIGNEE(S): (ONYX-N) ONYX PHARM INC; (TEXA) UNIV TEXAS SYSTEM

COUNTRY COUNT: 82

PATENT INFORMATION:

PATENT NO KIND DATE WEEK LA PG

WO 9947557 A2 19990923 (199948)\* EN 75

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ UG ZW

W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI
GB GE GH GM HR HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT
LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL

TJ TM TR TT UA UG UZ VN YU ZW

AU 9931038 A 19991011 (200008)

EP 1064373 A2 20010103 (200102) EN

R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE

#### APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 9947557	A2	WO 1999-US6051	19990318
AU 9931038	A	AU 1999-31038	19990318
EP 1064373	A2	EP 1999-912727	19990318
		WO 1999-US6051	19990318

## FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 9931038	A Based on	WO 9947557
EP 1064373	A2 Based on	WO 9947557

PRIORITY APPLN. INFO: US 1998-78634 19980318

AN 1999-571821 [48] WPIDS

AB

WO 9947557 A UPAB: 19991122

NOVELTY - Isolated RGS-guanine nucleotide exchange factor (GEF) polypeptides are new.

DETAILED DESCRIPTION - A novel isolated RGS-GEF polypeptide or a biologically active fragment consists of an RGS domain of a GEF protein.

INDEPENDENT CLAIMS are also included for the following:

- (1) an isolated RGS-GEF polypeptide or a biologically active fragment comprising an RGS domain of a GEF protein, with the proviso that the polypeptide does not comprise a dbl homology (DH) domain or a pleckstrin homology (PH) domain;
- (2) an isolated RGS-GEF polypeptide, or a biologically active fragment, where the polypeptide is selected from p115 Rho-GEF, Lsc, KIAA380, and where the polypeptide is mutated in the RGS domain, and where the polypeptide has a specific binding affinity for a G protein alpha subunit (GAS), or a GTPase activating activity for a GAS;
- (3) an isolated RGS-GEF nucleic acid consisting of a nucleotide sequence (NS) encoding a polypeptide comprising an RGS domain of a GEF protein;
- (4) a nucleic acid as in (3) but, where the polypeptide does not include a DH domain or a PH domain;
  - (5) a transformed cell containing a nucleic acid as in (4);
  - (6) a vector comprising a nucleic acid as in (4), and
  - (7) identifying or assaying a molecule that:
- (a) inhibits or enhances binding of a monomeric G protein guanine nucleotide exchange factor to a GAS comprising:
- (i) incubating the GAS, or fragments with the monomeric G protein nucleotide exchange factor, or fragments, in the presence and absence of a test molecule, and
- (ii) determining whether the presence of the test molecule inhibits or enhances binding between the monomeric G-protein guanine nucleotide exchange factor and the GAS;
- (b) inhibits or enhances a stimulatory effect of a GEF on a GAS GTPase activity comprising:
  - (i) as in (ai), and
- (ii) determining whether the presence of the test molecule inhibits or enhances the stimulatory effect of the GEF protein on GAS GTPase activity;
- (c) specifically inhibits the stimulatory effect of an activated GAS on GEF mediated nucleotide exchange of a monomeric G protein, comprising conducting a first assay by:
- (i) incubating an activated GAS, or its fragments, with a GEF protein, or fragments, and a monomeric G protein, or its fragments, in the presence and absence of a test inhibitor;
- (ii) conducting a second assay by incubating a GEF protein, or fragments, and a monomeric G protein. or fragments in the presence

and absence of the test inhibitor, and

- (iii) determining whether any inhibitory effect of the test inhibitor in the first assay is greater than any inhibitory effect of the test inhibitor in the second assay;
- (d) specifically enhances the stimulatory effect of an activated GAS on GEF mediated nucleotide exchange of a monomeric G protein, comprising:
- (i) conducting a first assay by incubating an activated GAS, or fragments with a GEF protein. and fragments, and a monomeric G protein, or fragments in the presence and absence of a test enhancer;
- (ii) as in (cii), but in the presence/absence of the test enhancer, and
- (iii) determining whether any enhancing effect of the test enhancer in the first assay is greater than any enhancing effect of the test enhancer in the second assay;
- (e) mimics the stimulatory effect of an activated GAS on GEF mediated nucleotide exchange of a monomeric G protein comprising:
- (i) identifying a test compound that exhibits a binding affinity for the RGS domain of GEF proteins, or fragments, incubating a GEF protein or fragments, and monomeric G protein, or fragments in the presence or absence of the test compound, and
- (ii) determining whether the test compound exhibits a stimulatory effect on GEF mediated nucleotide exchange of a monomeric G protein, and
- (f) mimics the stimulatory effect of an RGS domain of a GEF protein on GTPase activity of a GAS comprising:
- (i) identifying a test compound that exhibits a binding affinity for a GAS, and
- (ii) incubating a GTP loaded GAS in the presence or absence of the test compound to determine whether the test compound has a stimulatory effect on GAS GTPase activity.
- USE The RGS-GEF polypeptides can be used for modulating an activity of a GAS (claimed). The products can be used for the regulation of biological pathways in which a RGS-GEF polypeptide is involved, particularly pathological conditions, e.g. cell proliferation (e.g. cancer), growth control, morphogenesis, stress fiber formation, and integrin-mediated interactions, such as embryonic development, tumor cell growth and metastasis, programmed cell death, hemostasis, leukocyte homing and activation, bone resorption, clot retraction, and the response of cells to mechanical stress. The products can also be used for detection, diagnosis and production of transgenic animals.

ADVANTAGE - None given. Dwg.0/18

L14 ANSWER 4 OF 9 MEDLINE ACCESSION NUMBER: 1999439712

MEDLINE

DUPLICATE 1

#### 09/587574

DOCUMENT NUMBER:

99439712 PubMed ID: 10508919

TITLE:

A novel ADP-ribosylation like factor (ARL-6),

interacts with the protein-

conducting channel SEC61beta subunit.

AUTHOR:

Ingley E; Williams J H; Walker C E; Tsai S; Colley S;

Sayer M S; Tilbrook P A; Sarna M; Beaumont J G;

Klinken S P

CORPORATE SOURCE:

Laboratory for Cancer Medicine, Department of

Biochemistry, The University of Western Australia and

Royal Perth Hospital, Perth, W.A., Australia.

SOURCE:

FEBS LETTERS, (1999 Oct 1) 459 (1) 69-74.

Journal code: EUH; 0155157. ISSN: 0014-5793.

PUB. COUNTRY:

Netherlands

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE:

English

Engil

FILE SEGMENT:

Priority Journals

OTHER SOURCE:

GENBANK-AF031903; GENBANK-AF133669; GENBANK-AF133670;

GENBANK-AF133910; GENBANK-AF133911; GENBANK-AF133912;

GENBANK-AF133913

ENTRY MONTH:

199911

ENTRY DATE:

Entered STN: 20000111

Last Updated on STN: 20000111

Entered Medline: 19991101

AB We report here the isolation of a new member of the ADP-ribosylation factor (ARF)-like family (ARL-6) present in the J2E erythroleukemic cell line, but not its myeloid variants. Consistent with this lineage-restricted expression, ARL-6 mRNA increased with erythropoietin-induced maturation of J2E cells, and decreased with interleukin 6-induced differentiation of M1 monoblastoid cells. In tissues, ARL-6 mRNA was most abundant in brain and kidney. While

tissues, ARL-6 mRNA was most abundant in brain and kidney. While ARL-6 protein was predominantly cytosolic, its membrane association increased following exposure to GTP-gammaS, like many members of the ARF/ARL family. Using the yeast two-hybrid system, six molecules which interact with ARL-6 were identified including SEC61beta, a subunit of the heterotrimeric protein conducting

channel SEC61p. Co-immunoprecipitation of ARL-6 confirmed a stable association between ARL-6 and SEC61beta in COS cells. These results demonstrate that ARL-6, a novel member of the ADP-ribosylation factor-like family, interacts with the SEC61beta subunit.

L14 ANSWER 5 OF 9 JAPIO COPYRIGHT 2001 JPO

ACCESSION NUMBER:

1997-183797

**JAPIO** 

TITLE:

PHYSIOLOGICALLY ACTIVE PROTEIN RHOTEKIN

INVENTOR:

NARUMIYA SHU

PATENT ASSIGNEE(S):

KIRIN BREWERY CO LTD, JP (CO 330755)

PATENT INFORMATION:

PATENT NO

KIND DATE

ERA

MAIN IPC

Searcher

Shears

308-4994

19970715 Heisei (6) C07K014-47 JP 09183797 A

JP

APPLICATION INFORMATION

JP1995-354328 19951228 ST19N FORMAT:

JP07354328 Heisei ORIGINAL:

PATENT ABSTRACTS OF JAPAN (CD-ROM), Unexamined SOURCE:

Applications, Vol. 97, No. 7

1997-183797 JAPIO AN

PURPOSE: TO BE SOLVED: To obtain a new protein having activated AB

Rho-protein\_binding\_ability,\_inhibiting\_Rho-protein\_GTPase\_activity,\_\_\_\_

thus capable of inhibiting tumor development and

metastasis through neutralizing Rho-protein involving tumor

development and metastasis.

CONSTITUTION: protein is a new physiologically active protein Rhotekin (or its modified product), which has activated Rho-protein binding ability and inhibits Rho-protein GTPase activity, containing part or the whole of an amino acid sequence of the formula, or an equivalent sequence thereto. This protein is capable of neutralizing the Rho protein closely involving tumor development and metastasis, thus of inhibiting tumor development and metastasis. This new protein is obtained by conducting a library screening by yeast-two-hybrid system using mouse fetal cDNA library to isolate the gene of mouse's activated Rho- protein-binding protein followed by integrating a vector with the gene which is then manifested in host cells.

**DUPLICATE 2** L14 ANSWER 6 OF 9 MEDLINE

96408699 MEDLINE ACCESSION NUMBER:

96408699 PubMed ID: 8813706 DOCUMENT NUMBER:

Co-translational effects of temperature on membrane TITLE:

insertion and orientation of P-glycoprotein

sequences.

**AUTHOR:** Zhang J T; Chong C H

Department of Physiology and Biophysics, University CORPORATE SOURCE:

of Texas Medical Branch, Galveston 77555-0641, USA.

Shears

308-4994

CA-64539 (NCI) CONTRACT NUMBER:

MOLECULAR AND CELLULAR BIOCHEMISTRY, (1996 Jun 7) 159 SOURCE:

(1) 25-31.

Journal code: NGU; 0364456. ISSN: 0300-8177.

Netherlands PUB. COUNTRY:

Journal; Article; (JOURNAL ARTICLE)

English LANGUAGE:

FILE SEGMENT: Priority Journals

199612 ENTRY MONTH:

Entered STN: 19970128 ENTRY DATE:

Last Updated on STN: 19970128

Searcher

#### Entered Medline: 19961210

AB P-glycoprotein (pgp) is a membrane transport protein that causes multidrug resistance (MDR) by actively extruding a wide variety of cytotoxic agents out of cells. It may also function as a peptide transporter, a volume-regulated chloride channel, and an ATP channel. Previously, it has been shown that hamster pgp 1 Pgp is expressed in more than one topological form and that the generation of these structures is modulated by charged amino acids flanking the predicted transmembrane (TM) segments 3 and 4 and by soluble cytoplasmic factors. Different topological structures of Pgp may be related to its different functions. In this study, we examined the effects of translation temperature on the membrane insertion process and the topologies of Pgp. Using the rabbit reticulocyte lysate expression system, we showed that translation at different temperatures affects the membrane insertion and orientation of the putative TM3 and TM4 of hamster pgp 1 Pgp in a co-translational manner. This observation suggests that the membrane insertion process of TM3 and TM4 of Pgp molecules may involve a protein conducting channel and/or the interaction between TM3 and TM4, which act in a temperature sensitive manner. We speculate that manipulating temperature may provide a way to understand the structure-function relationship of Pop and help overcome Pgp-related multidrug resistance of cancer cells.

L14 ANSWER 7 OF 9 MEDLINE

DUPLICATE 3

ACCESSION NUMBER:

96381595 MEDLINE

DOCUMENT NUMBER:

96381595 PubMed ID: 8789608

TITLE:

Expression of mRNAs of multiple growth factors and

receptors by neuronal cell lines: detection with

RT-PCR.

**AUTHOR:** 

Zaheer A; Zhong W; Lim R

CORPORATE SOURCE:

Department of Neurology, University of Iowa College of Medicine and Veterans Affairs Medical Center, Iowa

City 52242, USA.

SOURCE:

NEUROCHEMICAL RESEARCH, (1995 Dec) 20 (12) 1457-63.

Journal code: NX9; 7613461. ISSN: 0364-3190.

PUB. COUNTRY:

United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE:

English

FILE SEGMENT:

Priority Journals

ENTRY MONTH:

199610

ENTRY DATE:

Entered STN: 19961106

Last Updated on STN: 20000303 Entered Medline: 19961018

AB Neurons and glia are capable of both secreting and responding to a large variety of growth factors. However, information on multiple expression of growth factors and their receptors was usually obtained from uncorrelated observations, using cells from various

animals of origin, developmental stages, growth phases, culture ages and culture conditions. Because of its specificity and extreme sensitivity, reverse transcription-polymerase chain reaction (RT-PCR) is uniquely suitable to study a large panel of growth factors and their receptors from a limited cell sample, free of these intervening variables. In this paper we evaluate the expression of mRNA of a total of 35 growth factor-related proteins by conducting RT-PCR on three neuronal cell lines: the PC12 rat pheochromocytoma line, the MAH rat sympathoadrenal progenitor line, and the N18 mouse neuroblastoma line. Three types of results are presented. The first confirms the existing knowledge such as the presence of Trk-A (NFG receptor) in PC12. The second consists of new information that expands and extends earlier observations, such as the presence of CNTF receptor complex in PC12, which explains our previous report that CNTF enhances the biological effects of NGF on these cells. The third consists of novel information that leads the way to further experimentation by the more conventional methods. These include the strong expression of Trk-B by MAH, predicting the biological responsiveness of MAH to BDNF and NT-4, and the expression of CNTF receptor in N18. Our results also suggest that CNTF is an autocrine factor for PC12 and MAH, since both lines express the growth factor as well as the receptor. Thus, RT-PCR is a valuable tool in growth factor research that can be used in complement to, and interactively with, other approaches such as bioassay, receptor binding, and immunochemical determination. It will be particularly useful for screening a large number of growth factors in minute areas of the brain in patients suffering from neurodegenerative diseases such as Parkinson's and Alzheimer's.

L14 ANSWER 8 OF 9 BIOSIS COPYRIGHT 2001 BIOSIS

ACCESSION NUMBER:

1991:333595 BIOSIS

DOCUMENT NUMBER:

CORPORATE SOURCE:

BR41:30145

TITLE:

REGULATION OF SQUAMOUS CELL MARKER SMALL PROLINE-RICH

PROTEIN IN CONDUCTING AIRWAY

EPITHELIUM.

AUTHOR (S):

AN G; ROBINSON C B; TESFAIZZI J; CARLSON D M; WU R CALIF. PRIMATE RES. CENT., UNIV. CALIF., DAVIS,

CALIF. 95616.

SOURCE:

INTERNATIONAL CONFERENCE OF THE AMERICAN LUNG ASSOCIATION AND THE AMERICAN THORACIC SOCIETY, ANAHEIM, CALIFORNIA, USA, MAY 12-15, 1991. AM REV

RESPIR DIS, (1991) 143 (4 PART 2), A515.

CODEN: ARDSBL. ISSN: 0003-0805.

DOCUMENT TYPE:

Conference

FILE SEGMENT:

BR; OLD English

LANGUAGE:

## 09/587574

L14 ANSWER 9 OF 9 MEDLINE

DUPLICATE 4

ACCESSION NUMBER:

82216354

MEDLINE

DOCUMENT NUMBER:

82216354 PubMed ID: 7086652

TITLE:

Antitumor agents XLVIII: Structure-activity

relationships of quassinoids as in vitro protein synthesis inhibitors of P-388 lymphocytic leukemia

tumor cell metabolism.

**AUTHOR:** 

Liou Y F; Hall I H; Okano M; Lee K H; Chaney S G

CONTRACT NUMBER:

CA 17625 (NCI) CA 22929 (NCI) CA 26466 (NCI)

SOURCE:

JOURNAL OF PHARMACEUTICAL SCIENCES, (1982 Apr) 71 (4)

430-5.

Journal code: J07; 2985195R. ISSN: 0022-3549.

PUB. COUNTRY:

United States

Journal; Article; (JOURNAL ARTICLE)

LANGUAGE:

English

FILE SEGMENT:

Priority Journals

ENTRY MONTH:

198208

ENTRY DATE:

Entered STN: 19900317

Last Updated on STN: 19980206 Entered Medline: 19820826

AΒ A series of brusatol, bisbrusatol, and bruceantin esters were examined for their ability to inhibit protein synthesis in P-388 lymphocytic leukemia cells. Compounds which produced high T/C % values (170-272) resulted in ID50 of 5.4-15.5 microM for inhibition of whole cell protein synthesis, ID50 of 1.3-13 microM for inhibition of endogenous protein synthesis in cell homogenates, and ID50 of 1.9-6 microM for inhibition of polyuridine directed polyphenylalanine synthesis using "runoff" ribosomes and a "pH 5" enzyme preparation. The polyuridine directed polyphenylalanine synthesis requires neither initiation nor termination factors, suggesting that quassinoids are exclusively elongation inhibitors. Bruceantin, brusatol, and bisbrusatolyl malonate allowed a runoff of the polyribosomes to 80S free ribosomes. However, formation of the ternary complex and 80S initiation complex were not inhibited by the quassinoids. Thus, these agents do not affect the individual steps leading to the formation of a stable 80S initiation complex in P-388 cells. Brusatol, bruceantin, and bisbrusatolyl malonate inhibited the formation of the first peptide bond between puromycin and [3H] methionyl-transfer RNA bound to the initiation complex, indicating peptidyl transferase activity is inhibited by the quassinoids in P-388 cells. These studies also suggest that the free 80S ribosome is the site of binding by the quassinoid. Ribosomes actively conducting protein synthesis will continue protein synthesis and terminate before the quassinoids bind. This proves quassinoids are elongation inhibitors of tumor cells. A strong correlation was observed between

# 09/587574

potent antileukemic activity and the ability to inhibit protein synthesis in P-388 lymphocytic leukemia cells.

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N-PSDB; X23370.
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                                                                                                                                          783..833
                                                                                                                                                                            397..465
                                                                                                                                /note-
                                                                                                                                                               /note=
                                                                                                                                                                                                            343..396
                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                          Location/Qualifiers 78..200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                    "Beta-catenin
claim 14"
                                                                                                                                                                                                                    "Regulator of described in
                                                                                                                     "Dishevilled homology region claim 15"
                                                                                                                                                                                 "GSK 3-beta binding region as described claim 13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 639; DB 20;
Pred. No. 2.7e-66;
Mismatches 0;
                                                                                                                                                           binding domain
                                                                                                                                                                                                                    G protein signalling domain as claim 12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                              as
                                                                                                                                                             as
                                                                                                                            described
                                                                                                                                                             described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               840;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197
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RESULT
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Matches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
Newly isolated nucleic acid encoding "axis inhibition" (Axin) - useful for detecting, diagnosing and treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Axin; cancer; breast cancer; colorectal cancer; gastrointestinal cancer; esophageal cancer; carcinoma; melanoma; diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
                                                                                  N-PSDB; X09013.
                                                                                                          WPI; 1999-120510/10.
                                                                                                                                                             Constantini F,
                                                                                                                                                                                                                                                                  10-JUL-1997;
                                                                                                                                                                                                                                                                                                                  09-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                  21-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                     W09902179-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel human conductin protein which has anti-tumour activity. Detecting the presence or amount of conductin, at protein or nucleic acid levels, is used to diagnose tumours, while agents that (re)activate conductin are used for tumour therapy. Conductin binds to beta-cateni and induces its cytoplasmic degradation, resulting in blockade of the Mnt/Wingless signalling pathway in vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC) fragments and, in conjunction with APC, acts as a tumour suppressor.
                                                                                                                                                                                                                (UYCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     beta-catenin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murine axin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumor-suppressing protein conductin diagnosis of tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Fig 1; 22pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Behrens J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78
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                                                                                                                                                                                                                ) UNIV COLUMBIA NEW
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DB; X23369.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                840 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Birchmeier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                97US-0890865
                                                                                                                                                          Zeng
                                                                                                                                                                                                                                                                                                                98WO-US14414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   992 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 639; DB 20;
Pred. No. 2.7e-66;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ,
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  cancer
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RESULT
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CC gastrointestinal, esophageal, carcinomas or melanomas). The wild compose the property of the colorectal compositions are also useful for colorectal compositions are also useful for creating cancer by inhibiting tumorigenesis (by inducing degradation colorectal colorecta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 78; Conser
              Newly isolated nucleic acid encoding "axis inhibition" protein (Axin) - useful for detecting, diagnosing and treating cancer
                                                                            WPI; 1999-120510/10.
N-PSDB; X09012.
                                                                                                                                                                                                                                                                                                                                                   W09902179-A1
                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Axin; cancer; breast cancer; colorectal cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human axin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W96264;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                        Constantini F,
                                                                                                                                                                                                                                                                  09-JUL-1998;
                                                                                                                                                                                                                                                                                                           21-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                  beta-catenin.
                                                                                                                                                                                 (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                                                                                                                                         10-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     treatment; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      992 AA;
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                                                                                                                                        Zeng
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 407; DB
Pred. No. 5.3e
21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A
                                                                                                                                                                                                                                                                                                                                                                                                                                                     thyroid carcinoma; tumorigenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 20;
5.3e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 992;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding mutant and wild type Axin and oligonucleotides derived from them are useful for detecting mutations in the Axin gene and for determining whether a subject is likely to develop cancer (including breast, colorectal, gastrointestinal, esophageal, carcinomas or melanomas). The wild type Axin and homologues of Axin are useful for treating subjects who are likely to develop cancer (thyroid carcinomas). The nucleic acids are also useful for diagnosing cancer and for detecting mutations in cancerous cells. Wild type Axin, its antisense molecule and identified compounds form pharmaceutical compositions in the treatment of cancer. The compositions are also useful for
                                                              /note-
Misc-difference 107
                                                                                                                                                                                                                                                                                                                RGS; regulators of G-protein signaling; GTPase activating protein; GAP;
G-alpha protein; cell adhesion; chemotaxis; vulnerary; immunosuppressor;
anti-rheumatic; anti-arthritic; anti-diabetic; anti-inflamatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treating cancer by inhibiting tumorigenesis (by inducing degradation of beta-catenin). The nucleic acid encoding Axin acts through negative regulation of the Wnt pathway in the Nieuwkoop Center.
               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                    Human regulator of G-protein signaling protein.
                                                                                                                                                                                                                                                                                                                                                                                               04-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                           ¥97153;
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                                       Misc-difference
                                                                                             Misc-difference
                                                                                                                       Misc-difference
                                                                                                                                                  Misc-difference
                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                               Key
                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                  cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y97153 standard; Protein; 235
                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 diyley 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 DIYLEY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMNLKDT---KTLRVAKAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              yrkyildnngivsrqtkpatksfikgcimkqlidpamfdqaqteiqatmeentypsflks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       900 AA;
                                                                                                                                                                                                                                                                                                   hepatotropic; anti-anaemic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                             /note= "forms 104
                                                                                                                                                                                                                                 Location/Qualifiers
82..201
                                          109
                                                                                                                       103
                                                                                                                                                  100
                                                                                                                                                                              90
                                                                                                                                                                                                        83
                                                                                                                                    /note= "forms
 /note-
                          /note-
                                                     /note=
                                                                                                                                                                                          /note-
                                                                                                                                                               note- "forms
                                                                                                                                                                                                                   /label= RGS_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.8%; Score 401; DB 20; 62.7%; Pred. No. 2.3e-38;
                                                     "Makes
                                                                              "forms
                                                                                                                                                                                        "forms part of hydrophobic
                          "Makes
"Makes direct contact with G-alpha-i"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17;
                                                                                                                                                             part
                                                                                                                                    part
                            direct
                                                     direct
                                                                                part of hydrophobic
                                                                                                         part of hydrophobic
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                                                                                                                                                                ę,
                                                                                                                                     of
                          contact with G-alpha-i"
                                                     contact with G-alpha-i"
                                                                                                                                     hydrophobic
                                                                                                                                                               hydrophobic
                                                                                                                                                                                                                                                                                                   modulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 900;
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                                                                                core"
                                                                                                                                       core"
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                                                                                                                                                                                                                                                                                                  gene therapy
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N-PSDB; A52089
                     Hodge MR,
                                  (MILL-) MILLENNIUM
                                                 04-FEB-1999;
                                                               04-FEB-2000;
                                                                              10-AUG-2000
                                                                                                                Misc-difference
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Novel regulator of G-protein signaling useful as diagnostic and investigative signaling disorders nucleic acids and polypeptides, tools and to treat G-protein

Claim 8; Page 102; 105pp; English.

The RGS (regulators of G-protein signaling) protein genes, clones h16395 and m1975, were identified in human and murine spleen cDNA libraries, respectively. Both proteins have unique N- and C-terminal sequences. The C-terminal location of the RGS domain is consistent with RGSs known to act as GTPase activating proteins (GAPs) for G-alpha proteins. G-alpha-i linked receptors support rapid adhesion and directed migration of leukocytes and other cell types. The novel RGS proteins may be used to modulate cell adhesion and chemotaxis, e.g. for alding wound repair. The RGS proteins, related cDNAs and anti-RGS antibodies are useful for modulation, diagnosis and treatment of immune and respiratory disorders.

Sequence 235

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel regulator of G-protein signaling nucleic acids and polypeptides, useful as diagnostic and investigative tools and to treat G-protein signaling disorders
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Pred. No. 6.7e-13;
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RESULT

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ID Y41020 standard; protein; 116 AA
XX X41020;
XX AC Y41020;
XX PGS2 protein RGS region.
XX RGS2 protein RGS region.
XX RGS2 protein RGS region.
XX RGS2 protein alpha subunit; cell protein collaboration; clot retraction collaboration; clot retraction collaboration; clot retraction collaboration; clot retraction collaboration collaboration; clot retraction collaboration collaboration; clot retraction, clot retraction, cell proliferation; products can be used for the collaboration collaboration collaboration; cell proliferation collaboration collaboration; cell proliferation collaboration col
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                                                                  61 YIENNSVVSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDIY 119
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                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75pp; English
                                                                                                                                                                                                                                                                                                                     26.2%;
                                                                                                                                                                                                                                                                                        20;
                                                                                                                                                                                                                                                                                    Score 167.5; DB
Pred. No. 4e-12;
0; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polakis P, Sternweis P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to develop products for integrin-mediated interactions
                                                                                                                                                                                                                                                                                        57;
                                                                                                                                                                                                                                                                                                                                                              20;
                                                                                                                                                                                                                                                                                                                                                   Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kozasa
                                                                                                                                                                                                                                                                                        Ψ
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
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                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                             F15566 to F16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in B5333 to B57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antilnfective, gynecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. F16506 to F16514 to B57303 represent sequences
         B43847 standard; Protein;
                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Page 1946-1947; 2338pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorders such as prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-MAR-2000; 2000WO-US05988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200055174-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              wound; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gastrointestinal; pulmonary;
                                                                                       148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vulnerary; gastrointestinal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B56929 standard; Protein; 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-MAR-2001
                                                                                                                 61
                                                                                                                                                                                                                      Local Similarity
                                                                                                                                              89
                                         9
                                                                         YIENNSVVSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDIY 119 :|| : ::|| |:| || :|
                                                                                                                                       wseafdellaskyglaafraflksefceeniefwlacedfkktk-spqklsskarkiytd 147
                                                                                                                                                                       WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKR 60
                                                                                                                                                                                                                                                                                                          in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-587513/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prostate cancer antigen protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ROSEN
                                                                                                                                                                                                                                                                               220 AA;
                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0124270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer; prostate cancer antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic;
                                                                                                                                                                                                                    26.2%;
            217 AA
                                                                                                                                                                                                  Score 167.5; DB 21;
Pred. No. 9.1e-12;
Pred. No. 9.7e-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cardiovascular; proliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nephrotropic; antiinfective; gynaecological;
neural; immune; reproductive; renal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cardioactive;
                                                                                                                                                                                                                               DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ingen; detection; diagnosis;
immunomodulatory; muscular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID
                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                               Length
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59 KRYIENNSVVSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDI 118

wsqslekllanqtgqnvfgsflksefseeniefwlacedykktesdllpck----aeeiy 145 WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFR--QMNLKDTKTLRVAKAIY 58

90

Matches Query Match

Local

Similarity

25.8%;

Score 165; DB 21; Pred. No. 1.8e-11; Mismatches

Length 217; Indels

8,

Gaps

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Conservative

28;

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CC B4339 to B4423. The proteins can have activities based on the tissues CC and cells the genes are expressed in Example of activities include: CC cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; CC antiasthmatic; antirleumatic; antiarthritic; antiviral; dermatological; CC antithyroid; antiallergic; antibacterial; antiviral; dermatological; CC neuroprotective; cardiant; thrombolytic; coagulant; nootropic; antipsoriatic and antiangiogenic. The polynucleotides and CC vasotropic; antipsoriatic and antiangiogenic. The polynucleotides and CC conditions and diagnosing pathological conditions. Polynucleotides, antipodies, agonists and antagonists from the present CC invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune CC cells, to treat disorders of haematopoietic cells, autoimmune disorders, cardiovascular disorders, neurological disease and bacterial or concers, cardiovascular disorders, neurological disease and bacterial or crancers, cardiovascular disorders, neurological disease and bacterial or crancers, cardiovascular disorders, neurological disease and bacterial or concers, cardiovascular disorders, neurological disease and bacterial or crancers cardiovascular disorders, neurological disease and bacterial or crancers cardiovascular disorders, neurological disease and bacterial or crancers cardiovascular disorders antibodies, agonists and concers cardiovascular disorders described antipolical disease and crancers cardiovascular disorders described antipolical disease and conditions described antipolical disease and con
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acids comprising sequences useful for treating or diagnosing e.g. cancer - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antianglogenic; gene therapy; inflammation; immune disorder; haematopoletic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haematopoletic; cardiovascular disorder; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAR-2000; 2000WO-US05882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurological disease; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; cancer associated gene; cancer antigen; detection; diagnosis; cytostatic; proliferative; vulnerary; immunomou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000-587533/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to C78448 encode the human cancer associated proteins given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C78056
217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                associated protein sequence SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0124270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2352pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer;
                                                                                                                                                                                                                                                                                                                                                                                medical
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RESULT 10
V41021
XX Y41021
XX Y41021
XX O6-DEC
XX RGS;
XX RGS;
XX RGS;
XX RGS;
XX RGS;
XX ROS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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Query Match
Best Local Similarity
Matches 39; Conser
                                                                                                                                                                                                                                  The invention relates to isolated RGS-guanine nucleotide exchange factor (GEF) polypeptides. The novel isolated RGS-GEF polypeptide consists of an RGS domain of a GEF protein and does not comprise a dbl homology (DH) domain or a pleckstrin homology (PH) domain. The RGS-GEF polypeptides can be used for modulating an activity of a G protein alpha subunit (GAS). The products can be used for the regulation of biological pathways in which a RGS-GEF polypeptide is involved, particularly pathological conditions, e.g. cell proliferation (e.g. cancer), morphogenesis, growth control, stress fiber formation, and integrin-mediated interactions, such as embryonic development, tumor cell growth and metastasis, programmed cell death, hemostasis, leukocyte homing and activation, bone resorption, clot retraction, and the response of cells to mechanical stress. The products can also be used for detection, diagnosis and production of strengenic animals. Sequences Y41014-028 represent RGS regions of several
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated RGS-GEF polypeptides, used modulating, e.g. cell proliferation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bollag G,
Jiang X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               morphogenesis; stress fiber formation; integrin-mediated interaction; embryonic development; tumor cell growth; cell death; leukocyte homing; bone resorption; clot retraction; dbl homology domain; mechanical stress;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 18; 75pp; English
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                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ONYX-) ONYX PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RGS3 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3S; guanine nucleotide exchange factor; GEF; RGS domain; GAS; protein alpha subunit; cell proliferation; growth control; h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΥL
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                                                                                                                                                          116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   homology domain
      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                  25.7%;
32.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roscoe W,
   22;
Score 164.5; DB Pred. No. 9e-12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polakis P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                integrin-mediated interactions
                                                             DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sternweis P,
   55;
      Indels
                                                             Length
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   ω,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hemostasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer;
   Gaps
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WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFR--QMNLKDTKTLRVAKAIY 58 Query Match Best Local (

Similarity 39; Conserv

Conservative

25.2%; Score 161; DB 20; 32.2%; Pred. No. 2.3e-11; tive 28; Mismatches 46;

Length 115;

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                                    (GEF) polypeptides. The novel isolated RGS-GEF polypeptide coursists with the compression of a GEF protein and does not comprise a dbl homology (DH) domain or a pleckstrin homology (PH) domain. The RGS-GEF polypeptides can be used for modulating an activity of a G protein alpha subunit (GAS). The products can be used for the regulation of biological pathways in which a RGS-GEF polypeptide is involved, particularly pathological conditions, e.g. cell proliferation (e.g. cancer), morphogenesis, growth control, stress fiber formation, and integrin-mediated interactions, such as embryonic development, tumor cell growth and metastasis, programmed cell death, hemostasis, leukocyte homing and activation, bone resorption, clot retraction, and the response of cells to mechanical stress. The products can also be used for detection, diagnosis and production of transgenic animals. Sequences 741014-028 represent RGS regions of several
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bollag G,
Jiang X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGS; guanine nucleotide exchange factor; GEF; RGS domain; GAS; cancer; G protein alpha subunit; cell proliferation; growth control; hemostasis; morphogenesis; stress fiber formation; integrin-mediated interaction; embryonic development; tumor cell growth; cell death; leukocyte homing; bone resorption; clot retraction; dbl homology domain; mechanical stress; bone resorption; clot retraction; dbl homology domain; mechanical stress;
Sequence
                                                                                                                                                                                                                                                                      The invention relates to isolated RGS-guanine nucleotide exchange fac (GEF) polypeptides. The novel isolated RGS-GEF polypeptide consists o RGS domain of a GEF protein and does not comprise a dbl homology (DH)
                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 18; 75pp; English
                                                                                                                                                                                                                                                                                                                                                                                                          New isolated RGS-GEF polypeptides, used to develop products for modulating, e.g. cell proliferation and integrin-mediated interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-571821/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pleckstrin homology domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ONYX-) ONYX PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YIENNSVVSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDIY 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         wgeslekllvhkyglavfqaflrtefseenlefwlacedfkkvk-sqskmaskakkifae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hart MJ,
  115 AA;
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                                                                                                                                                                                  Matches
                                                                                                                                                                                               Query Match
Best Local 9
                                                                                                                                                                                                                                                                                         This amino acid sequence represents the human p26 protein. The gene sequence was isolated from a human thymus cDNA library by plaque hybridisation using the rat p26 cDNA sequence (V19303) and the screening isolated the corresponding 889 bp sequence. p26
                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                       useful as a reagent for screening for compounds having dephosphorylase inhibitory activity. It is also useful as a treating and preventive agent for diseases related to the haematogenic system.
                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 2; 40pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                      Mammalian p26 proteins and their related DNA - useful for screening for de-phosphorylase inhibitory compounds
                                             154 kh 155
                                                                 121 EY 122
                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-056555/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TAKE ) TAKEDA CHEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-MAR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; p26; brain; hybridisation; dephosphorylase inhibitory activity; probe; rat; haematogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W44834 standard; peptide; 181 AA
                                                                                           97
                                                                                                     61 YIENNSYVSKOLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDIYL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human p26 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W44834;
            13
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                                                                                                                                                                                             Local
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                                                                                                                            waaslenlledpegvkrfreflkkefseenvlfwlacedfkkmqdk-tqmqekakeiymt 96
                                                                            fl--sskassqvnvegqsrlnekileep-hplmfqklqdqifnlmkydsysrfiksdlfl
                                                                                                                                                 WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     у 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KRYIENNSVVSKOLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAVQVFLTSDI 118
                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                           181 AA;
                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96JP-0055196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96JP-0347877.
                                                                                                                                                                                          25.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 IND LTD
                                                                                                                                                                               30;
                                                                                                                                                                                       Score 160; DB 19;
Pred. No. 5.4e-11;
                                                                                                                                                                             Mismatches
                                   .-
                                                                                                                                                                             49;
                                                                                                                                                                                                 Length 181;
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                                                                                                                                                                                                                                                                                                                          The encoding
                                                                                                                                                                                                                                                                                                     as a probe
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                                                                                                                                                                        Gaps
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Db Qy

64 waaslenlledpegvkrfreflkkefseenvlfwlacedfkkmgdk-tqmqekakeiymt 122

1 WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKR 60

Query Match Best Local S Matches 39

Local Similarity

25.0%; S 32.0%; P tive 30;

Score 160; DB 21; Pred. No. 6.4e-11; 0; Mismatches 49;

Length 207; Indels

4.

Conservative

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C called pancreatic cancer antigens, given in $54008 to B54465. The human communomodulatory, relaxant, contraceptive, gynaecological, cardiant and cancer antigens have cytostatic, neuroprotective, nootropic, c immunomodulatory, relaxant, contraceptive, gynaecological, cardiant and contininflammatory activities, and can be used in gene therapy. The complynucleotide and proteins can be used in gene therapy. The cambiorating a medical condition or in assays for diagnosting a continer to the proteins and the activity of the proteins can be confident of the proteins and the activity of the proteins can be confident of the proteins and the activity of the proteins can be confident of the antigens can be used to design nucleic acid hybridisation can be used to design nucleic acid hybridisation can be used to design nucleic acid hybridisation confidentification and/or typing and a variety of forensic and diagnostic confidentify detect and target the polypeptides, including both in vivo cused to treat or prevent neural, immune system, muscular, reproductive, confidential, pulmonary, cardovascular, renal or proliferative confidence confidences in the proteins can be used to design nucleic acid hybridisation confidence conf
  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C98773 to C99231 encode the human pancreatic cancer associated proteins called pancreatic cancer antiques, given in R54008 to R54466 The human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-MAR-2000; 2000WO-US05989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiinflammatory; cardiant; gene therapy; chromosome mapping; linkage analysis; tissue identification; tissue typing; forensic; neural; immune system; muscular; reproductive; gastrointestinal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; pancreas; pancreatic cancer; pancreatic cancer antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detection; diagnosis; identification; cytostatic; neu:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human pancreatic cancer antigen protein sequence SEQ ID NO:812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000-579444/54.
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207 AA;
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RESULT 14
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       New regulators of G-protein signalling - useful for, e.g. diagnosis, prevention and treatment of cancer and inflammation
                                  WPI; 1998-557112/47.
N-PSDB; V45442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Regulator of G-protein signalling 2; RGPS-2; human; G protein coupled receptor; signal transduction; inflammation; cell proliferation; cancer; diagnosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JAN-1999 (first entry)
                                                                  Goli SK,
                                                                                    (INCY-) INCYTE PHARM INC
                                                                                                                            31-MAR-1998;
                                                                                                                                                08-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human regulator of G-protein signalling 2 (RGPS-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W30561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W30561 standard; Protein;
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                                                                                                                                                                                                                                                                                                    Modified-site
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                                                                 Hillman JL
                                                                                                        97US-0829110
                                                                                                                            98WO-US06336.
                                                                                                                                                                                                                                                                                                                       66..69
/note=
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/note=
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235..238
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                                                                                                                                                                                                                                                   "potential protein kinase C phosphorylation
site"
                                                                                                                                                                                                                                                                               "potential site"
                                                                                                                                                                                                                                                                                                                        "potential
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                                                                                                                                                                                                                                                                                                                                                                                                                          "RGF motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     "potential G-protein coupled receptor
                                                                                                                                                                                       "potential site"
                                                                                                                                                                                                                 site"
                                                                                                                                                                                                                                                                                                            site"
                                                                                                                                                                                                                                                                                                                                                                                                                                          signature"
                                                                                                                                                                                                                                                                                                                                                                       potential cAMP- and cGMP-dependent protein kinase phosphorylation site"
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                                                                                                                                                                                                protein kinase C phosphorylation
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissues. The invention provides 2 regulators of 6-protein signalling, i.e. RGPS-2 and RGPS-1 (see W30560). The invention also features nucleic acids encoding RGPS polypeptides, oligonucleotides, peptide nucleic acids, fragments, portions or antisense molecules, and expression vectors and host cells. It also features antibodies specific for RGPS, and pharmaceutical compositions comprising purified RGPS. It also provides methods for stimulating cell proliferation using an RGPS or an agonist of RGPS and for treating or preventing disorders (e.g. cancer) associated with cell proliferation and information.
                                                                                                                                                                                                                                                                   RGS; guanine nucleotide exchange factor; GBF; RGS domain; GAS; cancer; G protein alpha subunit; cell proliferation; growth control; hemostasis; morphogenesis; stress fiber formation; integrin-mediated interaction; embryonic development; tumor cell growth; cell death; leukocyte homing; bone resorption; clot retraction; dbl homology domain; mechanical stress;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 19; Page 45;
                                                                                                                                                                                                                                                                                                                                                                                                                            Y41001;
                            Jiang X;
                                          Bollag G,
                                                                                                                                  18-MAR-1999;
                                                                                                                                                                  23-SEP-1999
                                                                                                                                                                                              W09947557-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       associated with cell proliferation and inflammation using an
                                                                        (ONYX-) ONYX PHARM INC.
                                                                                                      18-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 WTKSLHSLLGDQDGAYLERTFLEREKCVDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                            Hart MJ,
                                                                                                                                                                                                                                                        homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                       98US-0078634
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                                            Roscoe
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                                             Polakis
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WPI; 1999-571821/48

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The invention relates to isolated RGS-guanine nucleotide exchange factor CC (GEF) polypeptides. The novel isolated RGS-GEF polypeptide consists of an CC RGS domain of a GEF protein and does not comprise a dbl homology (PH) CC domain or a pleckstrin homology (PH) domain. The RGS-GEF polypeptides can be used for modulating an activity of a G protein alpha subunit (GAS). CC which a RGS-GEF polypeptide is involved, particularly pathological cc conditions, e.g. cell proliferation (e.g. cancer), morphogenesis, growth CC control, stress fiber formation, and integrin-mediated interactions, such CC as embryonic development, tumor cell growth and metastasis, programmed CC clot retraction, and the response of cells to mechanical stress. The CC products can also be used for detection, diagnosis and production of CC transgenic animals. Sequences Y41000-008 represent conserved domain
                                                                                                              Query Match 24.5
Best Local Similarity 31.1
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                   Sequence
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118 AA;
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1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*

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4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*

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US-08-829-110-3
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US-08-8748-483-1
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   a 4, Appli 31, Appli 31, Appli 32, A
Query Match
Best Local Similarity
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US-08-748-483-4  Sequence 4, Application US/08748483  Sequence 4, Application US/08748483  Patent NO. 5955314  GENERAL INFORMATION: APPLICANT: Hillman, Jennifer L. APPLICANT: Hillman, Jennifer L. APPLICANT: Goli, SUTYA K. TITLE OF INVENTION: A NOVEL REGULATOR OF CELL SIGNUMBER OF SEQUENCES: 5  CORRESPONDENCE ADDRESS: 5  COUNTRY: US ZIF: 94304  COMPTER: 3174 POTTER DIAMAGEUTICALS, INC. STATE: CA  COUNTRY: US ZIF: 94304  COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM COMPATIBLE COMPUTER: IBM COMPATIBLE OPERATION SYSTEM: DOS SOFTMARE: FASTSEO Version 2.0  CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/748,483  FILING DATE: Herewith CUS/08/748,483  FILING DATE: HEREWITH APPLICATION NUMBER: US/08/748,483  FILING DATE: HEREWITH APPLICATION NUMBER: DF-0157 US FELEPHONE: 415-845-055  TELEPHONE: 415-845-055  TELEPHONE: 415-845-055  TELEPHONE: 415-845-016  TELEPHONE: 415-845-016  TELEPHONE: 415-845-016  TELEPHONE: 415-845-016  TELEPHONE: 415-845-016  THARDIATE SOURCE: LENGTH: 211 amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids THARDIATE SOURCE: LENGTH: 211 amino acids TYPE: amino acids THARDIATE SOURCE: LENGTH: 1108AT  LENGAL-1008: 292037  US-08-748-483-4	28 133 20.8 123 2 US-08-588-258B-39 29 133 20.8 123 5 PCT-US56-08395-39 30 124.5 19.5 555 2 US-08-588-258B-24 31 124.5 19.5 555 3 US-08-68-258B-24 32 124.5 19.5 555 5 PCT-US96-08395-24 33 116 18.2 118 2 US-08-588-258B-38 34 116 17.8 123 2 US-08-588-258B-38 35 114 17.8 123 2 US-08-588-258B-1 36 114 17.8 123 2 US-08-68-255-1 37 114 17.8 123 5 PCT-US96-08295-1 38 113 17.7 119 2 US-08-68-258B-30 40 113 17.7 119 2 US-08-68-258B-30 41 101 15.8 420 2 US-08-588-258B-40 42 101 15.8 420 2 US-08-588-258B-40 43 64 10.0 764 5 PCT-US96-08295-40 44 64 10.0 764 5 PCT-US95-16930-4 45 64 10.0 764 5 PCT-US95-16930-4
SIGNALLING	Sequence 39, Appl Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl Sequence 38, Appl Sequence 38, Appl Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 30, Appl Sequence 30, Appl Sequence 30, Appl Sequence 40, Appl Sequence 40, Appli Sequence 40, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli

26.2%;

Score 167.5; DB 2 Pred. No. 2.3e-13;

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Length 211;

Matches

39;

Conservative

20;

RESULT 2 US-08-588-258B-31

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

COUNTRY: US ZIP: 02110

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Sequence 31, Application US/08460505
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GENERAL INFORMATION:
APPLICANT: H. Robert Horvitz et al.
APPLICANT: TOVENTION: REGULATORS OF G-PROTEIN SIGNALLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER: 39,109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 39,109
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
                                                                                                                                                                                                                                                                                                  59 KRYIENNSVYSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDI 118
                                                                                                                                                                                                                                                                  58 KAFVHSDA--AKQINIDERTRESTAKKIKAPTPTCFDEAQKVIYTLMEKDSYPRFLKSDI 115
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                                                                                                                                                                                                                                                                                                                                                                                 2 WSQSLEKLLANQTGQNVFGSFLKSEFSEENIEFWLACEDYKKTESDLLPCK----AEEIY 57
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PCT-US96-08295-31
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                                                                                                                                                                                                                                                      Sequence 31, Application PC/TUS9608295
GENERAL INFORMATION:
APPLICANT: Massachusetts Institute of Technology
TITLE OF INVENTION: REGULATORS OF G-PROTEIN SIGNALLING
NUMBER OF SEQUENCES: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
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  COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA
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ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Horvitz, Robert APPLICANT: Koelle, Michael TITLE OF INVENTION: REGULA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 YL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 YL 120
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                                                                                                                     STATE:
                                                                                                                                                                    ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELLEFAX: 01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 KAFVHSDA--AKQINIDERTRESTAKKIKAPTPTCFDEAQKVIYTLMEKDSYPRELKSDI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 KRYIENNSVVSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDI 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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REGISTRATION NUMBER: 39,109
REFERENCE/DOCKET NUMBER: 01997/214001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 02-JUN-1995 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 WSQSLEKLLANQTGQNVFGSFLKSEFSEENIEFWLACEDYKKTESDLLPCK----AEEIY 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
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                                                                                                                                                  Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGULATORS OF G-PROTEIN SIGNALLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Robert H.
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US-08-588-258B-31

TOPOLOGY: 1: MOLECULE TYPE:

linear

protein

STRANDEDNESS:

INFORMATION FOR SEQ ID NO:

TELEFAX: 617-428-7045

CLASSIFICATION:

SEQUENCE CHARACTERISTICS: LENGTH: 119 amino acids

amino acid

Query Match Best Local S Matches

Local Similarity 32.8 ses 40; Conservative

US-08-460-505-31

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Best Local Similarity
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CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/588,258
APPLICATION NUMBER: 12-JAN-96
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NAME: Bicker-Brady, Kristina
REGISTRATION NUMBER: 39,109
REFERENCE/DOCKET NUMBER: 01997/216001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/I
FILING DATE: 31-MAY-1996
                                                                SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hillman, Jennifer L. APPLICANT: Goli, Surya K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NOVEL REGULATORS OF G-PROTEIN TITLE OF INVENTION: SIGNALING
                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 YL 117
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TELEFAX: 200154
                                                                                                                                                                                                                            STREET: 3174 POI
CITY: Palo Alto
                               APPLICATION NUMBER: FILING DATE: Filed
                                                                                                                                                                              COUNTRY: U. ZIP: 94304
                                                                                                                                                                                                                 STATE:
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                                                                                                         OPERATING SYSTEM:
                                                                                                                        COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 KRYIENNSVVSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDI 118
                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFR--QMNLKDTKTLRVAKAIY 58
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APPLICATION DATA:
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3174 Porter Drive
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                                                                                                                                                                                               USA
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SYSTEM: PC-DOS/MS-DOS
                                 Filed Herewith
                                                                                                                                             Diskette
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                                                  US/08/829,110
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Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08748483 Patent No. 5955314
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                                                                                                       APPLICATION NUMBER: US, FILING DATE: Herewith CLASSIFICATION: 530 PRIOR APPLICATION DATA: APPLICATION NUMBER:
TELEPHONE: 415-855-0555
                                                                                                                                                                                         SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: A NOVEL REGULATOR OF CELL SIGNALLING NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hillman, Jenni
APPLICANT: Goli, Surya K.
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TELEPHONE: 415-855-0555
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                                                           ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
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LIBRARY: Gen-
-^NE: 299705
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                           REFERENCE/DOCKET NUMBER: 36
                                                                                                                                                                                                         OPERATING SYSTEM:
SOFTWARE: FastSE
                                                                                                                                                                                                                                                                                                                        CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 KRYIENNSVVSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDI 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 WSQSLEKLLANQTGQNVFGSFLKSEFSEENIEFWLACEDYKKTESDLLPCK----AEEIY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                         ZIP: 94304
                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                        STREET:
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                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH:
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                                        36,749
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                                PF-0157 US
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Pred. No. 4.3e-13;
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US-08-829-110-3
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Best Local Similarity
Matches 40; Conserv
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Patent No. 5882890
                                                                              TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/8:
FILING DATE: Filed Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FBSTSEQ for Windows Version
CURRENT APPLICATION DATA:
MMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hillman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL REGULATORS OF G-PROTEIN
TITLE OF INVENTION: SIGNALING
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                   TYPE: amino acid
STRANDEDNESS: single
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LIBRARY: GenBa
CLONE: 728966
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                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER:
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CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 WSQSLEKLLANQTGQNVFGSFLKSEFSEENIEFWLACEDYKKTESDLLPCK----AEEIY 124
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                                                                        Matches
                                                                                          Query Match
Best Local :
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Best Local Similarity 32.0
Matches 39; Conservative
                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Bicker-Brady, Kristina
REGISTRATION NUMBER: 39,109
REFERENCE/DOCKET NUMBER: 01997
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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STREET: BOSTON
CITY: BOSTON
TWATE: MA
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NUMBER OF SEQUENCES:
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                                                                    Local Similarity 31.9
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                                                                                                                                                                                                       STRANDEDNESS:
                   TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
FILING DATE: Januar
CLASSIFICATION: 435
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2 WSEAFDELLASKYGLAAFRAFLKSEFCEENIEFWLACEDFKKTK-SPQKLSSKARKIYTD 60
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                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 YIENNSYVSKQLKPATKTYIRDGIKKQQIGSYMFDQAQTEIQAVMEENAYQVFLTSDIYL 120
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                                                                                                                                                                                                                       amino acid
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                                                                                                                                                                                                                                     121 amino acids
                                                                                                                                                                                                                                                                                                          617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Clark & Elbing LLP
176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H. Robert Horvitz et al. VENTION: REGULATORS OF G-PROTEIN SIGNALLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THYMNOT 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                          January 12,
                                                                                                                                                                                                       not relevant
                                                                   24.7%; Score 158; DB 2; 1
31.9%; Pred. No. 1.7e-12;
7ative 20; Mismatches 59;
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                                                                   Indels
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                                                               2; Gaps
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61 YIENNSVVSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDIY 119

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Best Local Similarity
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                                                                                                                                             equence 32, Application PC/TUS9608295
GENERAL INFORMATION:
APPLICANT: Massachusetts Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 200154
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: BLEKET-Brady, Kristina
REGISTRATION NUMBER: 39,109
REFERENCE/DOCKET NUMBER: 01997/214001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                      CORRESPONDENCE ADDRESS
                                                                                                     APPLICANT: MASSACHUSETTS INSTITUTE OF TECHNOLOGY
TITLE OF INVENTION: REGULATORS OF G-PROTEIN SIGNALLING
NUMBER OF SEQUENCES: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: REGULATORS OF G-PROTEIN SIGNALLING
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Horvitz, Robert APPLICANT: Koelle, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 02-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                    CITY:
                                                   STREET:
                                                                                                                                                                                                                                                                        61 FIEKEAPKEINIDFQTKTLIA-AQNIQEATSGCFTTAQKRVYSLMENNSYPRFLESEFY 118
                                                                                                                                                                                                                                                                                                          61 YIENNSVVSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDIY 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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STATE: MA
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STREET: 22
COUNTRY:
                                                                   ADDRESSEE:
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                                                   E: Fish & Richardson P.C
225 Franklin Street
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                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                     24.7%; Score 158; DB 3; Length 121; 31.9%; Pred. No. 1.7e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/460,505
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                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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PCT-US96-08295-32
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                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                               ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                        APPLICANT: Hillman, Jennii APPLICANT: Goli, Surya K. TITLE OF INVENTION: NOVEL TITLE OF INVENTION: SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Bieker-Bradv, Kris
                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                  APPLICATION NUMBER: US/08/8 FILING DATE: Filed Herewith
                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                           STREET: 3174 POI CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 FIEKEAPKEINIDFQTKTLIA-AQNIQEATSGCFTTAQKRVYSLMENNSYPRFLESEFY 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1 CLASSIFICATION:
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CLASSIFICATION:
                                                                            SOFTWARE:
                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                                                                                                                                                                                  ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKR 60
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REFERENCE/DOCKET NUMBER: 019
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5. 5882890
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                                                                                                                                                                                                                                                                                                                                                                                     Hillman, Jennifer L.
                                                                            FastSEQ for Windows Version 2.0
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                                                                                                                                     Diskette
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12-JAN-96
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                                      US/08/829,110
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US-08-748-483-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                    CLASSIFICATION: 530
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 6:
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEB: INCYTE PHARMACEUTICALS, INC
STREET: 3174 PORTER Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hillman, Jennifer L. APPLICANT: Goli, Surya K.
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LIBRARY: GenBank
CLONE: 1216373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 205 amino acids
TYPE: amino acid
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                                                                                                                                                                          APPLICATION NUMBER: US
FILING DATE: Herewith
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CITY: Palo Alto
STATE: CA
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Local Similarity 30.8%;
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TOPOLOGY: lir
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REGISTRATION NUMBER: 36,749
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IBM Compatible
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                                 PF-0157 US
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Pred. No. 7.2e-12;
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RESULT 13
US-08-748-483-1
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; CLONE: 1216373
US-08-748-483-5
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Best Local Similarity
                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                      NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                          APPLICATION NUMBER: [FILING DATE: Herewit] CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hillman, Jenni
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: A NOV
NUMBER OF SEQUENCES: 5
IMMEDIATE SOURCE
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ADDRESSEE: INCYTE PHARMACEUTICALS,
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                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM CONCERNING SYSTEM:
                 TOPOLOGY:
                                                                                                                               TELEFAX: 415-845-4166
                                                                                                                                                                                                                                             FILING DATE:
                                                               LENGTH:
                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: INCLARAGE Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKR 60
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                                                amino acid
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US-08-748-483-1
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                                                                                                                             Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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NAME: LBUIB A. COTUZZI
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,228
FILING DATE: 04-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: FOR THE TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
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nes 36; Conserv
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ZIP: 10036-2711
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STATE: New York
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61 YIENNSV----VSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTS 116
                                                                                                                                                                                                                                         TOPOLOGY: linear
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                                    WRESFOLLLNSKNGVAAFHAFLKTEFSEEALEFWLACEEFKKIR-SATKLASRAHHIFDE 119
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29.3%; Pred. No. 5.3e-10;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LIM PC compatible
COMPUTER: DM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICANT: Gimeno, Carlos J.

TITLE OF INVENTION: RATH GENES AND POLYPEPTIDES AND METHODS

TITLE OF INVENTION: FOR THE TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 896-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Laura A. COTUZZI
REGISTRATION NUMBER: 30,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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                                  117 DIY 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 06-JUN-1997 CLASSIFICATION: 435
                                                                                                      61 YIENNSY----VSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
                                                                                                                                              61 WRESFDLLLNSKNGVAAFHAFLKTEFSEEALEFWLACEEFKKIR-SATKLASRAHHIFDE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                       YIRSEAPKEVNIDHETRELTKTNL-----QAATTSCFDVAQGKTRTLMEKDSYPRFLKS 173
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Pred. No. 5.3e-10;
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Search completed: June 7, 2001, 02:02:09 Job time: 5402 sec

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Result
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match
       June 7, 2001, 00:39:27; Search time 56.43 Seconds (without alignments)
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                                     T08423

T08423

S78089

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S718120

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S78236

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S7
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RESULT 2 TO8422 negative reg N;Alternate C;Species: R C;Date: 05-N C;Accession: R;Ikeda, S.; EMBO J 17, A;Title: Axi A;Reference A;Accession: A;Status: pr A;Molecule t A;Residues:	Matches Qy 1 Db 78 Qy 61 Db 138 Qy 121 Db 198	RESULT 1 T08423 Axin homolog Axil - rat N;Alternate names: Axil C;Species: Rattus norvegi C;Date: 05-Nov-1999 #seq C;Accession: T08423 R;Yamamoto, H.; Kishida, Mol. Cell. Biol. 18, 2867 A;Title: Axil, a member: Z1641 A;Accession: T08423 A;Status: preliminary; tr A;Molecule type: mRNA A;Residues: 1-838 YAM> A;Coss references: EMBL: A;Note: interacts with G; C;Keywords: phosphoprotei		44444333333333333333333333333333333333
ESULT 2 08422 (08422 (08422 (1) Alternate names: rAxx, Species: Rattus norw, Species: 05-Nov-1999 #s.) Accession: T08422 (1) I Accession: T08422 (1) I Accession: T1844 (1) I Axin, a negat, Title: Axin, a negat, Tefarence number: Z1 (1) Accession: T08422 (1) Status: preliminary; (1) MOLecule type: mRNA (1) Refarence number: MRNA (1) Refarence number: Z1 (2) Refarence number: Z1 (3) Residues: 1-832 (IKE)	Ō	SULT 1  Alternate names Species: Rattus Date: 05 Nov-19 Accession: T084 Yamamoto, H.; K J. Cell. Biol. Title: Axil, a Reference numbe Raccession: T084 Status: prelimi Molecule type: 1 Cross-reference Note: Interacts Keywords: phosp Ouery Match		73 72.5 71.5 71.5 71.5 70.5 70.5 70.5
or axin [impose: rAxin ss. rAxin s norvegicus [99] #sequency 422 422 1384, 1998 1 negative reper: Z16413; linary; trans mRNA mRNA	123; CONSETVA TKSILISLIGDQDGA             TKSLHSLLIGDQDGA	Axil - rat names: Axil names: Axil (attus norvegicus (bov-199) #sequenc T08423 H.; Kishida, S.; Liol. 18, 2867-28 Liol. 18, 2867-28 Liol. 19, 2867-28 Liol. 21, 2867-28 Liol.		11111111111111111111111111111111111111
ט מ א מ מ	TOU. Vative  JAYLERTI           SAYLERTI           SAYLERTI  SAYLERTI  PATKTYII  PATKTYII	- rat : Axil norvegicus (Norw porvegicus		1276 1291 382 431 190 1130 1157 268 421 785 798 798 190
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it) 05-Nov-1999 #text ishida, S.; Kikuc) the Wnt signaling 61 GB/EMBL/DDBJ	MO. /. 0e-53; matches 0; matches 0;	sion 05-Nov-1999 sion 05-Nov-1999 , T.; Ikeda, S.; n family, interac 8226558 from GB/EMBL/DDBJ from GB/EMBL/DDBJ nnD:g3080758; PI nd beta-catenin transduction: Score 639; DB 2	ALIGNMENTS	T09204 T09273 E64686 E71475 E711943 T41943 D82923 D82923 T43406 T343406 T343406 T343406 D82293 D82293 D82293
_change 21-Jul-2000 hi, A. pathway, forms a complex wit	Indels 0; Gaps 0;	<pre>change 21-Jul-2000  S.; Asashima, M.; Kikuchi, both glycogen synthase kin 10089.1; PID:g3080759 jth 838;</pre>		probable tail-host probable tail-host myosin-like protei hypothetical protei probable translati major DNA binding DNA-directed RNA p MHC Class I protei cymJ protein - Kle MG349 homolog G12 cullin 3 homolog - hypothetical protei isoleucyl-tRNA syn hypothetical protei translation elonga
rt	•	<b>5</b> `		

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G-0/G-1 switch regulatory protein 8 - human N;Alternate names: helix-loop-helix phosphoprotein; C;Species: Homo sapiens (man) C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #C;Accession: I53020; I65984 C;Siderovski, D.P.; Heximer, S.P.; Forsdyke, D.R.
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R;Druey, K.M.; Blumer, K.J.; Kang, V.H.; Kehrl, J.H.
Nature 379, 742-746, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-355, 'K', 357-519 < DRW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: Inhibition of G-protein-mediated A; Reference number: A58012; MUID: 96178495 A; Accession: S68436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-519 < DRU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data A; Reference number: $78089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Druey,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Date: 04-Dec-1997 t
C; Accession: S78089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G-protein signaling regulator RGS3 - human C; Species: Homo sapiens (man) C; Date: 04-Dec-1997 #sequence_revision 12-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
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                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                              WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKR
                                                                                                                                                                                                                                          YIAIQACKEVNLDSYTREHTKDNL--QSVTRGCFDLAQKRIFGLMEKDSYPRFLRSDLYL 507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMNLKDT---KTLRVAKAI 57
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40; Conserv
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; S68436
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Pred. No. 8.2e-09;
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Pred. No. 7
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No. 7.8e-31;
Mismatches
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                                   #text_change 29-Sep-1999
                                                                  regulator of G-protein signaling
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hypothetical protein F56B6.2 - C:Species: Caenorhabditis elega
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146

KH 147

elegans

Caenorhabditis elegans

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A;Molecule type: mRNA
A;Residues: 1-173 <HUN>
C;Superfamily: B-cell activation protein BL34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RGS10 protein - human
C;Species: Homo sapiens (man)
C;Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary; nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number:
A; Accession: $71812
                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: RGS10 is a selective activator of Galpha(i) GTPase activity A; Reference number: S71812; MUID:96371048
                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Hunt, T.W.; Fields, T.A.; Casey, P.J.; Peralta, E. Nature 383, 175-177, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: S7181
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A:Cross-references: GDB:355647; OMIM:600861
A:Map position: 1q31-1q31
A:Introns: 37/2; 71/2; 92/1; 147/3
C:Superfamily: B-cell activation protein BL34
C:Keywords: phosphoprotein
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A; Cross-references: GB:L13463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:L13391; NID:g292036; PIDN:AAA20680.1; PID:g292037
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A; Residues: 1-211 < RES>
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A;Title: A human gene encoding a putative basic helix-loop-helix phosphoprotein whose A;Reference number: I53020; MUID:94235158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
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                                                                                                                                        1 WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKR 60
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                                                                     YIENNSVVSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDIYL 120
                                                                                                                  WAASLENLLEDPEGVKRFREFLKKEFSEENVLFWLACEDFKKMQDK-TQMQEKAKEIYMT
                                  FL--SSKASSQVNVEGQSRLNEKILEEP-HPLMFQKLQDQIFNLMKYDSYSRFLKSDLFL
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                                                                                                                                                                                                     Similarity
39; Conser
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                                                                                                                                                                                                                        25.0%;
32.0%;
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                                                                                                                                                                                                                      Score 160; DB 2;
Pred. No. 3.7e-08;
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                                                                                                                                                                                                                                                                                                                                                                   sequence not shown;
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C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 *sequence_revision 13-Jan-1995 *text_change 31-Jan-2000
C;Accession: S43436; 156165; S34157
R;Newton, J.S.; Deed, R.W.; Mitchell, E.L.D.; Murphy, J.J.; Norton, J.D.
Biochim. Biophys. Acta 1216, 314-316, 1993
A;Title: A B cell specific immediate early human gene is located on chromosome A;Reference number: S43436; MUID:94060109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:U64599; pTDN:AAB04563.1
A;Experimental source: strain Bristol N2
C;Genetics:
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                                                                                                                                                             A;Gene: GDB:RGS1; IER1; 1R20; IR20; BL34
A;Cross-references: GDB:439178; OMIM:600323
A;Map position: 1q31-1q31
C;Superfamily: B-cell activation protein BL34
C;Keywords: B-cell; phosphoprotein
                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-180,'D',182-196 <HON>
A;Cross-references: GB:S59049; NID:g299704; PIDN:AAB26289.1; PID:g299705
                                                                                                                                                                                                                                                                                                                                                                     A;Title: Isolation and characterization of a novel B cell activation A;Reference number: I56165; MUID:93232596 A;Accession: I56165
                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X73427; NID:g313214; PIDN:CAA51826.1; PID:g313215 R;Hong, J.X.; Wilson, G.L.; Fox, C.H.; Kehrl, J.H. J. H. J. Immunol. 150, 3895-3904, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A; Accession: S43436
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A; Introns: 39/3; 235/2; 259/2; 322/3; 360/2; 405/1; 461/3; 503/2
A; Note: F5686.2
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A; Residues: 1-533 <STE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: Z20957
A; Accession: T31002
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Residues: 1-196 <NEW>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              451 SEFVAEHSPKEVNLDSDTRAATKAAVEAGCKPD----TFALAQSRVEQLMSKDSYRRFL 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59
                                                                                Local Similarity
WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFR--QMNLKDTKTLRVAKAIY 58
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elegans cosmid F56B6
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                                                             3; DB 2; 1
. 6.6e-08;
cches 47;
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Best Local S
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  source: embryo
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A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rosledues: 1-35, 'S', 37-39, 'S', 41-46, 'T', 48-67, 'N', 69-76, 'L', 78-177, 'T', 179-197, 'T', 1
A;Cross-references: EMBL:U27768
A;Experimental source: brain
C;Superfamily: B-cell activation protein BL34
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978221

G-protein signaling regulator RGP4 - human

G-protein signaling regulator RGS4

N;Alternate names: G-protein signaling regulator RGS4

C;Species: Homo sapiens (man)

C;Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #t
                                                                                                                          A; Title: Molecular cloning
A; Reference number: JC7228
A; Accession: JC7228
A; Molecule type: mRNA
A; Residues: 1-181 <SAI>
                                                                                                                                                                                                                                                     G-protein signaling regulator 5 homolog - clawed frog (;Species: Xenopus sp. (clawed frog) C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000 C;Accession: JC7228; PC7066
R;Saltch, O; Odagiri, M; Masuho, I; Nomoto, S; Kinoshita, N. Biochem. Biochem. Biochem. Biophys. Res. Commun. 270, 34-39, 2000
A;Title: Molecular cloning and characterization of Xenopus RGS5.
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Nature 3,746, 1996
A;Title: Inhibition of G-protein-mediated
A;Reference number: A58012; MUID:96178495
                                                             A;Cross-references: DDBJ:AB038436
A;Accession: PC7066
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A; Residues: 1-205 <DRU>
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A; Molecule type: protein A; Residues: 88-168 <SA2>
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R;Druey, K.M.; Blumer, K.J.; Kang, V.H.; Kehrl, J.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----NEFISVQ---ATKEVNLDSCTREETSRNMLEPTITCFDEAQKKIFNLMEKDSYRRF 168
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Pred. No. 1.2e-07;
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C;Comment: This protein has function as a genesis and cell differentiation. C;Superfamily: B-cell activation protein C;Keywords: differentiation; embryo
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A;Molecule type: DNA
A;Residues: 1-284 <FAV>
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A;Experimental source: strain Bristol N2
C;Accession: JC5503
R;Snow, B.E.; Antonio, L.; Suggs, S.; Gutstein, H.B.; Siderovski, D.P. Biochem. Biophys. Res. Commun. 233, 770-777, 1997
B;Title: Molecular cloning and expression analysis of rat Rgs12 and Rg A;Reference number: JC5502; MUID:97312490
A;Accession: JC5503
A;Molecule type: mRNA
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                                                                                                                      G-protein signaling regulator 14 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 05-Nov-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | -|| || : | :|::|| : ::|| || :::
WRDSLEKLLENSYGLSVFQSFLKSEFSEENIEFWMACEDYKKAKSPSKMTTK-AKKIYEE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKR 60
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                                                                                                                                                                                                                                                                                                                                                                                            WAQSFEGLLGNHVGRHHFRIFLRSIHAEENLRFWEAVVEFRSSRHKANAMNNLGKVILST
                                                                                                                                                                                                                                                                                                                                                                                                                             WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKR 60
                                                                                                                                                                                                                                                                                                                         YLAEGTTNEVFLPFGVRQVIERRIQDNQIDITLFDEAIKHVEQVLRNDPYVRFLQSSQYI
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                                                                                                                                                                                                                                                        278
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Pred. No. 1.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-Sep-1999 #text_change 20-Sep-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cosmid C29H12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 284;
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                                                                    Rgs14
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A;Residues: 1-544 <SNO>
A;Residues: 1-544 <SNO>
A;Cross-references: GB:U92279; NID:92088555; PIDN:AAC53175.1; PID:92088556
C;Comment: This protein functions as GTPase activating protein.
F;64-113/Domain: GH1 *status predicted <GH1>
F;117-152/Domain: GH2 *status predicted <GH2>
F;117-152/Domain: GH3 *status predicted <GH3>
F;151-180/Domain: GH3 *status predicted <GH3>
F;514-534/Region: conserved *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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submitted to the EMBL Data Library,
...afarence number: Z19427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-558 <WIL>
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A; Introns: 7/2; 76/1; 129/1; 176/2; 313/2; 364/2;
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A;Experimental source: clone F28C1
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RESULT 13
T21034
T21034
A; Reference number: 219363
Result 13
Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tes
C;Accession: T21034; T21270
R;Gardner, A.
Submitted to the EMBL Data Library, July 1995
A;Reference number: 219363
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Best Local S
Matches 34
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                                                                                                                                                                                                                                                                                                             YIENNSVVSK-QLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDIY 119
                                                                                                                                                                                                                                                                                                                                                  WEDSFEELLADSLGRETLQKFLDKEYSGENLRFWWEVQKLRKCSSRMVPVM--VTEIYNE
                                                                                                                                                                                                                                                                                                                                                                                  WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKR
                                                                                                                                                                                                        KDLV
                                                                                                                                                                                                                                                                           l Similarity
37; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                           19.5%;
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Pred. No. 9.4e-05;
23; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 124.5; DB 2, pred. No. 0.00032;
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                                                                                    15-Oct-1999 #text_change 21-Jul-2000
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A:Map position: X
A:Introns: 16/2; 31/2; 52/1; 91/3
C:Superfamily: B-cell activation protein BL34
                                                                                                                                                           A;Map position: X
A;Introns: 28/2; 43/2; 64/1; 103/3
C;Superfamily: B-cell activation protein BL34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
C;Accession: T21035; T21272
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A;Accession: T21035
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Status: preliminary; translated from A;Molecule type: DNA
A;Residues: 1-169 <WIL>
                                                                                                                                                                                                                                                A;Gene:
                                                                                                                                                                                                                                                                    A; Experimental source: clone F22E10 C; Genetics:
                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:Z67882; PIDN:CAB54230.1; GSPDB:GN00028; CESP:F16H9.1b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:Z50005; PIDN:CAB54219.1; GSPDB:GN00028; CESP:F16H9.1b
A;Experimental source: clone F16H9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-181 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, July 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F16H9.1b - Caenorhabditis elegans
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A;Experimental source: clone F22E10
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A;Residues: 1-169 <WI2>
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                                                                                                                                                                                                                                                                                                                                     Status: preliminary; translated from GB/EMBL/DDBJ; Molecule type: DNA; Mesidues: 1-181 <WIZ>
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                                                  Match 19.0%; Score 121.5; DB (Local Similarity 27.5%; Pred. No. 0.00018) Hes 33; Conservative 25; Mismatches 55
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                                                                                                                                                                                                                                             CESP: F16H9.1b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DFISILSPKEVSLDSRVREIVNTNMGRPSAST--FDEAQNQIYTLMQRDSYPRFLASNIY 155
  WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGF-RQMNLKDTKTLRVAKAIYK 59
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27.5%;
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WSQSFENLMKHRAGQKYFAEFLKGEYSDENILFWQACEELKREKNAE--KIEEKARIIYE 109

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C;Accession: JC5502
C;Accession: JC5502
R;Snow, B.E.; Antonio, L.; Suggs, S.; Gutstein, H.B.; Siderovski, R;Snow, B.E.; Antonio, L.; Suggs, S.; Gutstein, H.B.; Siderovski, R;Snow, Biophys. Res. Commun. 233; 770-777, 1997
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A; Residues: 1-1387 <SNO>
A; Cross-references: GB:U92280; NID:g2088557; PIDN:AAC53176.1; PID:g2088558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem. Biophys. Res. Commun. 233, 770-7777, 1997
A;Title: Molecular cloning and expression analysis of rat Rgs12 and Rgs14. A;Reference number: JC5502; MUID:97312490
A;Accession: JC5502
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 05-Nov-1999
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099211 homo sapien
p57095 brachydanio
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p57096 brachydanio
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.1; hosphorylation.	This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).	YTOPLASMIC. RESSED IN LUNG AND THI LATED BY GSK-3B AND DI RGS DOMAIN. DIX DOMAIN.	INCLUDED CONTROL OF THE WIT SIGNALING PATHWAY. DOWN INFORMATION: INHIBITOR OF THE WIT SIGNALING PATHWAY. DOWN BETA-CATENIN. PROBABLY FACILITATE THE PROSPHORYLATION CATENIN AND APC BY GSK-3B (BY SIMILARITY).  1- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BE AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BE OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CA	-9566905; Uochi T., Ikeda S., Koyama xin family, interacts with d beta-catenin and inhibits	y y pu puence update) notation update) IN 2) (CONDUCTIN) CONDUCTIN) Yertebr Sciurognathi; Mur	ALIGNMENTS PRT; 838 AA.	RGSE_MOUSE E610_CAEEL YUE1_CAEEL YUE1_CAEEL RGSB_HOUAN RGS9_MOUSE RGS9_BOUIN RGSS_BOVIN RGSS_BOVIN RGS9_HUMAN RGSC_HUMAN YKO7_CAEEEL
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RGS.
GSK-3B BINDING SITE (BY SIMILARITY).

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                                                                                       Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

- FUNCTION: INHIBITOR OF THE WINT SIGNLING PATHWAY. DOWN RE BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF CATERIN AND APC BY GSK-3B (BY SIMILARITY).

- ISUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-COCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN TERNARY COMPLEX (BY SIMILARITY).

- ISUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED PP2A (BY SIMILARITY): CONTAINS 1 RGS DOMAIN.

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                                                                                                                                                                                                                                                                                                                                                              Behrens J., Jerchow B.-A., Wuertele M., Grimm J., Wirtz R., Kuehl M., Wedlich D., Birchmeier W.; "Functional interaction of an axin homolog, conducatenin, APC, and GSK3beta."; Science 280:596-599(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Jenkins N.A., Warburton D., Costantini F.;
"Properties of mouse Axin2 and human AXIN2: chromosomal
expression pattern, interaction with Axin and effects on
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AXIN AND BETA-CATENIN
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MBL outstation -
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01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
AXIN 2 (AXIS INHIBITION PROTEIN 2) (CONDUCTIN)
                                    SEQUENCE FROM N.A.
TISSUE-Brain, and Lymphoblast;
Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G.,
Jenkins N.A., Warburton D., Costantini F.;
"Properties of mouse Axin2 and human AXIN2: chromosomal location,
                                                                                                                                                       Mai M., Qian C., Yokomizo A., "Cloning of the human homolog chromosome 17q23-q24."; Genomics 55:341-344(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HUMAN
AXN2_HUMAN
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                    expression pattern,
                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=99168905;
                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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AAF22800.1;
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Primates;
                    interaction with Axin and
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BETA-CATENIN BINDING SITE (BY
SIMILARITY).
POLY-HIS.
DIX.
R -> K (IN REF. 2).
H -> Y (IN REF. 2).
S -> P (IN REF. 2).
S -> A (IN REF. 2).
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Pred. No. 8.2
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4 -> Y (IN REF. 2).
5 -> P (IN REF. 2).
5 -> S (IN REF. 2).
6 -> A (IN REF. 2).
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RESULT 4

AXN2_BRARE
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Best Local Sim
Matches 118;
               AXN2_BRARE
P57095;
01-OCT-2000
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Developmental protein; Phosphorylation.
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EMBL; AF205888; AAF22799.1;
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SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN
OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.
TENNAY COMPLEX (BY SIMILARITY).
SUBCELLULAR LOCATION: CYTOPLASMIC.
TISSUE SPECIFICITY: EXPRESSED IN BRAIN AND LYMPHOBLAST.
PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: CONTAINS 1 RGS DOMAIN. SIMILARITY: CONTAINS 1 DIX DOMAIN.
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(Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation updats
S INHIBITION PROTEIN 2).
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MISSING
P -> S (
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BETA-CAPENIN BINDING SITE (BY
SIMILARITY).
POLY-HIS.
DIX.
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Pred. No. 2.1e-51;
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Q -> R (IN REF. 2).
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 RESULT 5
AXN1_BRARE
ID AXN1_B
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Bae V.-K., Hibi M., Hirano T.;

Bae V.-K., Hibi M., Hirano T.;

"Cooperative roles of Bozozok/Dharma and Nodal-related protein formation of the dorsal organizer in zebrafish.";

Mech. Dev. 91:293-303(2000).

-I- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN.

BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION O

CATENIN AND APC BY GSK-3B (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

-I- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYL

PP2A (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
NCBI_TaxID=7955;
AXN1_BRARE STANDARD; PRT; 835 AA P57094; 01-OCT-2000 (Rel. 40, Created) 01-OCT-2000 (Rel. 40, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation updat AXIN 1 (AXIS INHIBITION PROTEIN 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00615; RGS; 1. Pfam; PF00778; DIX; 1. PROSITE; PS50132; RGS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=20171051; PubMed=10704853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000342; ...
InterPro; IPR001158; -.
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BETA-CATENIN BIN
SIMILARITY).
POLY-SER.
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Pred. No. 2.2e-45;
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BINDING SITE (BY
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AXIN (AXIS INHIBITION E
AXIN OR AXN.
                                                                                             XENLA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cooperative roles of Bozozok/Dharma and Nodal-related proteins in the formation of the dorsal organizer in zebrafish.;

Mech. Dev. 91:293-303(200).

-i- FUNCTION: INHIBITOR OF THE WNT SIGNALING PARTHWAY. DOWN REGULATES BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-CATENIN AND APC BY GSK-3B (BY SIMILARITY).

-i- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB032262; HSSP; P49799; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shimizu T., Yamanaka Y., Ryu
Bae Y.-K., Hibi M., Hirano T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50132; RGS; Developmental protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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SIMILARITY: CONTAINS 1 RGS DOMAIN.
SIMILARITY: CONTAINS 1 DIX DOMAIN.
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                                                                                                                                                                                                                                                     IYLEY 213
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                                                                                                                                                                                                    KKYILDNNGIVSRQIKPATKSFIKDCVMKLHIDPAMFDQAQTEIQTMMEENTYPLFLKSD
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PROTEIN) (XAXIN).
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Phosphorylation.
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GSK-3B BINDING S
BETA-CATENIN BII
SIMILARITY).
DIX.
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Best Local
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O70239;
01-OCT-2000 (Rel. 40, C
01-OCT-2000 (Rel. 40, I
01-OCT-2000 (Rel. 40, I
AXIN 1 PROTEIN (AXIS IN
                                                                                         _RAT
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Hedgepeth C.M., Deardorff M.A., Klein
"Xenopus axin interacts with glycogen
expressed in the anterior midbrain.";
                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entities requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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PROSITE; PS50132; RGS; 1.
Developmental protein; Phosphorylation.
Developmental protein; Phosphorylation.
B8 211 RGS.
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HSSP; P49799; lAGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam;
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InterPro; IPR001158; -.
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FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-CATENIN AND APC BY GSK-3B (BY SIMILARITY).

SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

DEVELOPMENTAL STAGE: WEAKLY AND UBLOITOUSLY EXPRESSED THROUGHOUT EARLY DEVELOPMENT, AND HIGHLY EXPRESSED IN THE ANTERIOR MESSINCEPHALON ADJACENT TO THE FOREBRAIN-MIDBRAIN BOUNDARY.

PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PP2A (BY SIMILARITY).
SIMILARITY: CONTAINS 1 RGS DOMAIN.
SIMILARITY: CONTAINS 1 DIX DOMAIN.
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                                                                                                                                                                             DIYLEY
                                                                                                                                                                                                          YKKYVLDSNGIVSRQIKPATKSFIKDCVLRQQIDPAMFDQAQMEIQSMMEDNTYPVFLKS
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                                                                                                                                                                                                                                                                  DIYLEY
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                                                                                                                                                                                                                                                                                                                                            Similarity
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842 AA;
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434
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94459
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    , Last sequence update)
, Last annotation update)
INHIBITION PROTEIN 1) (R
                                                Created)
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                                                                                                                                                                                                                                                                                                                               Score 420; DB 1; I
Pred. No. 3.6e-32;
5; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                     DIX.
                                                                                                                                                                                                                                                                                                                                                                                                                               GSK-3B BINDING SITE (BY SIMILARITY).
BETA-CATENIN BINDING SITE (BY
SIMILARITY).
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(RAXIN)

(FRAGMENT).

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RESULT 8
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A Ikeda S., Kishida S., Yamamoto H., Murai H., Koyama S., Kikuchi A.;

A Ikeda S., Kishida S., Yamamoto H., Murai H., Koyama S., Kikuchi A.;

A Taxin, a negative regulator of the Wnt signaling pathway, forms a

complex with GSK-3beta and beta-catenin and promotes GSK-3beta-

A Templex with GSK-3beta and beta-catenin.*;

dependent.phosphorylation of beta-catenin.*;

LEMBO J. 17:1371-1384 (1998)

C -I- FUNCTION. INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES

C BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-

CATENIN AND APC BY GSK-3B AND BETA-CATENIN. THE INTERACTION

C CATENIN AND BETA-CATENIN OCCURS VIA THE ARMADILLO REPEATS

C CONTAINED IN BETA-CATENIN, TERNARY COMPLEX. ALSO BINUS TO

CONTAINED IN GAMMA-CATENIN). APC, DVL AND PP2A (BY SIMILARITY).

C -I- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

C -I- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS, THYMUS AND LUNG

FOLLOWED BY CEREBRUM, CEREBELLUM, HEART, KIDNEY, SKELETAL MUSCLE,

C SPLEEN AND LIVER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 78; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF017756; AAC40066.1; ALT_INIT. HSSP; P49799; LAGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Developmental protein; Phosphorylation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AXIN1 OR AXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50132; RGS; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                      151
                                                                                                                                                                                                                                                                                                      58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PP2A (BY SIMILARITY).
SIMILARITY: CONTAINS 1 RGS DOMAIN.
SIMILARITY: CONTAINS 1 DIX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPLEEN AND LIVER.
                                                                                                                                                                                       DIYLEY 122
                                                                                                                                                                                                                                                                                                                                                                      WAESLHSLLDDQDGISLFRTFLKQEGCADLLDFWFACSGFRKLEPCDSNEEKRLKLARAI 210
                                                                                                                                                                                                                                                                                                                                                                                                                            WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMNLKDT---KTLRVAKAI 57
                                                                                                                           DIYLEY 276
                                                                                                                                                                                                                                                                                                   YKRYI-ENNSVVSKOLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTS 116
                                                                                                                                                                                                                                             YRKYILDSNGIVSRQTKPATKSFIKDCVMKQQIDPAMFDQAQTEIQSTMEENTYPSFLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00778; DIX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR000342; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          277
498
567
893
99188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MΨ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 407; DB 1;
Pred. No. 6.4e-31;
1; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RGS.
GSK-3B BINDING SITE.
BETA-CATENIN BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3CCBD2224EDD384C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 893;
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214 WAESLHSLIDDQDGISLFRTFLKQEGCADLLDFWFACSGFRKLEPCDSNEEKRLKLARAI 58 YKRYI-ENNSVVSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTS 116

273

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                                                            Query Match
Best Local Similarity
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01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
AXIN 1 (AXIS INHIBITION PROTEIN 1) (FUSED PROTEIN) (FRAGMENT)
AXIN 1 (AXIS INHIBITION PROTEIN 1) (FUSED PROTEIN)
                                                                                                                           VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: INHIBITOR OF THE MNT SIGNALING PATHWAY. DOWN REGULATES BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-CATENIN AND APC BY GSK-3B (BY SIMILARITY).

-!- SUBUNTT: INPERACTS WITH GSK-3B AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN. TERNARY COMPLEX. ALSO BINDS TO PLAKOGLOBIN (GAMMA-CATENIN). APC, DVL AND PP2A (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING.

-!- FIRSUE SPECIFICITY: EXPRESSED IN EMBRYONIC STEM CELLS.

-!- DEVELOPMENTAL STAGE: WIDELY EXPRESSED AT E10.5 TO E16.5 DAY.

-!- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
                                                                                                                                                                                                                                                 Pfam;
                                                                                                                                                                                                                                                                                                                                     MGD; MGI:1096327; Axin.
InterPro; IPR000342; -.
InterPro; IPR001158; -.
                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF009011; AAC HSSP; P49799; 1AGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pathway that regulates embryonic axis formation."; Cell 90:181-192(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L. III,
Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.;
"The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AXN1_MOUSE
                                                                                                                                                             DOMAIN
                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090
                                                                                                                                                                                           DOMAIN
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                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                            DOMAIN
1 WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMNLKDT---KTLRVAKAI 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: CONTAINS 1 RGS DOMAIN. SIMILARITY: CONTAINS 1 DIX DOMAIN.
                                                                                                                                                                                                                                                                                                                        PF00615; RGS;
                                                                                                                            860
992
                                               Conservative
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109917
                                                                                                                                                                                           340
561
630
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Rodentia;
                                                            63.7%;
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                                               Score 407; DB 1; 1
Pred. No. 7.2e-31;
1; Mismatches 23;
                                                                                                                                                                        GSK-3B BINDING SITE (BY SIMILARITY).
BETA-CATENIN BINDING SITE (BY
SIMILARITY).
                                                                                                                            MISSING (IN ISOFORM 2).
N; 70EEB53D387BD26F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                           Length 992,
                                                Indels
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Matches
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Anterpro; ipR001150,
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Anterpro; ipR001150,
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Anterpro;
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01-OCT-2000 (Rel. 40, Last sequence up
01-OCT-2000 (Rel. 40, Last annotation
AXIN (AXIS INHIBITION PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF009012;
HSSP; P49799; 1
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MEDLINE-97373830; PubMed-9230313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AXIN OR AXN.
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                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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   85
                                                                                                                                                                                          Local
                                                                                                                                                                                                                              Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PP2A (BY SIMILARITY).
SIMILARITY: CONTAINS 1 RGS DOMAIN.
SIMILARITY: CONTAINS 1 DIX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGUL BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BET CATENIN AND APC BY GSK-3B (BY SIMILARITY).

SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

DEVELOPMENTAL STAGE: EXPRESSED AT STAGE 12 TO 15.

PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMN---LKDTKTLRVAKAI 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        way that regulates embryonic axis formation."; 90:181-192(1997).
   WAESLHSLLDDQDGINLFRTFLKQEDCADLLDFWFACSGFRKLEPCVSNEEKRLKLAKAI 144
                                                                                                                                                  Similarity 61.77; Conservative
                                                                                                                                                                                                                                                                                                                                             759
841 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC60245.1;
                                                                                                                                                                                                                                                                                                                                                     841
94931
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                                                                                                                                                                                          63.5%;
                                                                                                                                                                                                                                                                                                                                                     ₩;
                                                                                                                                                          22;
                                                                                                                                              Score 406; DB Pred. No. 7.5e 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        GSK-3B BINDING SITE (BY SIMILARITY).
BETA-CATENIN BINDING SITE (BY
SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                     400D0C90E72506FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
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                                                                                                                                                                                          DB 1;
.5e-31;
                                                                                                                                                          23;
                                                                                                                                                                                                                              Length 841;
                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGULATES
                                                                                                                                                          4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BETA-
                                                                                                                                                      Gaps
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Вb
                                      RESULT 10
AXN1_HUMAN
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                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
AXIN 1 (AXIS INHIBITION PROTEIN 1) (HAXIN) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AXN1_HUMAN
015169;
                                                                                                         NON_TER
                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J.,
Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97373830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AXIN1 OR AXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145
                                      SEQUENCE
                                                   DOMAIN
                                                                               DOMAIN
                                                                                                                                                                            InterPro; IPR000342; -.
InterPro; IPR001158; -.
Pfam; PF00615; RGS; 1.
                                                                                                                                                                                                                       MIM; 603816;
                                                                                                                                                                                                                                   HSSP;
                                                                                             DOMAIN
                                                                                                                                     Developmental protein;
                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205 DIYLEY 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BETA CATENIN. PROBABLY FACILIATION.

BETA CATENIN AND APC BY GSK-3B.

GATENIN AND APC BY GSK-3B.

GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)

SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)

AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN

OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.

OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN GAMMA-CATENIN),
                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: CONTAINS 1 RGS DOMAIN. SIMILARITY: CONTAINS 1 DIX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: CYTOPLASMIC. TISSUE SPECIFICITY: UBIQUITOUSLY E PTM: PROBABLY PHOSPHORYLATED BY GS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YKKYILDNNGIVSRQIKPATKSFIKDCVMKLQIDPDMFDQAQTEIQCMIEDNTYPLFLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DIYLEY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YKRYI-ENNSVVSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTS
                                                                                                                                                               PF00778; DIX; 1.
                                                                                                                                                                                                                                   AF009674; AAC51624.1; P49799; 1AGR.
                                                                                                                                                  PS50132; RGS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DVL AND PP2A.
                                        900
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                                   AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=9230313;
                                        900
99803

    Phosphorylation.

                                         ₩.
                                      RGS.
GSK-3B BINDING SITE (BY SIMILARITY).
BETA-CATENIN BINDING SITE (BY
SIMILARITY).
DIX.
EE5F990B11FC7B3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                 GSK-3B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M., Costantini F.;
an inhibitor of the Wnt signaling
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                                                                                                                                                                                                                                                                                                                                                                                                                                               EXPRESSED
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Length 900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perry W.L. III,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOWN REGULATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116
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Query Match Best Local

Similarity

62.8%; 62.7%;

Score Pred.

401; No.

L; DB 1; . 2.4e-30;

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Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                           MIM; 00--
Interpro; IPROUUS...,
Interpro; IPROUUS...,
Pfam; PFO0615; RGS; 1.
PRINTS; PRO1301; RGSPROTEIN.
PROTITE; PS50132; RGS; 1.
PROTITE; PS50132; RGS; 1.
PROTITE; PS50132; RGS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JLT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
REGULATOR OF G-PROTEIN SIGNALING 3 (RGS3) (RGP3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDILINE=96178495; PubMed=8602223;

Druey K.M., Blumer K.J., Kang V.H.,

"Inhibition of G-protein-mediated MA

mammalian gene family.";

Nature 379.742-746(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U27655; AAC50394.1; -. HSSP; P49799; 1AGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RGS3_HUMAN P49796;
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117
     121
                                                  450
                                                                                                                                                 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 YRKYILDNNGIVSRQTKPATKSFIKGCIMKQLIDPAMFDQAQTEIQATMEENTYPSFLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 WAESLHSLLDDQDGISLFRTFLKQEGCADLLDFWFACTGFRKLEPCDSNEEKRLKLARAI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEIR INACTIVE GDP-BOUND FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS 1 RGS DOMAIN.
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       EYV
                                                                                                                                            YKRYI-ENNSYVSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTS
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                                                  YIAIQACKEVNLDSYTREHTKDNL--QSVTRGCFDLAQKRIFGLMEKDSYPRFLRSDLYL
                                                                                                YIENNSVVSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDIYL 120
                                                                                                                                                                                                                                               60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79;
                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                    519 AA;
                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                    56601 MW;
                                                                                                                                                                                                                                                                 27.0%;
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                                                                                                                                                                                                                                                                                                                                              RGS.
; F1CFE3F27D4673A0 CRC64;
                                                                                                                                                                                                                                                                      Score 172.5;
Pred. No. 4.
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AP kinase activation
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                                                                                                                                                                                                                                                                      4.5e-09;
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                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                               56;
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                                                                                                                                                                                                                                                                                           Length 519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                  507
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                                                                                              RESULT 12
RRGS2_HRGS2_HRGS2_HRGS2_HRGS2_HRGS2_HRGS2_HRGS2_O O1-FEB
DT 01-FEB
DNA CC
MADDIIN
RA MINGE
RT 100A CC
RN MEDLIN
RA MINGE
RT 1031."
RT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  맑
Query.Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene, (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RGS2 OK GODGE (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Eukaryota; Metazoa; Primates;
                                                                                                                                                                                                                                                         EMBL; AL035407; CAB62512.1; -. HSSP; P49799; lAGR. MIM; 600861; -.
                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
REGULATOR OF G-PROTEIN SIGNALING 2 (RGS2) (G0/G1 SWITCH REGULATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wu H.-K., Heng H.H., Shi X.-M., Forsdyke D.R., Tsui L.-C., Mak T.W. Minden M.D., Siderovski D.P.; minden M.D., Siderovski D.P.; "Differential expression of a basic helix-loop-helix phosphoprotein gene, GOS8, in acute leukemia and localization to human chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A human gene encoding a putative basic helix-loop-helix phosphoprotein whose mRNA increases rapidly in cycloheximide-treated blood mononuclear cells.";

DNA Cell Biol. 13:125-147(1994).
                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHARACTERIZATION.
MEDLINE-95371353; Pubmed-7643615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RGS2_HUMAN
                                                                                                                                                                     PRINTS; PR01301; RGSPROTEIN. PROSITE; PS50132; RGS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bagguley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-94235158; PubMed-8179820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leukemia 9:1291-1298(1995)
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                                                                                                                                              ignal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO THEIR INACTIVE GDP-BOUND FORM. MAY PLAY A ROLE IN LEUKEMOGENESIS. TISSUE SPECIFICITY: EXPRESSED IN ACUTE MYELOGENOUS LEUKEMIA (AML) AND IN ACUTE LYMPHOBLASTIC LEUKEMIA (ALL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: CONTAINS 1 RGS DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTM: COULD BE PHOSPHORYLATED. MIGHT BE FUNCTIONALLY REGULATED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN KINASE(S)
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                                                                                                                                                                                                                   Pro; IPR000342; -. PF00615; RGS; 1.
                                                                                                                                                                                                                                                                                                                                           L13391; AAA20680.1; -.
L13463; AAC37587.1; -.
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                                                                                              83
211 AA;
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                                                                                                                            199
                                                                                                24382 MW;
                                                                                                                                            inhibitor;
  32
32
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8 8
                                                                                                                            RGS
Pred. No. 4.8e-09;
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                                                                                                                                              Cell cycle;
                                                                                                   EFFE4AE47EF9AD8F CRC64;
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                         DB 1;
                                                                                                                                                 Phosphorylation.
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                         Length
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RESULT 14
RGSA_HUMAN
ID RGSA_H
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
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01-NOV-1997 (Rel. 35, Last annotation update)
01-CCT-2000 (Rel. 40, Last annotation update)
REGULATOR OF G-PROTEIN SIGNALING 2 (RGS2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    008849;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:1098271; Rgs2.
InterPro; IPR000342; -.
Pfam; PF00615; RGS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RGS2_MOUSE
    RGSA_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97236828; PubMed=9079700;
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                                                                                                                                                                                                                                                           WTKSLHSLIGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKR 60
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                                                                                                                                                                    YIENNSVVSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDIY 119
                                                                                                                       FIEKEAPKEINIDFQTKSLIAQNI--QEATSGCFTTAQKRVYSLMENNSYPRFLESEFY 195
                                                                                                                                                                                                                   WAEAFDELLASKYGLAAFRAFLKSEFCEENIEFWLACEDFKKTK-SPQKLSSKARKIYTD 138
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31.9%;
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Q9V407; Q9XYC1;

Q1-QCT-2000 (Rel. 40, C
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01-OCT-2000
                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR01301; RGSPROTEIN. PROSITE; PS50132; RGS; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RGS10
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                                                      Ephydroidea; Drosophilidae; Drosophila
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RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
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RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu An. H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Barokstein P., Brottler P.,
RA Borkova D., Botchan M.R., Bouck J., Barokstein P., Brottler P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gebat S., Downes M., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbat W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibeywam C.,
RA Hartis N.L., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Llang Y., Lin X.,
RA Herkulov G., Milshina N.V., Mobarry C., Morris J., Molberson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Molberson D.,
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RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Virskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
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RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
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RA Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
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Development 126:4165-4173(1999).

-I- FUNCTION: INHIBITOR OF THE WG SIGNALING PATHWAY. DOWN REGULATES BETA-CATENIN (ARMADILLO-ARM). PROBABLY FACILITATE THE
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Suzuki A., Fujita F., Shibuya H., Toyoshima K., Ueno N., Akiyama T
"Negative regulation of Wingless signaling by D-axin, a Drosophila
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Science 283:1739-1742(1999).
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SUBUNIT: INTERACTS WITH ZW3 AND ARM. THE INTERACTION BETWEEN AXN AND ARM OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN ARM. SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY), DEVELOPMENTAL STAGE: UBIQUITOUSLY EXPRESSED THROUGHOUT THE
                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION OF BETA-CATENIN AND APC BY GSK-3B (ZESTE-WHITE
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POLY-SER.
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R -> Q (IN REF. 1).
MISSING (IN REF. 1).
; 31A502528CEE84BA CRC64;
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Listing first 45 summaries
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2: sp_bacteria
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177.851 Million cell updates/sec
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09uh84 homo sapien
09y2t1 homo sapien
09y2t1 homo sapien
09y990 xenopus lae
070239 rattus norv
035625 mus musculu
042400 gallus gall
015169 homo sapien
09ptp2 xenopus lae
09ns28 homo sapien
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Best Local Similarity
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01-AUG-1998 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=98226558; PubMed=9566905;
Yamamoto H., Kishida S., Uochi T., Ikeda S., Koyama S., Asashima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRODOM; PD001580; -; 1.
PRODOM; PD003639; -; 1.
SEQUENCE 838 AA; 92947 MW; 45B825C13BA07F37 CRC64;
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INTERPRO; IPR001158; -.
PFAM; PF00615; RGS; 1.
PFAM; PF00778; DIX; 1.
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Mol. Cell. Biol. 18:2867-2875(1998).
EMBL; AF017757; AAC40089.1; -.
HSSP; P49799; LAGR.
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61 YIENNSVVSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDIYL 120
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                                                                                                                  Conservative
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Best Local Similarity
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INTERPRO; IPR000342; -.
INTERPRO; IPR001158; -.
PFAM; PF00615; RGS; 1.
PFAM; PF00778; DIX; 1.
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01-NOV-1998
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Q9QXJ6;
01-MAY-2000
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Eukaryota; Metazoa; C
Mammalia; Eutheria; R
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                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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   Zhang T.,
                    SEQUENCE FROM N.A
                                                   NCBI_TaxID=10090;
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     Fagotto F.,
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ilarity 100.0%;
Conservative (
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Rodentia;
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      Hsu
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Pred. No. 7.8e-53;
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      Zeng
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PFAM; PF00778; DIX; 1.
PRINTS; PR01301; RGSPRO
SEQUENCE 840 AA; 928
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01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (NOV-1999) to the EMBL; AF205889; AAF22800.1; HSSP; P49799; 1AGR.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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PFAM; PF00778; DIX;
PRINTS; PR01301; RGS
                                                                                                                                                                                                                                             Submitted (NOV-1999) to the EMBL/GenBank/DDBJ EMBL; AF205888; AAF22799.1; -. HSSP; P49799; lAGR.
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YIENNSVVSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDIYL
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118; Conserv
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A; 92896 MW;
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A; 86857 MW;
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Pred. No. 1.5e-52;
1; Mismatches 0
                                                                                                     Score 624; DB 4;
Pred. No. 1.9e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                         Mismatches
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Best Local
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INTERPRO; IPRO01158; -.
PFAM; PF00615; RG; 1.
PFAM; PF00778; DIX; 1.
SEQUENCE 843 AA; 9355;
                                                                                                                                                                                                                                                                                                             09YGY0
09YGY0;
01-MAY-1999
01-MAY-1999
01-OCT-2000
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Q9Y2T1;
01-NOV-1999
MEDLINE=99173782; PubMed=10072781;
Hedgepeth C.M., Deardorff M.A., Klein
"Xenopus axin interacts with glycogen
expressed in the anterior midbrain.";
Mech. Dev. 80:147-151(1999).
                                                                                                                                                                                        Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Amphibla; Batrachia; Anura; Mesobatrachia; Pipoidea;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mai M., Qian C., Yokomizo A., "Cloning of the human homolog chromosome 17q23-q24.";
                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                           AXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomics 55:341-344(1999).
EMBL; AF078165; AAD20976.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P49799; 1AGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-99168905; PubMed-10049590;
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PFAM; PF00778; DIX; 1.
PRODOM; PD001580; -; 1.
PRODOM; PD003339; -; 1.
SEQUENCE 842 AA; 94459 M
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O702339;
01-AUG-1998 (TrEMBLTel. 0
01-AUG-1998 (TrEMBLTel. 0
01-OCT-2000 (TrEMBLTel. 1
                                                                                                                                                                                                                                                                                                                                                                                                    INTERPRO; IPRO00342; -.
INTERPRO; IPRO01158; -.
PFAM; PF00615; RGS; 1.
PFAM; PF00778; DIX; 1.
PRODOM; PD001580; -; 1.
PRODOM; PD003639; -; 1.
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EMBL; AF017756; AAC40066.1;
HSSP; P49799; lAGR.
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                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                Local Similarity 61.9 tes 78; Conservative
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61.1%;
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SEQUENCE FROM N.A.

MEDLINE=99151361; PubMed=9482734;

Ikeda S., Yamamoto H., Murai H., Kishida S., Kikuchi A.;

Ikeda S., Yamamoto H., Murai H., Kishida S., Kikuchi A.;

"Axin, a negative regulator of the Wnt signaling pathway,

complex with GSK-3beta and beta-catenin and promotes GSK-
dependent phosphorylation of beta-catenin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 YKKYVLDSNGIVSRQIKPATKSFIKDCVLRQQIDPAMFDQAQMEIQSMMEDNTYPVFLKS 204
                                                                                                             1 WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMNLKDT---KTLRVAKAI 57
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YKRYI-ENNSVYSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WAESLHSLLDDQDGIHLFRTFLQQENCADLLDFWFACSGFRKLEPNDSKVEKRLKLAKAI 144
                                          YKRYI-ENNSVVSKQLKPATKTYIRDGIKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTS
                                                                                       WAESLHSLLDDQDGISLFRTFLKQEGCADLLDFWFACSGFRKLEPCDSNEEKRLKLARAI
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Pred. No. 5.9e-32;
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Pred. No. 1e-30;
                                                                                                                                                                                                                                                                                                 B489504C7E594347 CRC64;
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[1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-97373830; PubMed-9230313;
Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perry
Zeng L., Fagotto F., Zhang T., Gumbiner B.M., Costantini F.
III Lee J.J., Tilghman S.M., Gumbiner B.M., an inhibitor of the
                                                                                                                                                                                                                                                                                                                                                             01-JAN-1998
01-JAN-1998
01-OCT-2000
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"The mouse Fused locus encodes Axin, an inhibitor of the pathway that regulates embryonic axis formation.";
Cell 90:181-192(1997).
EMBL; AFORGANIT.
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                                                                                                                                                                                                                                           Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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PFAM; PF00778; DIX; 1.
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HSSP; P49799; lAGR.
MGD; MGI:1096327; Axin.
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MEDLINE=97373830; PubMed=9230313;
Zeng L., Fagotto F., Zhang T., Hs
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01-OCT-2000
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(TremBLrel. 05, Last seq
(TremBLrel. 15, Last ann
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61.9%;
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Last annotation update)
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Pred. No. 1.2e-30;
1; Mismatches 23;
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; Murinae; Mus
                                                                                                   Perry W.L.,
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                            EMBL; AF009677; AACS1624.1; -
HSSP; P49799; 1AGR.
INTERPRO; IPRO01342; -.
INTERPRO; IPRO01158; -.
PFAM; PF00615; RGS; 1.
PFAM; PF00778; DIX; 1.
PRINTS; PR01301; RGSPROTEIN.
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015169;
01-JAN-1998
01-JAN-1998
01-OCT-2000
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MEDLINE=97373830; PubMed=9230313;
Zeng L., Fagotto F., Zhang T., Hs
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pathway that regulates embryonic axis Cell 90:181-192(1997)
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                                                                                         WTKSLHSLLGDQDGAYLFRTFLEREKCVDTLDFWFACNGFRQMNLKDT---KTLRVAKAI
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YRKYILDNNGIVSRQTKPATKSFIKGCIMKQLIDPAMFDQAQTEIQATMEENTYPSFLKS
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77; Conserv
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B (TrEMBLrel. 05,
O (TrEMBLrel. 15,
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62.7%;
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Last annotation updat
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Pred. No. 4.2e-30;
17; Mismatches 26
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Pred. No. 1.3e-30;
Pred. No. 23;
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122

Best Local Similarity

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RESULT 12
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ID 09NS28
AC Q9NS28
AC Q9NS28
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DT 01-OCT
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DT 01-OCT
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RN [1]
RP SEQUEN
RA Zhang
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Best Local
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                                                                                                                                           Q9NS28 PRELIMINARY; PRT; 235 AA.
Q9NS28;
Q1-QCT-2000 (TrEMBLrel. 15, Created)
Q1-QCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-QCT-2000 (TrEMBLrel. 15, Last annotation update)
REGULATOR OF G-PROTEIN SIGNALING 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9PTP2;
SEQUENCE FROM N.A.

Zhang W., Wan T., Yuan Z., He L., Cao X.;
"A novel regulator of G-protein signaling.";
"A novel regulator of the EMBL/GenBank/DDBJ
EMBL; AF076642; AAF80227.1;
SEQUENCE 235 AA; 27582 MW; 973ABDE8EC7DE3D
                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=OVARY;
Itoh K., Antipova A., Ratcliffe M., Sokol S.;
"Dishevelled transduces a signal by displacing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (APR-1999) to the EMBL; AF140243; AAF22574.1; INTERPRO; LPRO00342; -...INTERPRO; LPRO001158; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 DIYLEY
||||||
| 111|||
| 242 DIYLEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complex.";
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                                                                                           NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                     WTKSLHSLLGDQDGAYLFRTFLEREKCYDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKR 60
                                                                                                                                                                                                                                                                                                                                                                                           WGRSLNLLLDDQDGATLFRMYLEGEGLGDLLTFWFACNGFRAMDPLEPKTSKTAKAIYRW 128
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Pred. No. 5e-24;
  973ABDE8EC7DE3D5
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                                                                                                                                                            update)
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                           databases
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  CRC64;
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; Pipidae;
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Query Match

29

Score 186.5;

BB

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RESULT
Q9JL22
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Best Local S
Matches 39
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                                                             Q9JL22 PRELIMINARY; PRT; 297 AA.
Q9JL22;
Q0JL22;
Q1-CCT-2000 (TrEMBLrel. 15, Created)
Q1-CCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-CCT-2000 (TrEMBLrel. 15, Last annotation update)
Q1-CCT-2000 (TrEMBLrel. 15, Last annotation update)
REGULATOR OF G-PROTEIN SIGNALING 3 (FRAGMENT).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae.
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Q9JL23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "RGS molecule expression in murine B lymphocytes and regulate chemotaxis to lymphoid chemokines.";
J. Inmunol. 164:4720-4729(2000).
EMBL; AF215669; AAF34626.1; -.
SEQUENCE 192 AA; 22501 MW; BE66E0C1FE07952F CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
REGULATOR OF G-PROTEIN SIGNALING 3S.
SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-EMBRYO;
MEDLINE-20243574; PubMed=10779778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-KIDNEY;
MEDLINE-20243574; PubMed-10779778;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                    NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                             FIAIQACKEVNLDSYTREHTKENL--QSITRGCFDLAQKRIFGLMEKDSYPRFLRSDLYL
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25; Mismatches 43
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Pred. No. 1.3e-08;
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thi; Muridae;
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DP 01-OCT
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Search completed: June
Job time: 442 sec
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Best Local Similarity
Matches 39; Conserv
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"RGS molecule expression in murine B lymphocytes and ability to down-regulate chemotaxis to lymphoid chemokines.";
J. Immunol. 164:4720-4729(2000).
EMBL; AF215670; AAF34627.1; ...
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Q9JHXO;

Q9JHXO;

Q1-CCT-2000 (TrEMBLrel. 15, Created)

Q1-CCT-2000 (TrEMBLrel. 15, Last sequence update)

Q1-CCT-2000 (TrEMBLrel. 15, Last annotation update)

Q1-CCT-2000 (TrEMBLrel. 15, Last annotation update)

REGULATOR OF G-PROTEIN SIGNALING PROTEIN 2.

Rattus norvegicus (Rat).

Eukharyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Rattus.

MCBL_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-SPRAGUE DAWLEY; TISSUE-THORACIC AORTA SMOOTH MUSCLE;
STRAIN-SPRAGUE DAWLEY; TISSUE-THORACIC AORTA SMOOTH MUSCLE;
STRAIN-SPRAGUE DAWLEY; TISSUE-THORACIC AORTA SMOOTH MUSCLE.";
"RGS2 regulates angiotensin II signaling in vascular smooth muscle.";
"RGS2 regulates angiotensin II signaling in vascular smooth muscle.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF279918; AAF85981.1; -.
EMBL; AF279918; AAF85981.1; -.
EMBL; AF279918; AAF85981.1; -.
SEQUENCE 211 AA; 24323 MW; 84B5525CB41EA964 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 WSESLEKLILHKYGLEVFQAFIRTEFSEENLEFWLACEDFKKVK-SQSKMAAKAKKIFAE 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228 FIAIQACKEVNLDSYTREHTKENL--QSITRGCFDLAQKRIFGLMEKDSYPRFLRSDLYL 285
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                                                                                                                                                                                                                                                                            26.1%; Score 166.5; DB 11; Length 211; ilarity 32.8%; Pred. No. 1.8e-08; Conservative 19; Mismatches 58; Indels 3;
                           7,
                           2001, 02:09:39
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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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272
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/SIDS2/gcgdata/geneseq/geneseqp/AA198B.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp/AA198DAT:*
/SIDS2/gcgdata/geneseq/geneseqp/AA199D.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp/AA190D.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp/aa1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp/aa1982.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp/aa1983.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

11	10	9	80	7	σ	v	4	ω	2	н	Result
57	57	57	58	61.5	65	65	141.5	142.5	272	272	Score
21.0	21.0	21.0	21.3	22.6	23.9	23.9	52.0	52.4	100.0	100.0	Query Match Length DB
260	260	115	1816	995	463	462	900	992	840	840	Length
21	21	21	21	20	15	16	20	20	20	20	: B :
G61383	G56044	в27999	Y95440	Y04658	R48084	R78230	W96264	W96265	W93569	W93570	SUMMARIES
Arabidopsis thalia	Arabidopsis thalia	Human secreted pro	Caenorhabditis ele	L.lactis HsdR subu	C. antartica lipas	Candida antarctica	Human axin. Homo	Murine axin. Mus	Human conductin pr	Human conductin pr	IES Description

45	44	43	42	41	40	39	38	37	36	35	34	ω u	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12
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149	2234	803	7,22	478	422	1047	1257	908	900	758	453	406	406	406	406	406	406	406	347	824	626	439	267	578	398	856	349	535	534	321	321	306	306
14	21	21	19	20	14	18	20	18	17	21	22	21	21	21	21	20	20	20	17	19	20	20	21	18	19	21	19	17	17	21	21	21	21
R39358	Y81502	B00066	W55104	W92950	R39819	W01535	Y06427	W15473	R88616	B11540	B53070	Y86289	Y54496	B12426	B28212	Y05393	Y23627	Y31719	W05394	W68093	Y06292	W88235	B42487	W10422	W98441	B40894	W78102	R91310	R91309	G61381	G56042	G61382	G56043
r21	St:	KI	St	WO	2ml	Ce	МО	Hur	TNF-	SEI	Hur	Hur	Hur	Hur	NO	Hur	Α	Hur	MO!	Hur	Hur	Hur	Hur	Pei	н.	Hur	Ch:	Fu	Fu	Ara	Ara	Ara	Ara
ZPP.149. Sus scr	Streptococcus pneu	KIAA0160 polypepti	Streptococcus pneu	WO9905287 Seq ID 1	2mPK1 homologue pr	Cellular homologue	Mouse circadian re	Human P100 protein	F-R p55IC-bindin	SEN virus protein	Human angiogenesis	Human secreted pro	Human muscle angio		Novel human protei	Human TIE ligand N	A human growth fac	Human fibrinogen d	Mouse SH3P13 prote	Human neuronal PAS	Human transcriptio	Human prothrombina	Human ORFX ORF2251	Penicillium chryso	H. pylori GHPO 511	Human ORFX ORF658	Chimeric receptor	Fungal signal reco	CII		tha	İS	is tha

## ALIGNMENTS

Human conductin protein. 17-JUN-1999 (first entry) W93570;

W93570 standard; Protein; 840

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Tumor-suppressing protein conductin - diagnosis of tumors WPI; 1999-214706/18. N-PSDB; X23370. Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour; therapy; cytoplasmic degradation; blockade; Wnt signalling pathway; Adenomatous Polyposis Coli; APC; tumour suppressor. W09911780-A2. Behrens J, Birchmeier (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX 02-SEP-1997; 01-SEP-1998; 11-MAR-1999. Homo sapiens. 97DE-1038205. 98WO-DE02621. used for treatment and

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Best Local S
Matches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anti-tumour activity. Detecting the presence or amount of conductin, at protein or nucleic acid levels, is used to diagnose tumours, while agents that (re)activate conductin are used for tumour therapy. Conductin binds to beta-catenin and induces its cytoplasmic degradation, resulting in blockade of the Wnt/Wlingless signalling pathway in vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC) fragments and, in conjunction with APC, acts as a tumour suppressor.
                        Tumor-suppressing protein conductin
               diagnosis of tumors
                                                         WPI; 1999-214706/18
                                                                                                                                                   01-SEP-1998;
                                                                                                                                                                                                                                                                           Binding-site
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                                                                                                                                                                                                                                                                                                                                                                                                             Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour; therapy; cytoplasmic degradation; blockade; Wnt signalling pathway; Wingless signalling pathway; Adenomatous Polyposis Coli; APC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human conductin protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                N-PSDB;
                                                                                                                              02-SEP-1997;
                                                                                                                                                                         11-MAR-1999
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                                                                                                      (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX
                                                                                                                                                                                                WO9911780-A2
                                                                                                                                                                                                                                                                                                                                              Domain
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                                                                                                                                                                                                                                                                                      "GSK 3-beta binding region as claim 13"
                                                                                                                                                                                                                      "Dishevilled homology region claim 15"
                                                                                                                                                                                                                                                               "Beta-catenin binding domain
                                                                                                                                                                                                                                                     claim 14"
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Pred. No. 4.9e-25;
; Mismatches 0;
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in
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                         used for treatment and
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Nucleic acids encoding mutant and wild type Axin and coligonucleotides derived from them are useful for detecting mutations in the Axin gene and for determining whether a subject is likely to develop cancer (including breast, colorectal, gastrointestinal, esophageal, carcinomas or melanomas). The wild type Axin and homologues of Axin are useful for treating subjects who are likely to develop cancer (thyroid carcinomas). The nucleic acids are also useful for diagnosing cancer and for detecting mutations in cancerous cells. Wild type Axin, its antisense molecule and identified compounds form pharmaceutical compositions in the treatment of cancer. The compositions are also useful for treating cancer by inhibiting tumorigenesis (by inducing degradation of beta-catenin). The nucleic acid encoding Axin acts through
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Best Local (
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                                                                                                                                                                                                                       Claim 8;
                                                                                                                                                                                                                                                                  Newly isolated nucleic acid encoding "axis inhibition"
                                                                                                                                                                                                                                                                                                                WPI; 1999-120510/10.
                                                                                                                                                                                                                                                                                                                                              Constantini F,
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gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;
diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Fig 1; 22pp;
                                                                                                                                                                                                                                                    (Axin)
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                                                                                                                                                                                                                     Figure 8; 95pp;
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                                                                                                                                                                                                                                                  for detecting, diagnosing and treating
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Pred. No. 4.9e-25;
Mismatches 0;
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Matches
                                                                                        likely to develop cancer (including breast, colorectal, gastrointestinal, esophageal, carcinomas or melanomas). The wild type Axin and homologues of Axin are useful for treating subjects who are likely to develop cancer (thyroid carcinomas). The nucleic acids are also useful for diagnosing cancer and for detecting mutations in cancerous cells. Wild type Axin, its antisense molecule and identified compounds form pharmaceutical compositions in the treatment of cancer. The compositions are also useful for treating cancer by inhibiting tumorigenesis (by inducing degradation of beta-catenin). The nucleic acid encoding Axin acts through negative regulation of the Wnt pathway in the Nieuwkoop Center.
                                                                                                                                                                                                                                             Nucleic acids encoding mutant and wild type Axin and oligonucleotides derived from them are useful for detecting mutations in the Axin gene and for determining whether a subject is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Axin; cancer; breast cancer; colorectal cancer;
gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;
diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
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                                                                  Sequence
                                                                                                                                                                                                                                                                                                        Disclosure; Figure 11; 95pp; English.
                                                                                                                                                                                                                                                                                                                                  Newly isolated nucleic acid encoding "axis inhibition" protein (Axin) - useful for detecting, diagnosing and treating cancer
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30; Conservative
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Conservative
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             56.6%;
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Pred. No. 3.9e-09;
8; Mismatches 14
9
             Score 141.5; DB 20; Pred. No. 4.7e-09;
Mismatches
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                               E. colony transformants contg. Candida antarctica lipase A, chromosomal DNA of the C. antarctica strain LF058 (DSM 3855) were C prepd. The colonies are screened with the 32P-phosphorylated oligo C degenerate probe NOR 440, based on the N-terminal sequence determined from mature C. antarctica lipase. Plasmids were prepd. C from positive colonies and analysed by southern hybridisation. The probe for the southern is either the NOR 440 probe or a 32P-labelled probe NOR438. NOR 438 is an oligo corresp. to AA C sequence of the lipase in which, at 13 posms. a base has been chosen on the basis of codons used in yeasts and filamentous fungi. (Guess positions are indicated in 094949 FT). Only one plasmid, pMT1076, contains a band which hybridises both to NOR 440 c plasmid, pMT1076, contains a band which hybridises both to NOR 440 c plasmid, pMT1076, contains a band which hybridises both to NOR 440 c last two AAs of the propeptide (see R78230) are a typical c cleavage site for endoproteolytic processing by enzymes of the S.
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                                                                                                                                                                                                                                                                                                                  Aspergillus japonicus-type cells expressing heterologous protein - esp. fungal enzyme, provide high yields without significant prodn. of protease
                                                                                                                                                                                                                                                                                                                                                                                                      Berka RM,
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Sequence
                        cleavage site for endoproteolytic processing cerevisiae KEX-2 type.
                                                                                                                                                                                                                                                                           Example; Page 36-37; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                (NOVO ) NOVO NORDISK BIOTECH INC
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DB; Q94950.
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462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= propeptide 32..462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30..31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'label= mature lipase
                                                                                                                                                                                                                                                                                                                                                                                                      Takagi S,
                                                                                                                                                                                                                                                                                                                                                                                                        Yoder
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Query Match 23.9%; Best Local Similarity 48.3%; Matches 14; Conservative

Score 65; DB 16; Pred. No. 4.8; 5; Mismatches 8

8

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Gaps

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Length 462; Indels

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Y04658
ID YC
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AC YC
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                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                     Matches
                                                                                                                                                                                                                                   This sequence represents the C. antartica lipase A protein. This lipase has high thermostability and is active at acid pH. A varient of the mature lipase A in which Phel39 has been replaced by a Trp residue has increased specific activity compared to the parent lipase. The lipase or varient may be used in ester hydrolysis, ester synthesis or interesterification. They can also be used for avoiding pitch trouble in the process for the production of mechanical pulp or a paper-making process using mechanical pulp. They can also be used in detergents or as a digestive enzyme, eg. in the treatment of cystic fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lipase A; thermostability; specific activity; mechanical ester hydrolysis; ester synthesis; interesterification; epitch; paper-making; detergent; digestive enzyme; cystic
                 Y04658;
                                          Y04658 standard;
                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                          Claim 15; Page 39-40; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               New lipase variants, partic. from Candida antartica - have amino acid substitutions to increase specific activity against substrates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Borch K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Candida antartica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C. antartica lipase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R48084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R48084 standard;
                                                                                                                                                                                                                                                                                                                                                                                                 compared
                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; Q55463.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1994-035050/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Svendsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JAN-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9401541-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NOVO ) NOVO-NORDISK
                                                                                                   |: ||:| ||| | :| |: | :|||
336 asytvsvpkfprfiwhaipdeivpyqpaa 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        336 asytvsvpkfprfiwhaipdeivpyqpaa 364
                                                                                                                                                               Local
                                                                                                                            1 ANGQVSLPHFPR--THRLPKEMTPVEPAA 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ANGQVSLPHFPR--THRLPKEMTPVEPAA
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                                                                                                                                                    l Similarity 48.3
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                                                                                                                                                                                                                                                                                                                                                                                                  to parent lipase(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clausen G,
                                                                                                                                                                                                                463 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92DK-0000888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
                                          Protein;
                                                                                                                                                               23.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Egel-Mitani M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 463
                                        995 AA
                                                                                                                                                    5
                                                                                                                                                              Score 65;
Pred. No.
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                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hansen M,
                                                                                                                                                               DB
1.9;
                                                                                                                                                                            15;
                                                                                                                                                     8
                                                                                                                                                                            Length 463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pathar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ation; acid pH;
cystic fibrosis
                                                                                                                                                     Indels
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to polypeptides that constitute the HsdR, HsdM or HsdS subunit of a R/M [restriction/modification] type Ic bacteriophage resistance mechanism active against the phages of lactic acid bacteria, especially Lactococcus lactis. This sequence represents the Lactococcus lactis HsdR subunit. Nucleic acids encoding the HsdR, HsdM or HsdS fragment can be used for expression of at least one bacteriophage resistance mechanism in a lactic acid bacterium.
                                                                                                                           calcium release activated channel; therapy; diagnosis; lymphocyte proliferative disorder.
                                                                                                       Caenorhabditis elegans.
                                                                                                                                                     SOC/CRAC; calcium channel; store operated channel;
                                                                                                                                                                           Caenorhabditis elegans polypeptide at the c05c12.3 locus
                                                                                                                                                                                                    10-OCT-2000
                                                                                                                                                                                                                                                  Y95440 standard; Protein; 1816
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 18-22; 65pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chopin MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FR2767831-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HsdR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L.lactis HsdR subunit #1.
                                  20-DEC-1999;
                                                          13-JUL-2000
                                                                                 WO200040614-A2
                                                                                                                                                                                                                          Y95440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acid bacteria, especially Lactococcus lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteriophage resistance mechanism subunit polypeptides - of lactic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lactococcus lactis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lactic acid bacterium.
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                                                                                                                                                                                                                                                                                                            732
                                                                                                                                                                                                                                                                                                                        11 PRTHRLPKEMTPV--EPAAFAAELISRLEK------LKLELESRHSLEERLQ 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1999-183265/16.
                                                                                                                                                                                                                                                                                                           pqshqipk-ltpavqelkafagedfsqiprgekdlkqfvrlgletqnqiqqlvq 784
                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  995 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clier F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HsdS; restriction/modification; bacteriophage; resistance;
                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
98US-0114220
99US-0120018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97FR-0010885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97FR-0010885
                                  99WO-US29996
                                                                                                                                                                                                                                                                                                                                                                    22.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ehrlich SD,
                                                                                                                                                                                                                                                                                                                                                          17;
                                                                                                                                                                                                                                                                                                                                                                  Score 61.5;
Pred. No. 31;
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                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schouler
                                                                                                                                                                                                                                                                                                                                                                                Length 995;
                                                                                                                                                                                                                                                                                                                                                           Indels
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99US-0140415

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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptide at the c05c12.3 locus. The polypeptide was identified in a database search for putative calcium channel proteins. The c05c12.3 protein was noteable cause its central pore region had some similarity to, but was clearly distinct from, members of the Trp family of calcium chennels. The polypeptide was used in BLAST screening to isolate 2 other C. elegans homologues (see
                                                                                                                                                                                                                                                                                                                  Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New SOC/CRAC calcium channel polynucleotides and polypeptides used to diagnose and treat proliferative disorders associated with the channel and to screen for novel modulators of the channel -
Isolated nucleic acid molecule encoding a human secreted protein
                             WPI; 2000-638174/61.
                                                                                                                                                                09-MAR-2000;
                                                                                                                                                                                                                            WO200055171-A1
                                                                                                                                                                                                                                                         Homo saplens.
                                                                                                                                                                                                                                                                                                       cardiant;
                                                                                                                                                                                                                                                                                                                                                                               Human secreted protein BLAST search protein SEQ ID NO: 153
                                                                                                                                                                                                                                                                                                                                                                                                           02-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B27999 standard; Protein; 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y95441-42) and mouse melastatin-1 (see Y95438). These were used to screen EST databases for lymphocyte homologues. Human clones (see A4992-24) encoding members (see Y95435-37) of a new family SOC (store operated channel) or CRAC (calcium release activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is that of a Caenorhabditis elegans polypeptide at the c05c12.3 locus. The polypeptide was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-465957/40
                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                                                                                      12-MAR-1999;
23-NOV-1999;
                                                                                                                                                                                              21-SEP-2000
                                                                                                                                                                                                                                                                                       neurological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    channel) calcium channel polypeptides were identified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 72-76; 108pp; English.
                                                                                                                                                                                                                                                                                                     gene therapy; cancer; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1816 AA;
                                                           Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                2000WO-US06043
                                                                                                                      99US-0124146.
99US-0167061.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.38;
                                                                                                                                                                                                                                                                                       infection; human; secreted protein.
                                                           Komatsoulis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 58; DB Pred. No. 1.7e 6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1816;
                                                                                                                                                                                                                                                                                                     cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such
                                                                                                                                29-MAR-1999
01-APR-1999
                                                                                                                                                                                                                                                                                                                EP1033405-A2
                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                    Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana protein fragment SEQ ID NO: 71971.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G56044 standard; Protein; 260 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide fragment homologous to the protein encoded by the gene given in the descriptor line. The sequence is a search result from a BLASTX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 427-428; 438pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   used in preventing, treating or ameliorating a medical condition
                                                                        16-APR-1999;
19-APR-1999;
                                                                                                    08-APR-1999
                                                                                                                     06-APR-1999
                                                                                                                                                                            09-MAR-1999;
23-MAR-1999;
                                                                                                                                                                                                         05-MAR-1999
                                                                                                                                                                                                                                                                                  06-SEP-2000
                           23-APR-1999
23-APR-1999
                                                                                                                                                                                                                         25-FEB-1999;
                                                                                                                                                                                                                                                     25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                         termination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homology search. The genes and proteins are useful for preventing
                                                         21-APR-1999
                                                                                                                                                               25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 yfeslhtllmdisplfretfgsklisklselkke
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 HFPRTHRLPKEMTPVEPAAFAAELISRLEKLKLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention relates to the isolation of genes C59049-C59098 encoding human secreted proteins B27907-B27956. This sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bacterial, fungal and parasitic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115
                                                                                                                                                                                                                                                                                                                                                                         sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                     2000EP-0301439
99US-0128714.
99US-0129845.
99US-0130077.
99US-0130449.
99US-0130510.
99US-0131449.
99US-0132048.
                                                                                                                                                            99US-0123548.
99US-0125788.
99US-0126264.
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99US-0123180
                                                                                                                                990S-0126785
990S-0127462
                                                                                                                     990S-0128234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 57; DB
; Pred. No. 9.4;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42
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promoter;
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-1999	-1999 -1999	-1996	-1999	-199	1999	1999	-199	-1999	-1999 1-1999	1-1999	1999	7-1999 1-1999	1-1999	1-1999	9661-1 1999	7-1999 7-1999	1-1999	1-1999	1-1999 1-1999	1-1999	1-1999	1-1999 1-1999	1-1999	1-1999	I-1999 I-1999	1-1999	I-1999	-1999 2001-	-1999	1999	-1999	-1999	-1999	-1999	-1999	1999	-1999
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21-APR-1999

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990S-0121825

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11-MAY-1999
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99US-0125788

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99US-0128734

99US-0128734

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Best Local Similarity 37.5%; Fi
Matches 15; Conservative 10;
 25-FEB-1999
05-MAR-1999
09-MAR-1999
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28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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87 pkelipldpasynpaaylwkkie -- dipeerrhhliglie 124
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99US-0161992.
99US-0161993.
99US-0162142.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
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              Length 306;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; Protein; 321 AA.
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Matches 15
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PR 21 - COT-1999 99US-0152076.
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                    Score
   55 5512 5 555 55

50 11111 2 555 55

00 11111 2 555 555

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55115 555 555 555 555
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  US-09-587-574-3
272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185757 seqs, 19210857 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapop 10.0 , Gapext 0
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US-08-985-291-52
US-08-985-291-52
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US-08-964-671-4
US-08-960-507-19
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336	Query M Best Lo Matches	US-08-458-023B-2  Sequence 2, Application US-08-7990 GENERAL INFORMATION: APPLICANT: Barka, Rana APPLICANT: Takagi, Sh. APPLICANT: Takagi, Sh. APPLICANT: BOOMINATHAN TITLE OF INVENTION: APPLICANT: BOOMINATHAN TITLE OF INVENTION: APPLICANT: BOOMINATHAN TITLE OF INVENTION: APPLICATE: New YORK STATE: New YORK STATE: New YORK STATE: New YORK COUNTRY: USA ZIP: 10174-6201 COMPUTER READABLE FORM MEDIUM TYPE: Floppy COMPUTER: IBM PC CON OPERATION SYSTEM: PATLING SYSTEM: PATLING TONEY/AGENT INFORMATION NUMBER: FILING DATE: 01-JUN CLASSIFTCATION NUMBER: FILING DATE: 01-JUN CLASSIFTCATION NUMBER: REFERENCE/DOCKET NUMBER: REF		28 29 29 30 31 31 32 33 34 44 44 44 44 44 44 44 44 44 44 44
	/ Match Local Simi nes 14;	458-023B-2 ence 2, App. nt No. 5667; eral INFORM pPLICANT: 1 COUNTRY: New STARE: New ST		50.5 50.5 50.5 50.5 50.5 50.5 50.5 50.5
ANGQVSLPHFPR-  :   :      ASYTVSVPKFPRF	ilarity Conser	Application Septiments of the process of the proces		11111111111111111111111111111111111111
Η .	23.9 48.3 vative	OR-458-023B-2 -08-458-023B-2 -08-458-023B-2 -08-458-023B-2 Sequence 2, Application US/08458023B Sequence 2, Application US/08458023B Sequence 2, Application US/08458023B Sequence 2, Application US/08458023B Patent No. 5667990 APPLICANT: Boominathan, Karuppan TITLE OF INVENTION: ASPERGILLUS NUMBER OF SEQUENCES: 16 CORRESPONDENCE ADDRESS: ADDRESSEE: No. 5667990 No. 56 STREET: 405 Lexington Avenue CITY: New York CONMITY: USA ZIP: 10174-6201 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATION SYSTEM: PC-DOS/MS-DC SOFTWARE: Patentin Release #1. CURRENT APPLICATION NUMBER: US/08/458 FILING DATE: 01-UN-1995 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: REGISTRATION TOWNBER: 31,274 REFERENCE/DOCKET NUMBER: 4086. TELECOMMUNICATION NUMBER: 4086. TELECOMMUNICATION NUMBER: 4086. TELECOMMUNICATION NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 462 amino acids TYPE: protein		2089 2089 396 396 443 443 453 453 651 651 671 671 1780 1780 1780 1780 1780 1780 1780 17
-THRLPKEMTPVEPAA   :   :   :      WHAIPDEIVPYQPAA	*; Sc *; Pr	1.08 1.08 1.00 0.00 1.00 0.00 0.00 0.00	_	1 US-00 1 US-00 1 US-00 2 US-00 2 US-00 2 US-00 3 US-00 1 US-00 1 US-00 1 US-00 2 US-00 2 US-00 2 US-00 3 US-00 2 US-00 3 US-00 5 PGT-1
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US-09-111-556A-2
                                                                                                                                   Sequence 2, Application US/08360758 Patent No. 6074863
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TITLE OF INVENTION: C. ANTARCTICA LIPASE AND LIPASE VARIANTS
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
LENGTH: 463 amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
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APPLICATION NUMBER:
FILING DATE: 03-JUN-
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                       APPLICANT:
                                                                                       APPLICANT:
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CANT: Hansen, Mogens TO OF INVENTION: C. ANTAF
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                                                                   Pathar, Shamkant A Egel-Mitani, Michi
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Egel-Mitani, Michi
                                 Clausen,
                                                     Borch, Kim
                                                                                                   Svendsen, Allan
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   ANTARCTICA LIPASE
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   AND LIPASE VARIANTS
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US-08-360-758-2
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Best Local Similarity
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                                                                                                                             COMPUTER READABLE FORM:
MEDLIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
COMPUTER: LBM PC compatible
COMPUTER: DC PC DOS/MS-DOS
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             APPLICATION NUMBER: US/08/31
FILING DATE: 03-October-1994
ATTORNEY_AGENT INFORMATION:
NAME: Harrington, James J.
                                                                                         SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
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APPLICANT: Yaver, Debbie Sue
TITLE OF INVENTION: GENES ENCODING SIGNAL RECOGNITION PARTICLE
TITLE OF INVENTION: ASPERGILLUS NIGER
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                       STREET: 405 Lexil CITY: New York STATE: New York COUNTRY: U.S.A. COUNTRY: 10174-6401
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REGISTRATION NUMBER:
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405 Lexington Avenue, Suite 6400
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 1
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Best Local Similarity
                                                                                                                                                                                   TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 552 amino acids
TYPE: amino acids
STRANDEDNESS: single
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Patent No. 592256
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATEN: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,401E
FILING DATE: 03-October-1994
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein ORIGINAL SOURCE: ORGANISM: Aspergillus
                                                                                                                                     MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59225610 No. 5922561disk of No. 5922561th America,
STREET: 405 Lexington Avenue, Suite 6400
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LENGTH: 534 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: GENES ENCODING SIGNAL RECOGNITION PARTICLE TITLE OF INVENTION: ASPERGILLUS NIGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Thompson, Sheryl / APPLICANT: Yaver, Debbie Sue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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164 LTQTDPAIVAAEGVAKFKKERPEIIVDTSGRHKQEEEL 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
ZIP: 10174-6401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 534 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 4248.000-US
                                                                                                                                                                          TOPOLOGY:
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                  Conservative
                                                                                                                 Aspergillus niger
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33.3%;
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                                                                                                                                                                                                                                                                                                                                4248.000-US
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Pred. No. 21
                                Score 56.5;
Pred. No. 2:
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                  Mismatches
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                                                DB 2;
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                  13;
                                               Length 552;
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                  Indels
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                                                                                                                                                                                                              Sequence 2, Applic Patent No. 6054293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4,
                                                                                                                                                                                                                                                                                                                                                                                                Query Match 20.6%; Score 56; DB 3; Le Best Local Similarity 47.8%; Pred. No. 1.5e+02; Mismatches 9;
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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                                                                                                  APPLICANT: Tessier-Lav
APPLICANT: He, Zhigang
APPLICANT: Chen, Hang
APPLICANT: Chen, Hang
TITLE OF INVENTION: See
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                            1790 NSERGLPHEPRTHRTYRGLYPHE 1812
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
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APPLICANT: He, Z
APPLICANT: Chen,
                                                                                     CORRESPONDENCE ADDRESS:
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CITY: HILLSBOROUGH
STATE: CALIFORNIA
STATE: C
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                                     ADDRESSEE: SCIENCE CORRECT: 75 DENISE DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/936,135 FILING DATE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                CITY: HILLSBOROUGH
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                 CALIFORNIA
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75 DENISE DRIVE
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                                                                                                                                                         He, Zhigang
                                                                                                                                                                            Tessier-Lavigne, Marc
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                                                                    SCIENCE & TECHNOLOGY LAW GROUP
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                                                                                                                         Semaphorin Receptors
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                                                                    TELEPHONE: (415) 343-43-
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (650) 343-4342 INFORMATION FOR SEQ ID NO: :
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FLODS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/785,310A
FILING DATE: 21-0AN-1997
CLASSIFICATION: 536
CLASSIFICATION: 536
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
                             SEQUENCE CHARACTERISTICS:
LENGTH: 824 amino acids
                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UTS
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LENGTH: 2588 amino aci
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NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Neuronal PAS Domain Protein NUMBER OF SEQUENCES: 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
STRANDEDNESS:
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T: 268 BUSH STREET, SUITE 3200
SAN_FRANCISCO
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Similarity 47.8%;
11; Conservative
                 amino acid
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Pred. No. 1.5e+02;
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; MOLECULE TYPE:
US-08-785-310A-7
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                                                                                                               Matches
                                                                                                                             Best Local
                                                                                                                                         Query Match
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GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
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APPLICANT:
                                                                                                                                                                                                  TOPOLOGY: 1
MOLECULE TYPE:
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NAME: No.: 5874241thrup, Thomas
REGISTRATION NUMBER: 33,268
                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: C1
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                                         436 EASTPALPRSATLPQELPVPGLSQAATMPAPLPSPLSCDLTQQLLPQTVLQSTPAPMAQF 495
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496 SAQ-FSMFQTIKDQLEQRTRILQANIRWQQEELHKIQEQL 534
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CITY: Chicago
                           29 AAELISRLEKLKLELESR--
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                                                                                                                                                                                                                                               TYPE:
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                                                                                    4 QVSLPHFPRTHRLPKEM----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Illinois
7: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Dressler, Rockey, Milnamow & Katz
Two Prudential Plaza, Suite 4700
                                                                                                                                                                                                                                                           824 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pinto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                      312-616-5460
                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Turek, Fred W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Takahashi, Joseph S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                   312-616-5400
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                                                                                                                             19.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clock Gene and Gene Product
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                                                                                                                             Score 53.5;
Pred. No. 8
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Pred. No. 8
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                            -HSLEERL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84;
                                                                                                                                             DB 2;
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                                                                                     TPVEPAAF 28
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 52
LENGTH: 824
TYPE: PRT
ORGANISM: Mus musculus
US-08-885-291-52
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US-08-934-494-2
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Best Local Similarity
Matches 20; Conserv
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Patent No. 60571
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CURRENT PAPLICATION NUMBER: US/08/885,291A
CURRENT FILING DATE: 1997-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: 08/816,693
EARLIER FILING DATE: 1997-03-13
NUMBER OF SEQ ID NOS: 55
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                                               TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acid
                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P10
                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gurney, Austin TITLE OF INVENTION: Tie L. NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  496 SAQ-FSMFQTIKDQLEQRTRILQANIRWQQEELHKIQEQL 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           436 EASTPALPRSATLPQELPVPGLSQAATMPAPLPSPLSCDLTQQLLPQTVLQSTPAPMAQF 495
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STREET: 1 DNA Way
CITY: South San Francisco
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                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/934,494
                                                                                                                        TELEPHONE:
               ropology:
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                                Amino Acid
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                                                   406 amino acids
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650/952-9881
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15
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20.0%;
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                                                                                         US-08-699-103B-10
                                                                                                           RESULT
                                                         Sequence 10, Application US/08699103B Patent No. 6107462
                                                                                                                                                                                                                  Matches
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Best Local Similarity
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                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/143
FILING DATE: 28-Aug-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 406 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
APPLICANT: Rine, Jasper D.
APPLICANT: Hampton, Randolph
TITLE OF INVENTION: GENES AND PROTEINS CONTROLLING
                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
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                                                                                                                                                       161 RRKRLPEMAQPVDP----AHNVSRLHRLPRDCQELFQVGER 197
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                                                                                                                                                                        12 RTHRLPKEMTPVEPAAFAAELISRLEKLKLELESRHSLEER 52
                                                                                                                                                                                                                                                                                                                            TYPE: Amino Acid
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STATE: California
                                                                                                                                                                                                                  Local Similarity 34.
                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
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NVENTION: Tie Ligand Homologues
STATIFNCES: 17
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650/952-9881
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Hillan, Kenneth
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Goddard, Audrey
Godowski, Paul J.
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Pred. No.
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Pred. No.
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US-08-699-103B-12
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Best Local
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NFORMATION FOR SEQ ID NO: 10:
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/699,103B
FILING DATE: 16-ADG-1996
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MEDIUM TYPE: Diskett
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/322-5070
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APPLICATION NUMBER: 60/002,581
FILING DATE: 17-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 853 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                          ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
SOFTWARE: FastSEQ for Windows Version CORRENT APPLICATION UNMBER: US/08/699,103B FILLING DATE: 16-AUG-1996
PRIOR APPLICATION UNMBER: 60/002,581
PAPPLICATION WINDER: 60/002,581
FILLING DATE: 17-AUG-1995
                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                        APPLICANT: HAMPTON, RANDOLPH
TITLE OF INVENTION: CHOLESTEROL SYNTHESIS

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                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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CITY: Menlo Park
STATE: CA
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                                                                                                                                                                                                         STREET: 2200 Sand
CITY: Menlo Park
STATE: CA
                                                                                                           OPERATING SYSTEM:
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amino acid
OGY: linear
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2200 Sand Hill Road, Suite 100
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2200 Sand Hill Road, Suite 100
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                                                                                                                                                                                              USA
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                                                                                                                            IBM Compatible
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16-AUG-1996
                                                                                                                                               Diskette
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; MOLECULE TYPE: protein US-08-699-103B-12
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Search completed: June Job time: 5403 sec
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                                                                                                                                             Query Match
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CURRENT FILING DATE: 1998-12-24
EARLIER APPLICATION NUMBER: US 60/068,886
EARLIER FILING DATE: 1997-12-26
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lee, Cheng-Chi
APPLICANT: Sun, Zhong Sheng
APPLICANT: Albrecht, Urs
APPLICANT: Elchele, Gregor
TITLE OF INVENTION: Mammalian Circadian Regulator M-RIGUIZ (M-PERZ)
FILE REFERENCE: D6067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 650/854-08/5 INFORMATION FOR SEQ ID NO: 12:
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## ALIGNMENTS

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negative regualtor axin [imported] - rat
N;Alternate names: rAxin
C:Species: Rattus norvegicus (Norway rat)
C:Species: Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000
C;Accession: T08422
R;Ikeda, S:; Yamamoto, H:; Murai, H:; Kishida, .S.; Kikuchi, A.
EMBO J. 17, 1371-1384, 1998
A;Title: Axin, a negative regulator of the Wnt signaling pathway, forms a co
A;Reference number: Z16413; MUID:98151361
A;Accession: T08422
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mkNA
A;Residues: 1-832 < TKE>
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-838 <YAM>
A;Cross-references: EMBL:AF017757; NID:g3080758; PIDN:AAC40089.1; PID:g3080759
A;Note: interacts with GSK-3beta and beta-catenin
C;Keywords: phosphoprotein; signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOI. Cell. Biol. 18, 2867-2875, 1998
A;Title: Axil, a member of the Axin family, interacts with A;Reference number: Z16414; MUID:98226558
A;Accession: T08423
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N;Alternate names: Axil
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jul-2000
C;Accession: T08423
C;Accession: T08423
R;Yanamoto, H.; Kishida, S.; Uochi, T.; Ikeda, S.; Koyama, S.; Asashima, M.; Kikuchi,
                                                                                                                 A;Cross-references: EMBL:AF017756; NID:g2982197; PIDN:AAC40066.1; PID:g2982198 A;Note: GSK-3beta interacting protein C;Keywords: phosphoprotein; signal transduction
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A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Reger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; A; Reference number: A69580; MUID:98044033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: strain PAO1 C; Genetics: A; Gene: PA1624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic A;Reference number: A82950; MUID:20437337 A;Accession: C83442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: C83442
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, Lory, S.; Olson, M.V.
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                                                                                                                                                                                                                       A; Cross-references: GB:Z99110; GB:AL009126; A; Experimental source: strain 168
                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-141 <KUN>
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A; Residues: 1-268 <STO>
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conserved hypothetical protein yklA - Bacillus subtilis
C; Species: Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE004590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein PA1624 [imported] -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000; Accession: D69857
                                 Query Match
Best Local
                                                                                                                                       Superfamily: hypothetical protein ykla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary
     Matches
                                                                                                                                                                                                                                                                                                                          Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ANGQVSLPHFPRTHRLPKEMTPVEPAAFAAELISRLEKL----KLELESRHSLEER 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N
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     l Similarity
16; Conserv
23.2%;
nilarity 33.3%;
Conservative 1:
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  ; Score 63; DB 2; ; Pred. No. 2.4; 11; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 64.5;
Pred. No. 3.
9; Mismatche
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                                                                                                                                                                                                                                               NID:g2633472; PIDN:CAB13171.1; PID:g2633668
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     13;
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                                                    Length 141;
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        Indels
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        Gaps
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K.; Lim,
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  A; Molecule type: DNA
A; Residues: 1-333 <LOG>
C; Superfamily: unassigne
C; Keywords: DNA binding;
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C48423
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        ;Superfamily: unassigned homeobox proteins; ;Keywords: DNA binding; homeobox; nucleus;
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A;Cross-references: EMB::AF020713; NID::g3025478; PID::g3025578; PIDN::AAC13073.1
A;Cross-references: EMB::AF020713; NID::g3025478; PID::g3025578; PIDN::AAC13073.1
C; Bron, S; Broullet, S; Bruschi, C.V.; Caldwell, B; Capuano, V; Carter, N.M.;
A; Ebrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J; Fabret, C; Ferrari,
Nature 390, 249-256, 1997
A; Authors: Foulger, D; Fritz, C; Fujita, M; Fujita, Y; Fuma, S; Galizzi, A; Gal
A; Authors: Foulger, D; Fritz, C; Fujita, M; Fujita, Y; Fuma, S; Hosono, S; Hullo, M
iech, J; Harwood, C.R.; Henaut, A; Hilbert, H; Holsappel, S; Hosono, S; Hullo, M
Koetter, P; Koningstein, G; Krogh, S; Kumano, M; Kurita, K; Lapidus, A; Lardino
A; Authors: Lauber, J; Lazarevic, V; Lee, S,M.; Levine, A; Liu, H; Masuda, S; Mau
Y, M; Ogawa, K; Ogiwara, A; Oudega, B; Park, S.H.; Parro, V; Pohl, T.M.; Portete
Rieger, M; Rivolta, C; Rocha, E; Roche, B; Rose, M; Sadale, Y; Sato, T; Scanl
A; Authors: Schleich, S; Schroeter, R; Scoffone, F; Sekdyuchi, J; Sekowska, A; Se
akeuchi, M; Tamakoshi, A; Tamanoto, H; Yamane, K; Yasumoto, K; Yata, K; Yoshida
A; Authors: Yoshikawa, H, F; Zumstein, E; Yoshikawa, H; Danchin, A.
A; Title: The Complete genome sequence of the Gram-positive bacterium Bacillus subtili
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Lazarevic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, submitted to the EMBL Data Library, August 1997 A;Description: The complete nucleotide sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable antirepressor - Bacillus subtilis phage SPBC2
C;Species: Bacillus subtilis phage SPBC2
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 20-Jun-2000
                                                                   R;Logan, C.; Hanks, M.C.; Noble-Topham, S.; Nallainathan, Dev. Genet. 13, 345-358, 1992
A;Title: Cloning and sequence comparison of the mouse, hum A;Reference number: A48423; MUID:93185339
                                                                                                                                                                                                                                                                homeotic protein engrailed 1 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Oct-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: yoqD
C;Superfamily: phage Pl kilA protein
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R; Lazarevic, V.; Duesterhoe
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A; Status: preliminary; not compared with conceptual translation
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A;Experimental source: strain:
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                                             A; Accession: C48423
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ANGQVSLPHFPRTHR----LPKEMTPVEPAAFAAELISRLEKLKLELESRHSL 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 62.5; DB 2; Pred. No. 5.3;
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                                                                                                                            and
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                                                                                                                                chicken engrailed
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homeobox homology

regulation

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C;Accession: T46149
R;Bloecker, H.; Mewes, H.W.;
submitted to the Protein Sequence
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A;Accession: S57018
                                                                               A;Map position: 3
A;Introns: 66/2; 111/3; 177/1; 217/3; 269/3
A;Note: T3A5.100
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote
                                                                                                                                                                                                                                                                                                                                          protein kinase ATN1-like protein - Arabidopsis thaliana
N;Alternate names: protein T3A5.100
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
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N;Alternate names: hypothetical protein J1415; hypothetical protein YJR83.30
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 04-Mar-2000
C;Accession: S55190; S57018
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                                                                                                                                                                       A;Cross-references: EMBL:AL132979
A;Experimental source: cultivar Columbia;
                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-377 <BLO>
                                                                                                                                                                                                                                                            A; Reference number: 223024
A; Accession: T46149
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A; Residues: 1-539 <ZAG>
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A; Residues: 1-539 <DEH>
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A; Accession: S55190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;de Haan, M.; Smits, P.H.M.; Grivell, L.A. submitted to the EMBL Data Library, May 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F; 245-301/Domain:
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 th 22.1%; Similarity 30.6%; Post Conservative 11;
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38.8%;
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 Score 60; DB
Pred. No. 16;
11; Mismatches
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Pred. No. 16;
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Pred. No. 8.2;
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltvell, T.; Gentles, S.; Hamlin, N.; Hc Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authbors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complet A;Reference number: A70500; MUID:98295987
A;Accession: E70826
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R;Huttly, A.K.; Phillips, A.L.
Plant Mol. Biol. 27, 1043-1052, 1995
A;Title: Gibberellin-regulated expression
A;Reference number: S56638; MUID:95284341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable membrane protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X79993; NID:g871983; PIDN:CAA56314.1; PID:g871984 C;Superfamily: kinase-related transforming protein; protein kinase homolog; C;Keywords: ATP: phosphotransferase; protein kinase C;Keywords: ATP: phosphotransferase; protein kinase F;33-322/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                          C;Genetics:
A;Gene: mmp
                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AL021943; GB:AL123456; NID:g3261530; A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-964 <COL>
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C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 18-Jun-1999
C;Accession: S56638
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N;Alternate names: MAP1 kinase
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                                                                                                                                                         ; Score 59.5; D; Pred. No. 53; 10; Mismatches
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human (fragment)

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A;Title: The genome sequence of the plant pathogen Xylella fastidiosa A;Reference number: A82515; MUID:2035717
A;Note: for a complete list of authors see reference number A59328 be A;Accession: A82561
A;Status: preliminary
A;Cross-references: GB:AE004050; GB:AE003849; NID:g9107594; PIDN:AAF85213.1; GSPDB:GN00:A;Experimental source: strain 9a5c R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; &
                                                                                                                                                                                                                                                                       C;Accession: A82561
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequer Nature 406, 151-157, 2000
                                                                                                                                                                                                                                                                                                                                                         hypothetical protein XF2414 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-20
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A;Title: Coordinate embryonic expression of three zebrafish engrailed genes A;Reference number: S30437; MUID:93201987
A;Accession: S30438
                                                                                     A; Molecule type: DNA
A; Residues: 1-601 <SIM>
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A; Residues: 1-231 <EKK>
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C;Date: 13-Jan-1995 #sequence_revision 13
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A;Map position: 2q31-2q31
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A; Residues: 1-7962 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 59; DB Pred. No. 12;
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A;Cross-references: EMBL:D14693; NID:g287572; C;Superfamily: unassigned homeobox proteins;
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A;Authors: Ferreira, V.C.A.; Eraga, J.S.; Franca, S.C.; Franco, M.C.; Fr J.D.; Junquelra, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, R.V.; Sawa A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.B.; de Sa, R.G.; Santelli, R.V.; Sawa A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.B.; de Sa, R.G.; Santelli, R.V.; Sawa A;Authors: da Silva, V.; Valada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L. A;Reference number: A59328
                                                                                                                                                                                                                                       homeotic protein En-1b - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein C47D12.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
A; Molecule type: mRNA
A; Residues: 1-171 <WAT>
                                                                              A; Accession: S35638
                                                                                                         A; Title: Nucleotide sequence of Xenopus homeobox gene, En-1 A; Reference number: S35638; MUID:93281404
                                                                                                                                                         R;Watanabe, M.; Hayashida, T.; Nishimoto, T.; Kobayashi, H. Nucleic Acids Res. 21, 2513, 1993
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A; Introns: 40/3; 150/3; 476/3; 577/2;
C; Superfamily: threonine--tRNA ligase
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                                                       A;Status: preliminary
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A; Residues: 1-725 <WIL>
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A; Accession: T19994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:269902; PIDN:CAA93762.1; GSPDB:GN00020; CESP:C47D12.6
A;Experimental source: clone C47D12
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Pred. No. 41;
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; PIDN:BAA03519.1; PID:d1004030; PID:g287 homeobox homology

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Result
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AXNN_ENICA
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HUMAN
MML5_METH
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MML5_METH
HMEB_LENERE
SYTC_CAEEL
HMEB_XENLA
HMEB_BRARE
SYTC_CAEEL
HMEB_XENLA
HMEB_MOUSE
SYTC_CAEEL
HMEB_ARAPNG
HMEB_BRARE
THI4_HALN1
SYE_BARE
THI4_HALN1
SYE_BARE
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HYEC_AMBME
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PCB3_HUMAN
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ING SITE (BY SIM	SWISS-PROT entry is copyright. It is produced three the Swiss Institute of Bioinformatics and the uropean Bioinformatics Institute. There are no by non-profit institutions as long as its contied and this statement is not removed. Usage by ies requires a license agreement (See http://www.nd an email to license@isb-sib.ch).	-1- SUBCELULLAR LOCATION: CYTOPLASMIC1- TISSUE SPECIFICITY: EXPRESSED IN LUNG AND THYMUS1- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY PP2A1- SIMILARITY: CONTAINS 1 RGS DOMAIN1- SIMILARITY: CONTAINS 1 DIX DOMAIN.	MAI. Cell. Biol. 18:2867-2875(1998).  MOI. Cell. Biol. 18:2867-2875(1998).  -i. FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES BETA-CATEMIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-CATEMIN AND APC BY GSK-3B (CY SIMILARITY).  -i. SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B) AND BETA-CATEMIN. THE INTERACTION BETWEEN AXIN AND BETA-CATEMIN.  OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATEMIN.	[1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. TISSUE-Brain; MEDLINE-98226558; PubMed-9566905; Yamamoto H., Kishida S., Uochi T., Ikeda S., Koyama S., Asashima M., Kikuchi A.; Kikuchi A.; A member of the Axin family, interacts with both glycogen Synthase kinase 3beta and beta-catenin and inhibits axis formation of	_RAT 1 _RAT

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SEQUENCE
                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INHIBITOR OF THE WAT SIGNALING PATHWAY. DOWN REGULATES
BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G., Jenkins N.A., Warburton D., Costantini F.; "Properties of mouse Axin2 and human Axin2: chromosomal location, expression pattern, interaction with Axin and effects on embryoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Behrens J., Jerchow B.-A., Wuertele M., Grimm J., Asbrand C., Wirtz R., Kuehl M., Wedlich D., Birchmeler W.; "Functional interaction of an axin homolog, conductin, with betacatenin, APC, and GSK3beta.";
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01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
                                                                                              EMBL; AF073788;
                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   axis formation."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AXN2_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              343
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                                                                                                                                                                                      European Bioinformatics Institute.
                                                                                                                                                                                                                                                  SIMILARITY: CONTAINS 1 RGS DOMAIN. SIMILARITY: CONTAINS 1 DIX DOMAIN.
                                                                                                                                                                                                                                                                                            TERNARY COMPLEX (BY SIMILARITY).
SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY)
PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOS
                                                                                                                                                                                                                                                                                                                                  CATENIN AND APC BY GSK-3B (BY SIMILARITY).

SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN

OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.
                                                                                                                                                                                                                                                                                PP2A (BY SIMILARITY).
                                                               ; AF205889; AJ
MGI:1270862;
                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANGQVSLPHFPRTHRLPKEMTPVEPAAFAAELISRLEKLKLELESRHSLEERLQ 396
                                                  P49799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 100.0%;
Similarity 100.0%;
54; Conservative 0
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838 i
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                                                                             AAC26047.1;
AAF22800.1;
                                                                Axin2.
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838
92947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BETA-CATENIN BINDING SITE SIMILARITY).
POLY-HIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 272; DB 1;
Pred. No. 1.7e-24
; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45B825C13BA07F37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2) (CONDUCTIN) (AXIN-LIKE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  840
                                                                                                                                                                                    There are no
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                                                                                                                                                                                                                                                                                              AND DEPHOSPHORYLATED
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                                                                                                                                                                                      restrictions
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RESULT AND LID                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12_HUMAN STANDARI

AXN2_HUMAN STANDARI

Q9Y2TI; Q9UH84;

01-CCT-2000 (Rel. 40, C

01-CCT-2000 (Rel. 40, I

01-CCT-2000 (Rel. 40, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                       axis formation.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY, DOWN REGULATES BETA-CATENIN, PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-CATENIN AND APC BY GSK-3B (BY SINTLARITY).
-i- SUBUNT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mai M., Qian C., Yokomizo A., Smith D.I., I "Cloning of the human homolog of conductin chromosome 17q23-q24.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                              Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G., Jenkins N.A., Warburton D., Costantini F.; "Properties of mouse Axin2 and human AXIN2: chromosomal location,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                            expression pattern, interaction with Axin and
                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Brain, and Lymphoblast;
Zhang T., Fagotto F., Hsu W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomics 55:341-344(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99168905; PubMed=10049590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AXIN 2 (AXIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR01301; RGSPROTEIN. PROSITE; PS50132; RGS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00615; RGS; 1. Pfam; PF00778; DIX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PP2A (BY SIMILARITY)
SIMILARITY: CONTAINS
SIMILARITY: CONTAINS
                                                                                                           OCCURS VIA THE ARMADILLO REPEATS CONTAINED TERNARY COMPLEX (BY SIMILARITY).
SUBCELLULAR LOCATION: CYTOPLASMIC.
TISSUE SPECIFICITY: EXPRESSED IN BRAIN AND PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 100.
54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 758
101
474
484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Human).
~+azoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INHIBITION PROTEIN 2) (CONDUCTIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phosphorylation
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840
101
474
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503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                           1 RGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MW.
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R -> K (IN REF. 2)

H -> Y (IN REF. 2)

S -> P (IN REF. 2)

F -> S (IN REF. 7)

-> A (IN REF. 7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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GSK-3B BINDING SITE (BY SIMILARITY).
BETA-CATENIN BINDING SITE (BY
SIMILARITY).
POLY-HIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 272; DB 1;
Pred. No. 1.8e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X -> K (IN REF. 2).
1 -> Y (IN REF. 2).
5 -> P (IN REF. 2).
7 -> S (IN REF. 2).
7 -> A (IN REF. 2).
A07D5EFB25DE7277
                                             DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu W.;
n (AXIN2),
                                                                                                                                                                                                                                                                                                                                                                                   effects on embryonic
                                                                                                                                                                                                  KINASE-3 BETA (GSK-3B)
AXIN AND BETA-CATENIN
IN BETA-CATENIN.
                                                                                                                LYMPHOBLAST.
DEPHOSPHORYLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AXIN-LIKE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   840;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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collaboration

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Swiss Institute of Bioinformatics

and the

outstation

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                     SEQUENCE FROM N.A.

MEDITINE-20171051; PubMed-10704853;

MEDITINE-20171051; PubMed-10704853;

Shimizu T., Yamanaka Y., Ryu S.-L., Hashimoto H., Yabe T.,

Bae Y.-K., Hibi M., Hirano T.;

"Cooperative roles of Bozozok/Dharma and Nodal-related pro
formation of the dorsal organizer in zebrafish.";

Mech. Dev. 91:293-303(2000).

1- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN
BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                              AXN2_BRARE
P57095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                  Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
AXIN 2 (AXIS INHIBITION PROTEIN 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001158; -.
Pfam; PF00615; RGS; 1.
Pfam; PF00778; DIX; 1.
PRINTS; PR01301; RGSPROTEIN.
PROSITE; PS50132; RGS; 1.
Developmental protein; Phosphorylation.
                                                                                                                                                                                                                                         Cypriniformes; Cyprinidae; NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIM; 604025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF078165;
                                                                                                                                                                                                                                                                                                               AXINZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              343
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PP2A (BY SIMILARITY).
SIMILARITY: CONTAINS 1 RGS DOMAIN.
SIMILARITY: CONTAINS 1 DIX DOMAIN.
                                                                  PTM: PROBABLY PHOSPHORYLATED BY GSK-3B
                                                                               CATENIN AND APC BY GSK-3B (BY SIMILARITY).
SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF078165; AAD20976.1; -. AF205888; AAF22799.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 98.:
53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  696
93557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                474
843
62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200
413
476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.5%;
copyright. It
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::
                                                                                                                                                                                                                                                          Rasborinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HVCLFQHQAERRWV (IN REF. 2).

Q -> R (IN REF. 2).

MISSING (IN REF. 2).

P -> S (IN REF. 2).

Q -> H (IN REF. 2).

Q -> H (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 268; DE
Pred. No. 5.26
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSK-3B BINDING SITE (BY SIMILARITY).
BETA-CATENIN BINDING SITE (BY
SIMILARITY).
POLY-HIS.
DIX.
OPGVGKGQVTKPMSVSSNTRRNEDGL -> HHGGQG
                                                                                                                                                                                                                                                                                                                                                                                           812
                                                                                                                                                                                                                                                          Danio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
.2e-24;
                                                                                                                                                                                                                                                                                                                                                                                          ξ
                                                                    AND
                                                                    DEPHOSPHORYLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 843;
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the Euro
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Cell 90:181-192(197).

-I- FUNCTION: INHIBITOR OF THE WHT SIGNALING PATHWAY. DOWN REGULATES BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-CATENIN AND APC BY GSK-3B (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

-I- DEVELOPMENTAL STAGE: EXPRESSED AT STAGE 12 TO 15.

-I- PIM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
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the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@fisb-sib.ch).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasiani
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Pfam; PF00778; DIX; 1.
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Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J.,
Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F
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"Cooperative roles of Bozozok/Dharma and Nodal-related proformation of the dorsal organizer in zebrafish.";

Mech. Dev. 91:293-303(2000).

-i- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN
BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brachydanio rerio (Zebrafish) (Zebra danio).

Eukaryota; Metazoa; Chordata; Craniata; Futeleostomi;

Eukaryota; Metazoa; Chordata; Teleostei; Euteleostei; Ostariophysi

Actinopterygii; Meleostei; Euteleostei; Ostariophysi

Cypriniformes; Cyprinidae; Rasborinae; Danio.
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Developmental protein; Phosphorylation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATENIN AND APC BY GSK-3B (BY SIMILARITY).
SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY)
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32; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         759
841 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
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94931 MW;
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59.3%;
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Pred. No. 5.5e
ll; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIX.
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zebrafish.";
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5.5e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 841;
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RESULT
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Best Local S
                           InterPro; IPR000342; -.
InterPro; IPR001158; -.
Pfam; PF00615; RGS; 1.
Pfam; PF00778; DIX; 1.
PROSITE; PS50132; RGS; 1.
Developmental protein; Pho
                                                                                                                                                                                                                                                                                                                                                                                        dependent phosphorylation of beta-catenin.;

dependent phosphorylation of beta-catenin.;

EMBO J. 17:1371-1384(1998).

-I- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-CATENIN AND APC BY GSK-3B (BY SIMILARITY).

-I- SUBGUNIT: INTERACTS WITH GSK-3B AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN. TERNARY COMPLEX. ALSO BINDS TO PLAKOGLOBIN (GAMMA-CATENIN), APC, DVL AND PP2A (BY SIMILARITY).

-I- SUBGELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

-I- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS, THYMUS AND LUNG FOLLOWED BY CEREBRUM, CEREBELLUM, HEART, KIDNEY, SKELETAL MUSCLE.
                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ikeda S., Kishida S., Yamamoto H., Murai H., Koyama S., Kikuchi "Axin, a negative regulator of the Wnt signaling pathway, forms complex with GSK-3beta and beta-catenin and promotes GSK-3beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         070239;
NON_TER
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                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AXIN1 OR AXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (Rel. 40, Last annotation update)
AXIN 1 PROTEIN (AXIS INHIBITION PROTEIN 1) (RAXIN) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence up
01-OCT-2000 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AXN1_RAT
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                                                                                                                                HSSP; P49799; 1AGR.
                                                                                                                                              EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          366 NGRVPLPHIPRTINRIPKDI-HVEPEKFAAELISRLEGVLREREAQEKLEERLK 417
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                                                                                                                                                                                                                                                                                                             PP2A (BY SIMILARITY).
SIMILARITY: CONTAINS 1 RGS DOMAIN.
SIMILARITY: CONTAINS 1 DIX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
                                                                                                                                                                                                                                                                                                                                                                              SPLEEN AND LIVER.
                                                                                                                                              AF017756;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32;
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351
437
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                                                                                                                                              AAC40066.1;
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436
512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Rat
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                                Phosphorylation.
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                                                                                                                                               ALT_INIT.
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Pred. No. 3.7e-10;
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GSK-3B BINDING SITE (
BETA-CATENIN BINDING
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1C62FCF1F5937C87 CRC64
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DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zeng L., Pagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L. III, Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.;
"The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling pathway that regulates embryonic axis formation.";
Cell 90:181-192(1997).

Cell 90:181-192(1997).

BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-CCT-2000 (Rel. 40, Created)
01-CCT-2000 (Rel. 40, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
AXIN 1 (AXIS INHIBITION PROTEIN 1) (FUSED PROTEIN) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AXN1_MOUSE
035625;
Pfam; PF00615; RGS; 1.
Pfam; PF00778; DIX; 1.
PROSTTE; PS50132; RGS; 1.
Developmental protein; Phosphorylation; NON_TER 1 1 1
DOMAIN 10 18 POLY-ALA.
DOMAIN 217 340 RGS.
                                                                                                           EMBL; AF009011; AAC53285.1; HSSP; P49799; 1AGR. MGD; MGI-1096327; Axin. InterPro; IPR000342; -. InterPro; IPR001158; -.
                                                                                                                                                                                                     modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatice Institute. There are no restrue by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS 1 AN MEDLINE-97373830; PubMed-9230313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AXIN1 OR AXIN OR FU.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: EXPRESSED IN EMBRYONIC STEM CELLS. DEVELOPMENTAL STAGE: WIDELY EXPRESSED AT E10.5 TO E16.5 DAY PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED
                                                                                                                                                                                                                                                                                                                                                                                                                     BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN. TERNARY COMPLEX. ALSO BINDS TO PLAKOGLOBIN (GAMMA-CATENIN), APC, DVL AND PP2A (BY SIMILARITY). SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY). ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 1 RGS DOMAIN. SIMILARITY: CONTAINS 1 DIX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATENIN AND APC BY GSK-3B (BY SIMILARITY).
SUBUNIT: INTERACTS WITH GSK-3B AND BETA-CATENIN. THE INTERACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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567
893
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Pred. No. 3.5e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sciurognathi;
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                                                   Alternative
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Best Local s
Matches 30
                                                           Interpro; IPR000342; -.
Interpro; IPR001158; -.
Pfam; PF00615; RGS; 1.
Pfam; PF00778; DIX; 1.
PROSITE; PS50132; RGS; 1
Developmental protein; Pl
NON TER
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Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L. III,

Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.;

"The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling
pathway that regulates embryonic axis formation.";

Cell 90:181-192(1997).

Cell 90:181-192(1997).

-I- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES

BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARSPLIC
SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.
PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND
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SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN
OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TERNARY COMPLEX. MAY ALSO BINDS APC, DVL AND PP2A.
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INHIBITION PROTEIN 1) (HAXIN) (FRAGMENT).
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Pred. No. 3.9e
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BETA-CATENIN BINDING SITE (BY
SIMILARITY).
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GSK-3B BINDING
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                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as its content is in no modified and this statement is not removed. Usage by and for commer entitles requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                           Hedgepeth C.M., Deardorff M.A., Klein P.S.;
"Xenopus axin interacts with glycogen synthase kinase-3 beta and is expressed in the anterior midbrain.";
Mech. Dev. 80:147-151(1999).

-I- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-CATENIN AND APC BY GSK-3B (BY SIMILARITY).

-I- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
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SEQUENCE
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                                                                                                                                                                                                   EMBL; AF097313; AAC71036.1; -.
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01-OCT-2000 (Rel.
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DOMAIN 88 211 RGS.
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                                        GSK-3B BINDING SITE (BY SIMILARITY).
BETA-CATENIN BINDING SITE (BY
SIMILARITY).
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Pred. No. 4.6e-09;
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DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a light content content to the content                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HME1_CHICK Q05916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
PROSITE; PS00033; ENGRAILED; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00024; HOMEOBOX. PRINTS; PR00026; ENGRAILED.
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01-FEB-1994 (Rel. 28, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
HOMEOBOX PROTEIN ENGRAILED-1 (GG-EN-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                         8 PHFPRTHRLPKEMTPVEP----AAFAAELISRLEKLKLELE-SRHSLEERLQ
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SIMILARITY: BELONGS TO THE ENGRAILED FAMILY OF HOMEOBOX PROTEINS.
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PSSPRTRKLKKKKTEKEDKRPRTAFTAE - - - QLQRLKAEFQANRYITEQRRQ
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                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                    DNA-binding; Developmental protein; Nuclear protein.

22 29 POLY-GLY.
36 65 PRO-RICH.
59 65 POLY-PRO.
97 104 POLY-GLY.
244 303 HOMEOBOX.
333 AA; 34515 MW; DOFIBIF917E1FBAD CRC64;
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IPR000747; -.
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30-MAY-2000
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YANDARD; PRT; 539 AA.
P47084;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
40-MAY-2000 (Rel. 39, Last annotation update)
50-MAY-2000 (Rel. 39, Last annotation update)
50-MAY-2000 (Rel. 39, Last sequence update)
50-MAY-2000 (Rel. 30, Last sequence u
                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Bacteria; Firmicutes; Bacillus/Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-S288C / FY1679;
de Haan M., Smits P.H.M., Grivell L.A.;
submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AJ002571; CAA05593.1; -.
EMBL; Z99110; CAB13171.1; -.
SUBtiList; BG13238; ykla.
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                                       EMBL; X87611; CAA60924.1; -. EMBL; Z49503; CAA89525.1; -.
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PROTEIN IN PROA-METC INTERGENIC
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us group; Bacillus.
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Pred. No. 1;
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HME1_HUMAN
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Best Local 9
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EMBL; L12699;
HSSP; P02836;
TRANSFAC; T020
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DNA_BIND
SEQUENCE
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Q05925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Logan C., Hanks M.C., Noble-Topham Provart N.J., Joyner A.L.; and sequence comparison of engrailed genes reveal potential fu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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01-FEB-1994 (Rel. 28,
01-OCT-2000 (Rel. 40,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 131290;
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InterPro; IPR001356; -.
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                           PHFPRTHRLPKEMTPVEP----AAFAAELISRLEKLKLELE-SRHSLEERLQ
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PSSPRTRKLKKKKNEKEDKRPRTAFTAE---QLQRLKAEFQANRYITEQRRQ
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19; Conser
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PS50071;
PS00033;
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000 (Rel. 40, Last annotation update)
PROTEIN ENGRAILED-1 (HU-EN-1).
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199 218
224 231
302 361
391 AA; 400
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HOMEOBOX_2; 1.
ENGRAILED; 1.
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Pred. No. 7;
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Pred. No.
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Best Local Similarity
Matches 22; Conserv
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MEDLINE-97422617; PubMed-9268643;

Hanna M.C., Platts J.T., Kirkness E.F.;

"Identification of a gene within the tandem array of red and green color pigment genes.";

Genomics 4:384-386(1997).

-i- TISSUE SPECIFICITY: TESTIS-SPECIFIC.

-i- SIMILARITY: SOME, TO HUMAN KIAA0481.
                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     015482;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
TESTIS-SPECIFIC PROTEIN TEX28.
CXORF2 OR TEX28.
                                                                                                                                                                                                                                                                                   SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                       NCBI_TaxID=9606;
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410 AA; 46131 MW;
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              7, 2001, 02:10:31
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272
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Compugen Ltd.
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sp_invertebrate:*
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o35625 mus musculu
o15169 homo sapien
O9y9y0 xenopus lae
O9w7r4 brachydanio
O9rbi0 acinetobact
O34449 bacillus su
O64113 bacteriopha
O96565 junonia coe
O68167 lactococcus
                                                                                                               070240 rattus norv
088566 mus musculu
099x16 mus musculu
09y2t1 homo sapien
09uh84 homo sapien
042400 gallus gall
09ptp2 xenopus lae
070239 rattus norv
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        081599 triticum ae
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20.6	20.8	20.8	20.8	20.8	20.8	21.0	21.0	21.0	21.0	21.1	21.1	21.1	21.3	21.3	21.5	21.5	21.5	21.7	21.7	21.7	21.9	21.9	21.9	21.9	21.9
501	1100	526	. 483	207	90	722	435	287	156	1454	978	254	1707	259	1061	883	601	1327	884	363	7962	2715	442	369	129
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Q9uud0 sch1zosacch	Q9xim3 arabidopsis	Q9usx7 schizosacch	087270 bartonella	Q9m8w6 arabidopsis	Q74750 human immun	Q9xuj7 caenorhabdi	Q9v539 drosophila	Q9ssl8 arabidopsis	Q22757 caenorhabdi	Q9xii7 arabidopsis	067124 aquifex aeo	067279 aquifex aeo	Q17652 caenorhabdi	N	. Q9nqv6 homo sapien	Q9uli9 homo sapien				Q9zgq7 myxococcus	O O	Q9wts6 mus musculu	Q9nzj2 homo sapien	Q43379 avena sativ	047954 trypanosoma

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RESULT
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Best Local Similarity
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INTERPRO; IPRO01158; -.
PFAM; PF00615; RGS; 1.
PFAM; PF00778; DIX; 1.
PRODOM; PD001580; -; 1.
PRODOM; PD003639; -; 1.
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01-AUG-1998 (TrEMBLrel.
01-AUG-1998 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus embryos.";
MO1. Cell. Biol. 18:2867-2875(1998).
EMBL; AF017757; ARC40089.1; -.
HSSP: P49799; lAGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kikuchi A.; "Axil, a member of the Axin family, interacts with both glycogen synthase kinase 3beta and beta-catenin and inhibits axis formation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-98226558; PubMed-9566905;
Yamamoto H., Kishida S., Uochi T., Ikeda S.,
                                                                                                                                                                                                                                                                                                     SEQUENCE
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Mammalia; Eutheria;
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      343
838 AA;
                                                                                                                                     Conservative
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Rodentia;
                                                                                                                                                                                                                                                                                                  92947 MW; 45B825Cl3BA07F37 CRC64;
                                                                                                                              100.0%; Score 272; DB 1: 100.0%; Pred. No. 3e-23; tive 0; Mismatches
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Q9scq4 arabidopsis

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Query Match
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Best Local
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INTERPRO; IPRO01158; -.
PFAM; PF00615; RGS; 1.
PFAM; PF00778; DIX; 1.
PFAM; PF0071580; -; 1.
PRODOM; PD003539; -; 1.
PRODOM; PD003539; -; 1.
SEQUENCE 840 AA; 92934 MW; /
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Q9QXJ6;
Q1-MAY-2000
01-MAY-2000
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01-NOV-1998;
01-NOV-1998;
01-OCT-2000;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                 expression pattern, interaction axis formation.";
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Jenkins N.A., Warburton D., Costantini F.; "Properties of mouse Axin2 and human AXIN2: chromos
                                                                                                                                                                    PFAM;
                                                                                                                                                                                               PFAM;
                                                                                                                                                                                                                   EMBL; AF205889; AAF22800.1; HSSP; P49799; 1AGR. INTERPRO; IPR000342; -. INTERPRO; IPR001158; -.
                                                                                                                                                                                                                                                                                                                                                Submitted (NOV-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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MGD; MGI:1270862; Axin2.
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EMBL; AF073788; AAC26047.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-98221239; PubMed-9554852;
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Local Similarity 100.0%;
nes 54; Conservative
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PF00778; DIX; 1.
S; PR01301; RGSPR
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Pred. No. 3e-23;
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Score 272;
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Length 840;
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Best Local Similarity
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Q9UH84;
Q1-MAY-2000
Q1-MAY-2000
Q1-CCT-2000
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Q9Y2T1;
Q1-NOV-1999
01-NOV-1999
01-OCT-2000
                                                                                                                                   Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G., Jenkins N.A., Warburton D., Costantini F.; "Properties of mouse Axin2 and human AXIN2: chromosomal location, expression pattern, interaction with Axin and effects on embryoni axis formation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (NOV-1999) to the EMBL; AF205888; AAF22799.1; HSSP; P49799; LAGR.
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EMBL; AF078165; AAD20976.1; -.
                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                       INTERPRO; IPR000342; ~.
INTERPRO; IPR001158; ~.
                                                                                                                                                                                                                                                                                                                                                                                AXIN2
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HSSP; P49799; 1AGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99168905; PubMed=10049590; Mai M., Qian C., Yokomizo A., Smith "Cloning of the human homolog of con
                                                                                                                                                                                                                                         TISSUE=BRAIN, LYMPHOBLAST;
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM; PF00615; PFAM; PF00778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ANGQVSLPHFPRTHRLPKEMTPVEPAAFAAELISRLEKLKLELESRHSLEERLQ
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  PF00615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR000342; -. IPR001158; -.
                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 13, ) (TrEMBLrel. 13, ) (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
  RGS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGS;
                                                                                                                                                                                                                                                                                                                    Chordata;
Primates;
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93557 MW;
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98.1%;
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Pred. No. 8.6e
0; Mismatches
                                                                                                                    EMBL/GenBank/DDBJ databases
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; Mismatches
                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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.6e-23;
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Matches
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Best Local
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PFAM; PF00778; DIX; 1.
PR0DOM; PD001580; -; 1.
PR0DOM; PD003639; -; 1.
SEQUENCE 841 AA; 94931
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REDLINE-97373830; PubMed-9230313;

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01-JAN-1998
01-OCT-2000
                                                                                                                                                                                                                   Q9PTP2
Q9PTP2;
Q9PTP2;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-JUN-2000 (TrEMBLrel. 14, Last annotation update)
AXIN-RELATED PROTEIN.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pathway that regulates embryonic Cell 90:181-192(1997).
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SEQUENCE 777 AA
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INTERPRO; IPRO01158; ...
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HSSP; P49799; 1.
                                                              TISSUE-OVARY;
                                                                                                                                                                                                  Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9031;
                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                   NCBI_TaxID=8355;
Itoh K., Antipova A., Ratcliffe M.,
"Dishevelled transduces a signal by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          342
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52; Conserv
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32; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC60245.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RGSPROTEIN.
A; 86857 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.9%;
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Pred. No. 4.8e-10;
1; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 264; DB 4;
Pred. No. 2.3e-22;
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Sokol S.;
displacing
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   from
                                                                                                                                                                                                                              Euteleostomi;
; Pipidae;
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   axin-GSK3
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Best Local S
Matches 30
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Best Local
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musculus (Mouse).
Eukaryota; Metazoa; Chordata; C.
Mammalla; Eutheria; Rodentia; Sc
NCBI_TaxID-10090;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERPRO; IPRO00342; -.
INTERPRO; IPRO01158; -.
PFAM; PF00778; DIX; 1.
PRINTS; PR01301; RGSPROTI
SEQUENCE 706 AA; 79196
                                                                                                                                 035625 PRELIMINARY;
035625;
01-JAN-1998 (TrEMBLrel. 0
01-JAN-1998 (TrEMBLrel. 0
01-OCT-2000 (TrEMBLrel. 1
AXIN (FRAGMENT).
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INTERPRO; IPRO01158; -.
PRAM; PP00615; RGS; 1.
PPAM; PF00778; DIX; 1.
PRODOM; PD001580; -; 1.
PRODOM; PD003639; -; 1.
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070239;
01-AUG-1998
01-AUG-1998
01-OCT-2000
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MEDILINE-98151361; PubMed=9482734;

Ikeda S., Yamamoto H., Murai H., Kishida S., Kikuchi A.;

Ikeda S., Yamamoto H., Murai H., Kishida S., Kikuchi A.;

Raxin, a negative regulator of the Wnt signaling pathway, forms complex with GSK-3beta and beta-catenin and promotes GSK-3beta-dependent phosphorylation of beta-catenin.";

EMBO J. 17:1371-1384(1998).

EMBL; AF017756; AAC40066.1; -.

HSSP; P49799; LAGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases. EMBL: AF140243; AAF22574.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complex.";
Submitted (APR-1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                              368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           832
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illarity 56.6%;
Conservative
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A; 79196 MW;
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Rodentia;
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 142.5;
pred. No. 2.6e
8; Mismatches
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Pred. No. 1.5e-08;
7; Mismatches 17;
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                                                  Craniata; Vertebrata; I
Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                   PRT;
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                                                                           Euteleostomi;
                                                    Murinae;
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RESULT 11
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Best Local 9
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INTERPRO; IPRO01158; -.
PFAM; PF00615; RGS; 1.
PFAM; PF00778; DIX; 1.
PRINTS; PR01301; RGSPROTEIN.
NON_TER 1
 Q9YGYO;
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01-JAN-1998 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF009674;
HSSP; P49799; 1
                                                                                                                                                                                                                                                                                                                                                                                                                   pathway that regulate Cell 90:181-192(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Peri
III Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F
"The mouse Fused locus encodes Axin, an inhibitor of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=97373830; PubMed=9230313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
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HSSP; P49799; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L., III Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.; "The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling
                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
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                                                                                                      2 NGQYSLPHFPRTHRLPKEMTPVEPAAFÄAELISRLEKLKLELESRHSLEERLQ
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00 NGRVPLPHIPRTYRVPKEVR-VEPQKFAEELIHRLEAVQRTREAEEKLEERLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 NGQVSLPHFPRTHRLPKEMTPVEPAAFAAELISRLEKLKLELESRHSLEERLQ 54
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PF00778; DIX; 1.
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                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   that regulates embryonic
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                                                                                                                                                                                                                                                              900 AA;
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                     PRELIMINARY;
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Primates;
                                                                                                                                                                                                                                                                  99803 MW;
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15,
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; Pred. No. 3.1e
8; Mismatches
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Last annotation updat
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                                                                                                                                                                        Score 141.5; DB 4;
Pred. No. 3.6e-08;
""amatches 14;
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                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hsu W.,
                                                                                                                                                                                                                                                                  EE5F990B11FC7B3B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       formation.";
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nes 14;
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                                                                                                                                                                                                            DB 4; Length
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; Homo.
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RESULT
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Query Match
Best Local S
Matches 22
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Best Local :
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INTERPRO; IPRO01158; -.
PFAM; PF00615; RGS; 1.
PFAM; PF00778; DIX; 1.
PRODOM; PD001580; -; 1.
PRODOM; PD003639; -; 1.
PRODOM; PD003639; -; 1.
SEQUENCE 842 AA; 94459 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999
01-NOV-1999
01-OCT-2000
                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
Mieda M., Kikuchi Y., Hirate Y.,
Mieda M., Kikuchi Y., Hirate Y.,
"Compartmentalized expression of
"Compartmentalized expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE=99173782; PubMed=10072781;

Hedgepeth C.M., Deardorff M.A., Klein
"Xenopus axin interacts with glycogen
expressed in the anterior midbrain.";

Mech. Dev. 80:147-151(1999).
                                                                                                                                                                                                                                                                                                                                      Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AXIN.
                                                                                                                                                                                          Mech. Dev. 0:0-0(1999).
EMBL; AB026979; BAA81892.1;
HSSP; P02468; 1KLO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; (
Amphibia; Batrachia;
                                                                               PRINTS; PRO0011; EGFLAMININ.
PROSITE; PS00022; EGF_1; UNKNOWN_B.
PROSITE; F001186; EGF_2; 7.
SEQUENCE 2590 AA; 288587 MW; 59
                                                                                                                                                                                                                                                                                                                                                                                                                                         TEN-M3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9W7R4;
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                                                                                                                                                                                                                                           system."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=8355;
                                                                                                                                                PFAM; PF00008; EGF; 5.
                                                                                                                                                              INTERPRO; IPR000561; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    362 ANGRGPLPHIPRTYHMPKDI-HVDPEKFAAELISRLEGVLRDREAEQKLEERLK
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                Similarity
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Anura; Mesobatrachia; Pipoidea; Pipidae;
               25.0%;
31.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10,
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Score 68; DB Pred. No. 33; 6; Mismatches
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Last sequence up
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Last sequence update)
Last annotation update)
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0; Mismatches
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Pred. No. 1.3e-07;
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f zebrafish
nm /odd Oz g
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                                                                                                                                                                                                                                                            Okamoto H.;
h ten-m3 and ten-m4,
gene, in the centra
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                                 Length 2590;
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Conservative

--PVEPAAFAAELISRLEKLKLE---

19;

Indels

24;

Gaps

2

42

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76

**COSTLPPVPPPHKQQPSVTALNHNSLSSRRNVSPAPPAALPAELQTTPESVPLQDSWVLG** 

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RESULT 14
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Best Local
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MEDLINE-98044033; PubMed-9384377;

Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

Borriss R., Bourster L., Brans A., Braun M., Brignell S.C., Bron S.,

Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

Fritz C., Fujita M., Fujita Y., Funa S., Galizzi A., Galleron N.,

Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,

Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,

Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
                                                                                                                                                                                                                                                                                                              O34449;
01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERPRO; IPR001789; -.
INTERPRO; IPR001867; -.
PFAM; PF00072; response_reg; 1.
PFAM; PF00486; trans_reg_C; 1.
SEQUENCE 226 AA; 26423 MW; B3C1E641015C74DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2000 (TrEMBLrel. 15, Last annotation update)
PUTATIVE 2-COMPONENT REGULATORY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jones R.M., Collier L.S., Neidle E.L., Williams P.A.; "areABC genes determine the catabolism of aryl esters in Acinetobacter sp. strain ADP1.";
                                                                                                                                                                              STRAIN-168
                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                      Bacteria; Firmicutes; Bacillus/Staphylococcus NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                          034449
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                                                                                                                                                                                                                                                                   Bacillus subtilis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                135 GQVQL--FPNTHRILKDGQPINLSTKEWSILEPMMMYPNQIFSKQMLEEKL 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                     Firmicutes; Bacillus/Clostridium
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Pred. No. 7
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RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
Median N., Wellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Medina N., Wellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Parro V., Pohl T.M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Scrokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Sorokin A., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA Viari A., Wambutt R., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
"The complete genome sequence of the gram-positive bacterium Bacillus subtilis.";
                                                              Matches
                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kunst F., Ogasawara N., Yos
Submitted (NOV-1997) to the
EMBL; Z99114; CAB13959.1; -
EMBL; Z99115; CAB13985.1; -
SEQUENCE 251 AA; 28593 M
                                                                                                                                                                                                                                                                                                                                 01-AUG-1998 (TrEMBLrel.
01-AUG-1998 (TrEMBLrel.
01-AUG-1998 (TrEMBLrel.
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064113;
                                                                                                                                       Lazarevic V., Duesterhoeft A., Soldo B., Hilbert H., Man Karamata D.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases EMBL; AF020713; AAC13073.1; -.
SEQUENCE 251 AA; 28593 MW; BE79F500A3A0E3C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Kl
Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                     Viruses;
                                                                                                                                                                                                                                                                                  Bacteriophage SPBc2
                                                                                                                                                                                                                                                                                                                   PUTATIVE ANTIREPRESSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                     NCBI_TaxID-66797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
62
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390:249-256(1997).
                                                                          Similarity
                                                                                                                                                                                                                                                                     dsDNA viruses,
                                                              Conservative
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28593 MW;
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32.1%;
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07,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
                                                                                                                                                                                                                                                                     RNA stage; Tailed phages; Siphoviridae.
                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
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Pred. No. 13;
13; Mismatches
                                                                           Score 62.5;
Pred. No. 13;
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                                                            Mismatches
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21 G10503 Arabidopsis		٠.	61	23
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Y53920 A Bcl-2 a		·	۳	21
G21146		17.1	61.5	20
G27248		17.1		19
G59723 Arabidopsis			62	18
G59724 Arabid			62	17
W01437	348 1	17.2	62	16
G59725			62	15
B11726		17.4	N	14
B11732	1042 2:	17.4	62.5	13
21 Y57950 Human transmembran		17.6	63.5	12

## ALIGNMENTS

RESULT W93570

W93570;

W93570 standard; Protein; 840

8

Human conductin protein. 17-JUN-1999 (first entry)

Tumor-suppressing protein conductin diagnosis of tumors WPI; 1999-214706/18. N-PSDB; X23370. Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour; therapy; cytoplasmic degradation; blockade; Wnt signalling pathway; Wingless signalling pathway; Adenomatous Polyposis Coli; APC; Behrens J, Birchmeier W; 02-SEP-1997; 01-SEP-1998; 11-MAR-1999. WO9911780-A2. Homo sapiens (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX tumour suppressor 97DE-1038205. 98WO-DE02621. . used for treatment

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Best Local
  N-PSDB;
          WPI; 1999-214706/18
                                Behrens J,
                                                                           02-SEP-1997;
                                                                                                   01-SEP-1998;
                                                                                                                        11-MAR-1999
                                                                                                                                                                                                                                                                                                                                                        Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour; therapy; cytoplasmic degradation; blockade; Wnt signalling pathway; Wingless signalling pathway; Adenomatous Polyposis Coli; APC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel human conductin protein which has anti-tumour activity. Detecting the presence or amount of conductin, at protein or nucleic acid levels, is used to diagnose tumours, while agents that (re)activate conductin are used for tumour therapy. Conductin binds to beta-catenin and induces its cytoplasmic degradation,
                                                                                                                                              WO9911780-A2
                                                                                                                                                                                          Region
                                                                                                                                                                                                                          Binding-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            resulting in blockade of the Wnt/Wingless signalling pathway in vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC) fragments and, in conjunction with APC, acts as a tumour suppressor.
                                                                                                                                                                                                                                                                                                      Key
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                                                                                                                                                                                                                                                                                                                                                                                                       Human conductin protein
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                                                     (DELB-) DELBRUECK CENT MOLEKULARE
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                                 Birchmeier W;
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                                                                           97DE-1038205
                                                                                                  98WO-DE02621
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                                                                                                                                                                                          783..833
                                                                                                                                                                                                                                                                     /note= "Regulator of G protein signalling
  described in claim 12"
                                                                                                                                                                               /note-
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                                                                                                                                                                                                   "Beta-catenin
claim 14"
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                                                                                                                                                                                                                                    "GSK 3-beta binding region as claim 13"
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Pred. No. 2.9e-35;
Mismatches 0;
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                                                      MEDIZIN MAX
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Nucleic acids encoding mutant and wild type Axin and oligonucleotides derived from them are useful for detecting mutations in the Axin gene and for determining whether a subject likely to develop cancer (including breast, colorectal, gastrointestinal, esophageal, carcinomas or melanomas). The wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel human conductin protein which has anti-tumour activity. Detecting the presence or amount of conductin, at protein or nucleic acid levels, is used to diagnose tumours, while agents that (re)activate conductin are used for tumour therapy. Conductin binds to beta-catenin and induces its cytoplasmic degradation, resulting in blockade of the WntyWingless signalling pathway in vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC)
                                                                                                                                                                                                                                                                                                                                                                                      Axin; cancer; breast cancer; colorectal cancer; gastrointestinal cancer; esophageal cancer; carcinoma; melanoma; diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis; beta-catenin.
                                                                                    Claim
                                                                                                           Newly isolated nucleic acid encoding "axis inhibition" protein (Axin) - useful for detecting, diagnosing and treating cancer
                                                                                                                                                                                              Constantini F,
                                                                                                                                                                                                                                                   10-JUL-1997;
                                                                                                                                                                                                                                                                                09-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W96265 standard; Protein; 992 AA.
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DB; X09013.
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                                                                                   8; Figure 8; 95pp; English.
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Pred. No. 2.9e-35;
Mismatches 0;
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Nucleic acids encoding mutant and wild type Axin and oligonucleotides derived from them are useful for detecting mutations in the Axin gene and for determining whether a subject is likely to develop cancer (including breast, colorectal, gastrointestinal, esophageal, carcinomas or melanomas). The wild type Axin and homologues of Axin are useful for treating subjects who are likely to develop cancer (thyroid carcinomas). The nucleic acids are also useful for diagnosing cancer and for detecting mutations in cancerous cells. Wild type Axin, its antisense molecule and identified compounds form pharmaceutical compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      type Axin and homologues of Axin are useful for treating subjects who are likely to develop cancer (thyroid carcinomas). The nucleic acids are also useful for diagnosing cancer and for detecting mutations in cancerous cells. Wild type Axin, its antisense molecule and identified compounds form pharmaceutical compositions in the treatment of cancer. The compositions are also useful for treating cancer by inhibiting tumorigenesis (by inducing degradation of beta-catenin). The nucleic acid encoding Axin acts through negative regulation of the Wnt pathway in the Nieuwkoop Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Axin; cancer; breast cancer; colorectal cancer;
gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;
diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Constantini F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human axin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W96264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                            Disclosure; Figure 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Newly isolated nucleic acid encoding "axis inhibition"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-120510/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  beta-catenin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W96264 standard; Protein; 900 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                        (Axin) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 DDHLSRVLKTPGCQSPGVGRYSPRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity es 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QIREDEEKEGSEQALSSRDGAPVQHPLALLPS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dehvqrvmrtpgcqspgpghrspds 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful for detecting, diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         992 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97us-0890865
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                                                                                                                                                                                                                                                                                                                                            95pp; English.
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Pred. No. 2.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68
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Best Local S
Matches 33
                                                            Query Match
Best Local S
Matches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in the treatment of cancer. The compositions are also useful for treating cancer by inhibiting tumorigenesis (by inducing degradation of beta-catenin). The nucleic acid encoding Axin acts through negative regulation of the Wnt pathway in the Nieuwkoop Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                      Steroid; hormone;
                                                                                                                                                                                                                                                                                                                                                                                                         Steroid hormone receptor (NUCI).
                                                                                                                                                                                                                                                                                                                                                                                                                             13-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                 R41875
                                                                                                                                                                                                                                                                                                                                               GB2265376-A
                                                                                                                                                                                                                                                                                                                                                                    Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R41875 standard; Protein; 441 AA
                                                                                                            Sequence
                                                                                                                                The steroid hormone receptor (designated NUCI) is identify and evaluate chemical entities that bind
                                                                                                                                                             Claim 5; Page 39-40; 62pp;
                                                                                                                                                                                New human steroid hormone receptor NUCI -evaluate ligands binding to the receptor
                                                                                                                                                                                                                N-PDSB;
                                                                                                                                                                                                                                            Rodan GA,
                                                                                                                                                                                                                                                                (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                     24-MAR-1992;
                                                                                                                                                                                                                                                                                                         23-MAR-1993;
                                                                                                                                                                                                                                                                                                                             29-SEP-1993
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                               QIREDEEKEGSEQALSSRDGAPVOH--PLALLPSGSYEE-----DPOTILDDHLSRVLKT 53
                                                                                                                                                                                                                       1993-305586/39.
  PGCQSPGVGRYSPRSR 69
                     evreeeekeevaea----egapelnggpqhalpsssytdlsrsssppslldq-----lq
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                                                                      Similarity
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                                                                                                               441
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                                                                                                                                                                                                                                                                                     92US-0857055
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                                                                                                                                                                                                                                                                                                                                                                                       receptor; osteosarcoma; superfamily.
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                                                                      19.0%;
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                                                                                                                                                                                                                                             Schmidt A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                            ; Pred. No. 3.8; 10; Mismatches
                                                                                                                                                              English
                                                                      Score
Pred.
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                                                                      No. 3
                                                                                                                                                                                                                                             Vogel RL
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to it
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RESULT
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R89214
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Best Local 9
                                                                                                                                                                                                                                                                                                       Matches
                                                                                              07-JUL-1999
                                Nuclear receptor agonist; antagonist; identification; PPAR; peroxisome proliferator activated receptor.
                                                                     Human PPAR-delta protein sequence
                                                                                                                       Y05472;
                                                                                                                                             Y05472 standard;
                                                                                                                                                                                                                                                                                                                                                                                       A novel human peroxisome proliferator activated receptor (PPAR) designated hNUClB (R89214), is expressed from a cDNA clone (T10) isolated from a human kidney cDNA library. hNUClB is a member of the PPAR family and can be used to screen NUC protein inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 44; Page 29-31; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1996-087756/09.
N-PSDB; T10583.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypercholesteremia and hyperlipoproteinemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Screening methods for identifying NUC protein inhibitors - as potential agents for the treatment of hyperlipidemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mukherjee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LIGA-) LIGAND PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9601430-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hNUC1B; peroxisome proliferator activated receptor; hypercholesterolemia; hyperlipoproteinemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peroxisome proliferator activated receptor hNUC1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R89214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R89214 standard;
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                                                                                                                                                                                                                               54 PGCQSPGVGRYSPRSR
                                                                                                                                                                                                                                                                               1 QIREDEEKEGSEQALSSRDGAPVQH--PLALLPSGSYEE-----DPQTILDDHLSRVLKT 53
                                                                                                                                                                     7
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                                                                                                                                                                                                                                                      evreeeekeevaea----egapelnggpqhalpsssytdlsrsssppslldq-----lq
                                                                                                                                                                                                                                                                                                       l Similarity 30.3
23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                   441 AA;
                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94US-0270635
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                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein; 441 AA
                                                                                                                                                                                                                                                                                                                                                                                     R89214), is expressed from a cDNA clone (T10583) an kidney cDNA library. hNUClB is a member of can be used to screen NUC protein inhibitors.
                                                                                                                                                                                                                                                                                                                 19.0%;
                                                                                                                                                                                                                                69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hyperlipoproteinemia
                                                                                                                                             441
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                                                                                                                                                                                                                                                                                                     Score 68.5; DB Pred. No. 3.8; 10; Mismatches
                                                                                                                                             B
                                                                                                                                                                                                                                                                                                                              DB 17;
                                                                                                                                                                                                                                                                                                        26;
                                                                                                                                                                                                                                                                                                                              Length 441;
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                                                                                                                                                                                                                                                                                                       17;
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RESULT
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Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             agonists and antagonists comprises measuring fluorescent resonance transfer between fluorescent-labelled nuclear receptors and co-activators. The method can be used for identifying agonists and antagonist of nuclear receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence is the human peroxisome proliferator activated receptor-delta (PPAR-delta).

The invention relates to a method for identifying nuclear receptor
                                                                                                                                                                             antimitotic factor; mitosis.
                                                                                                                                                                                      Human; MIN1; cell cycle; G2/M border; progression; cdc2 kinase; yeas
functional complementation; weel; mik1; mutant; cancer; development;
                                                                                                                                                                                                                                          08-AUG-1996 (first entry)
                 N-PSDB; T05406.
                             WPI; 1995-399339/51.
                                                                     05-APR-1994;
                                                                                          05-APR-1994;
                                                                                                               24-OCT-1995
                                                                                                                                   JP07274971-A
                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                     Human cell
                                                                                                                                                                                                                                                               R77417;
                                                                                                                                                                                                                                                                                  R77417 standard; Protein; 1132 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 10a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying nuclear receptor agonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-263998/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cummings RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-OCT-1997;
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                                                (SHKJ ) SHINGIJUTSU JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9918124-A1
                                                                                                                                                                                                                                                                                                                                                         54 PGCQSPGVGRYSPRSR 69
                                                                                                                                                                                                                                                                                                                                                                              10 evreeeekeevaea----egapelnggpqhalpsssytdlsrsssppslldq-----lq 59
                                                                                                                                                                                                                                                                                                                                     60 mgcdgascgslnmecr
                                                                                                                                                                                                                                                                                                                                                                                          1 QIREDEEKEGSEQALSSRDGAPVQH--PLALLPSGSYEE-----DPQTILDDHLSRVLKT 53
                                                                                                                                                                                                                                                                                                       œ
                                                                                                                                                                                                                     cycle protein min1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          441 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hermes
                                                                      94JP-0093033.
                                                                                          94JP-0093033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0061385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-US21049
                                                                                                                                                                                                                                                                                                                                                                                                                                  19.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ą,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60pp; English.
                                                                                                                                                                                                                                                                                                                                       75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Moller
                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 68.5;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhou
                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ç;
                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
                                                                                                                                                                                                                                                                                                                                                                                                                         26;
                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 441;
                                                                                                                                                                                                                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              energy
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Human derived cell cycle gene encoding an anti:mitotic factor -

used

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RESULT W29659
ID W2965
AC W296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
          Query Match 18.9
Best Local Similarity 32.9
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1033 vktpqcqhvspgm 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is the amino acid sequence of the human MIN1 gene product. The protein has a mol. wt. about 129 kD. The gene is expressed at the G2/M border of the cell wycle and can inactivate the cell cycle progression protein cdc2 kinase. The gene was isolated by functional complementation of a yeast weel/mik1 mutant strain. The gene and protein can be used in the determination of cancer cell development and as an antimitotic
                                                                                                                                                                                                                                                                                           New isolated nucleic acids and secreted proteins - obtained from human adult ovary, human foetal kidney, human foetal brain and human adult brain cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   secreted protein; BP202_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 4; 5pp; Japanese
                                                                                                                                         Sequence
                                                                                                                                                                                          The sequence is that of a novel, isolated secreted protein.
                                                                                                                                                                                                                                           Disclosure; Page 67-68; 113pp; English
                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; V40520.
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-413686/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-JAN-1998;
09-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens BP202_3 clone secreted protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W29659 standard; Protein; 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         factor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Agostino MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                976 qfleqlpkddhddffst---tplqhqrillpsfqgseddddilpnmdknpttpssvifpl 1032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 LKTPGCQ--SPGV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QIREDEEKEGSEQALSSRDGAPVQHPLALLPSGSYEEDPQTILDDH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J, Jacobs K,
Spaulding V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1132 AA;
                                                                                                                                         397 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0004684.
97US-0780814.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-US00543.
18.9%; pre
32.9%; pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lavallie ER,
Treacy M;
          Score 68; DB;
Pred. No. 3.9;
10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 68.5; DE Pred. No. 12; 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      мсСоу ЈМ,
                                                           DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26;
             23;
                                                           Length 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ö
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             18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
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          Gaps
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B 8

11 SEQALSSRDGAPVQHPLALLPSGSYEEDPQTILDDHLSRVLKTPGCQSPGVG--RYSPRS 68

seq--sasesapedqp-----dreedpragaed--pkaekspgadskglgckrgspka 232

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                                                                          RESULT 10
W44865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
Matches
            Query Match
Best Local Similarity
                                                                                                therapeutic agents, and for diagnostic tests. In addition, peptides corresponding to TPC2 or TPC3 proteins can also be used to regulate telomere length and telomerase activity in mammalian cells. Immunogenic peptides and proteins of the invention can also be used in therapeutic immunisation and vaccination procedures. Antibodies that specifically bind to TPC2 or TPC3 proteins can be used in screening, diagnosing and monitoring diseases and other conditions, such as cancer, pregancy or fertility.
                                                                                                                                                                                                                                         telomere length or modulates telomerase activity. Its amino acid sequence was deduced from a cDNA clone (see V19480) obtained from a human 293 cell library. TPC3 and TPC2 (see W4864) proteins can be obtained by purification from natural sources, by in vitro synthesis or by purification from recombinant host cells. They have application in methods for reconstituting in vitro telomerase or other enzymatic activities that maintain telomeres and regulate
                                                                                                                                                                                                                                                                                                                                                     This polypeptide comprises human TPC3, a protein that regulates
                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 6A-C; 86pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; V19480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-207373/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adams RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ·13-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-MAR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnosis; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TPC3; telomere length;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human TPC3 telomere length and telomerase regulatory protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W44865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W44865 standard; Protein; 382 AA.
                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                 telomerase activity
                                                                                                                                                                                                                                                                                                                                                                                                                               Human TPC2, TPC3 and TR genes - regulate telomere length or modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GERO-) GERON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238 qmrefleqlpkddhddffst---tplqhqrillpsfqdsedddilpnmdknpttpssv1 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295 fplvktpqcqhvspgm 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48 SRVLKTPGCQ--SPGV 61 ::||| || |||:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QIREDEE---KEGSEQALSSRDGAPVQHPLALLPSGSYEEDPQTILDDH------L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Andrews WH,
                                                                          382 AA;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96WO-US14679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96WO-US14679
              17.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        telomerase; human; cancer; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Feng J,
9;
              Score 63.5;
Pred. No. 13;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Villeponteau
                            DB
                              19;
17;
                            Length
 Indels
                               382;
 13;
 Gaps
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Y57950
ID Y55
XX Y5
AC Y5
XX Y5
DT 23
DT 23
DX HU
XX HU
XW HU
KW AN
KW AN
KW GE
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                                                                                                                                                                                                                                                        Matches
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05-JAN-1996;
13-SEP-1996;
                                                                                                                                                                                                                                                                                                                                   This sequence is the human TPC3 protein, which is contained within the recombinant mammalian host cell of the invention. The invention provides methods and reagents for regulating telomera length and modulating telomerase activity in mammalian cells as well as for detecting, diagnosing, and treating related diseases and conditions as cancer, pregnancy, or fertility in humans and other mammals.
           antiproliferative; neuroprotective; immune disorder;
reproductive disorder; smooth muscle disorder; neurological disorder;
gastrointestinal disorder; developmental disorder;
                                              Human; transmembrane protein; HTMPN; diagnosis; immunospecific;
                                                                      Human transmembrane protein HTMPN-74.
                                                                                                23-MAR-2000
                                                                                                                                              Y57950 standard;
                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                              {\tt DNA} encoding proteins TPC2 and TPC3 - useful for regulating telomere length or modulating telomerase activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPC2; TPC3; human; telomere length regulation; cancer;
fertility; diagnosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams RR, Andrews WH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US5858777-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human TPC3 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W73959;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W73959 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GERO-) GERON CORP.
                                                                                                                                                                                                        236 seq--sasesapedqp-----dreedpragaed--pkaekspgadskglgckrgspka 284
                                                                                                                                                                      12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11
                                                                                                                                                                                                                              11 SEQALSSRDGAPVQHPLALLPSGSYEEDPQTILDDHLSRVLKTPGCQSPGVG--RYSPRS 68
                                                                                                                                                                                                                                                                    Local
  proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1999-152104/13.
                                                                                                                                                                                                                                                       Similarity
21; Conserv
                                                                                                                                                                                                                                                                                                                  434 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                        Fig 6; 59pp; English.
                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                               (first entry)
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96US-0583808.
96US-0710249.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-0710249
                                                                                                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                17.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feng
                                                                                                                                               605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            434
                                                                                                                                                                                                                                                       9;
                                                                                                                                                                                                                                                                Score 63.5;
Pred. No. 15;
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                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Villeponteau
                                                                                                                                                                                                                                                                               DВ
                                                                                                                                                                                                                                                      17;
                                                                                                                                                                                                                                                                               20;
                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pregnancy;
                                                                                                                                                                                                                                                                               434;
                                                                                                                                                                                                                                                       13;
                                                                                                                                                                                                                                                      Gaps
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RESULT
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Best Local S
Matches 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-JUL-1998;
02-OCT-1998;
24-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                       neuroprotective activities. The human transmembrane proteins, polynucleotides encoding them and other compositions and methods from the present invention, can be used for the diagnosis, treatment or prevention of immune, reproductive, smooth muscle, neurological, gastrointestinal, developmental and cell proliferative disorders. The HTMPN's can be used to treat or prevent disorders associated with a decreased expression or activity of HTMPN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 256698 to 256776 encode Y57877 to Y57955 which represent human transmembrane proteins designated HTMPN-1 to HTMPN-79, respectively. The transmembrane protein have immunospecific, antiproliferative and neuroprotective activities. The human transmembrane proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proteins, polynucleotides, vectors, host cells and antibodies used to diagnose, treat or prevent immune, reproductive, smooth muscle, neurological, gastrointestinal, developmental and cell proliferative disorders
                                                                                                           GP900;
                                                                                                                                    Cryptosporidium parvum Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
                      US6071518-A
                                            Cryptosporidium
                                                                      cytoplasmic
                                                                                   merozoite; diarrhoea; protozoacide;
                                                                                              competitive inhibition; attachment;
                                                                                                                                                              28-OCT-2000
                                                                                                                                                                                                            B11732 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 172-174; 229pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INCY-)
                                                                                                                                                                                                                                                                       161 reeeeeeeeeemekeevekqdveeeeellpvngsqeeakpqvrdfsltsssqtpg
                                                                                                                                                                                                                                     <u>, 1</u>
                                                                                                                                                                                                                                                                                      3 REDEEKEGSEQALSSR--DGAPVQHPLALLP-SGSYEEDPQTILDDHLSRVLKTPG 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000-072605/06.
DB; Z56771.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens
                                                                                                            Iowa
                                                                                                                                                                                                                                                                                                                        19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INCYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lal
                                                                                                                                                                                                                                                                                                                                                                                     605 AA;
                                                                       domain.
                                                                                                           isolate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patterson
                                                                                                                                                           (first entry)
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98US-0102954.
98US-0109869.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US11904
                                              parvum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hillman
                                                                                              glycoprotein; antibody; cryptosporidiosis;
on; attachment; invasion; ligand binding; s
                                                                                                                                                                                                                                                                                                                        17.6%; Score 63.5; 33.9%; Pred. No. 23; tive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ç
                                                                                                                                                                                                           1042
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                                                                                                                                    isolate GP900, domain
                                                                                                                                                                                                            AA
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                                                                                   invasion; domain 5;
                                                                                    domain
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Kaser MR, 1
                                                                                                                                                                                                                                                                                                                                                 DB 21;
                                                                                                                                                                                                                                                                                                                         24;
                                                                                    transmembrane
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                                                                                                                                                                                                                                                                                                                                                 Length 605;
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                                                                                     domain;
                                                                                                 sporozoite;
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GG GP900 antibody production, and to a method of cryptosporidiosis treatment CG or prophylaxis comprising administration of anti-GP900 antibodies to an chindvidual. Cryptosporidium parvum GP900 and GP900 fragments are able to competitively inhibit sporozoite or merozoite attachment or invasion, and care also useful for the generation of anti-GP900 antibodies. The cc antibodies also inhibit sporozoite or merozoite attachment/invasion, and cadditionally inhibit the binding of GP900 ligands to GP900. GP900 cc proteins, fragments and antibodies may therefore be used to treat or prevent cryptosporidiosis. Infection with Cryptosporidium is a common cc use of diarrhoea in humans and causes life-threatening diarrhoea in immunocompromised persons. Cryptosporidiosis can be contracted from cc contaminated municipal water supplies (e.g., public swimming pools). It is also a cause of disease in animals, resulting in financial losses in cc agriculture. GP900 fragments, fusion proteins and antibodies may also be used for the diagnosis of Cryptosporidium parvum infections, and for the cused for the diagnosis of Cryptosporidium parvum infections, and for the detection of the parasite in the environment. Sequences B11728-B11732 cc for GP900, which contains a putative transmembrane domain and a cortant contains a putative transmembrane domain and a
                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-SEP-1996;
01-JUN-1993;
29-MAY-1992;
03-APR-1995;
             Cryptosporidium parvum Iowa isolate
                                                  28-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to the GP900 glycoprotein of the protozoan Cryptosporidium parvum, DNA encoding it, GP900 fragments, and fusion proteins comprising GP900 fragments. The invention also relates to the administration of GP900 or fragments thereof to a host to elicit anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New GP900 protein fragments and fusion proteins of Cryptosporidium parvum, useful for detecting the presence of the parasite, and diagnosing or treating Cryptosporidium infections by competitive inhibition of the function of GP900 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (REGC ) UNIV
                                                                                        B11726;
                                                                                                                           B11726 standard; Protein; 1837
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytoplasmic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Column 73-80; 59pp; English.
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                                                                                                                                                                                                                                                      QSPGVGRYSPRS 68
                                                                                                                                                                                                                                                                                                                 KEGSEQALSSRDGAPVQHPLALLPSGSYEEDPQT----
                                                                                                                                                                                                                                                                                                                                                                     21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1042 AA;
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92US-0891301.
95US-0415751.
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                                                                                                                                                                                                                                                                                                                                                                  Score 62.5; D
Pred. No. 59;
8; Mismatches
                 GP900
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                                                                                                                                                                                                                                                                                                                                                                                                      Length 1042
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QSPGVGRYSPRS

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kagsqskssdesgnpid----

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1706 aapkkggvipes 1717

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                                                                                                                                                                               Cryptosporidium parvum, DNA encoding it, GP900 fragments, and fusion CC cryptosporidium parvum, DNA encoding it, GP900 fragments, and fusion CC administration of GP900 or fragments thereof to a host to elicit anti-CC GP900 antibody production, and to a method of cryptosporidiosis treatment CC or prophylaxis comprising administration of anti-GP900 antibodies to an individual Cryptosporidium parvum GP900 and GP900 fragments are able to CC competitively inhibit sporozoite or merozoite attachment or invasion, and CC are also useful for the generation of anti-GP900 antibodies. The CC antibodies also inhibit sporozoite or merozoite attachment or invasion and CC anditionally inhibit the binding of GP900 ligands to GP900. GP900 proteins, fragments and antibodies may therefore be used to treat or prevent cryptosporidosis. Infection with Cryptosporidium is a common CC cause of diarrhoea in humans and causes life-threatening diarrhoea in immunocompromised persons. Cryptosporidiosis can be contracted from CC inmunocompromised persons. Cryptosporidiosis can be contracted from CC instantiated municipal water supplies (e.g., public swimming pools). It is also a cause of disease in animals, resulting in financial losses in agriculture. GP900 fragments, fusion proteins and antibodies may also be used for the diagnosis of Cryptosporidium parvum infections, and for the CC detection of the parasite in the environment. The present sequence CC represents the GP900 protein of the Iowa isolate of Cryptosporidium
                                       Matches
                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-SEP-1996;
01-JUN-1993;
29-MAY-1992;
03-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New GP900 protein fragments and fusion proteins of Cryptosporidium parvum, useful for detecting the presence of the parasite, and diagnosing or treating Cryptosporidium infections by competitive inhibition of the function of GP900 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GP900; Iowa isolate; glycoprotein; antibody; cryptosporidiosis; competitive inhibition; attachment; invasion; ligand binding; s
                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to the GP900 glycoprotein of the protozoan Cryptosporidium parvum, DNA encoding it, GP900 fragments, and fu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Petersen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         merozoite; diarrhoea; protozoacide
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                                                         Local Similarity
8 KEGSEQALSSRDGAPVQHPLALLPSGSYEEDPQT----
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)B; A61846, A61847.
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                                       21;
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                                                                                                                                 1837
                                       Conservative
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93US-0071880.
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                                                                                                                                 A,
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                                                         17.48;
29.28;
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                                   Score 62.5; DB 21;
Pred. No. 1.2e+02;
Pred. No. 1.2e+02;
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   -----ILDDHLSRVLKT-PGC 56
                                                                          Length 1837;
                                         Indels
                                         17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G59725
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PR 23.AUG-1999 99US-014993.
PR 25.AUG-1999 99US-0150864.
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd
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/cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/1aa/backfiles1.pep:*
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US-08-726-320-4
US-08-928-361B-30
US-08-700-651-5
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US-08-404-531B-28
US-08-476-900A-28
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US-08-488-546A-29
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US-08-415-655-13
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US-08-928-361B-5
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                                      US-08-928-361B-6
US-09-102-204-1
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32.521 Million cell updates/sec
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              Sequence 4, Appli Sequence 5, Appli Sequence 15, Appli Sequence 15, Appli Sequence 29, Appli Sequence 29, Appli Sequence 29, Appli Sequence 29, Appli Sequence 39, Appli Sequence 30, Appli Sequence 5, Appli Sequence 2, Appli Sequence 6, Appli Sequence 7, Appli Sequence 1, Appli Sequ
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US-08-710-249-4
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5. 4	54.5	54.5	54.5	55.5	55.5	56	56	56	56	56	56.5	56.5	56.5	56.5	56.5	56.5	56.5
15.0	15.1	15.1	15.1	15.4	15.4	15.6	15.6	15.6	15.6	15.6	15.7	15.7	15.7	15.7	15.7	15.7	15.7
993	222	222	206	242	242	1199	1162	432	432	432	711	711	471	471	459	449	449
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US-09-060-410-4	5185431-4	US-09-040-483-3	5185431-1	US-09-206-537-2	US-08-845-998-2	US-09-208-742-2	US-08-728-323A-2	US-08-480-912-8	US-08-488-382A-8	US-08-522-166-8	US-08-465-473B-7	US-08-235-838-7	PCT-US94-02539-31	US-08-657-392-31	US-08-673-312-2	PCT-US94-02539-2	US-08-657-392-2
Sequence 4, Appli	Patent No. 5185431	Sequence 3, Appli	Patent No. 5185431	Sequence 2, Appli	•	Sequence 2, Appli	•	•	Sequence 8, Appli	Sequence 8, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 31, Appl	Sequence 31, Appl	Sequence 2, Appli		Sequence 2, Appli

## ALIGNMENTS

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; TOPOLOGY: 11; MOLECULE TYPE: US-08-710-249-4
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                                                                                                                                                                                                                                        CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/583,808
FILING DATE: 05-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/003,492
FILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REGISTRATION NUMBER: 32,944
                                                                                                                                  TELEFAX: (415) 576-03
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acids
                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Methods and Reagents for Regulating TITLE OF INVENTION: Telomere Length and Telomerase Activity NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Andrews, William H. APPLICANT: Adams, Robert R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Villepontea APPLICANT: Feng, Junli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Two Embarca
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 13-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
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                                                                amino acid
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; Sequence 5, Application US/08928361B
; Patent No. 6071518
                                RESULT 3
US-08-928-361B-5
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Best Local :
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INFORMATION FOR SEQ ID NO: 11:
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                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1042 amino acids
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APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 650-324-1677
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MEDIUM TYPE: Floppy disk
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                                                                                                       911 AAPKKGGVIPES 922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 48
                                                                                                                                        57 QSPGVGRYSPRS 68
                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS
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35.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES INFECTIONS
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Pred. No. 18;
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                                                                                                                                                                                                                        Sequence 5, Application Patent No. 6025480
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INFORMATION FOR SEQ ID NO: 5:
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                                                                                                                   TITLE OF INVENTION: TITLE OF INVENTION:
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ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                    APPLICANT: Massague, Joan APPLICANT: Lee, Mong-hong
                                                                                                                                                                                                                                                                                                                                                                                              1652 KAGSQSKSSDESGNPID-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1837 amino acids
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ADDRESSEE: PETERS, VERNY, JONES & BIKSA STREET: 385 Sherman Avenue, Suite 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
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                                                                                                                                                                                                                                                                                                                                                              57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity nes 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Verny, Hana REGISTRATION NUMBER:
                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 12-SEP
                                                                 ADDRESSEE:
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               New York
New York
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                                                                                                                                                                                                                                         Application US/08415655
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                                                 E: Cooper & Dunham
1185 Avenue of the Americas
United States of America
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SYSTEM: PC-DOS/MS-DOS
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12-SEP-1997
                                                                                                                   ISOLATED NUCLEIC ACID MOLECULES ENCODING p75KIP2, A CYCLIN-DEPENDENT KINASE INHIBITOR AND USES SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.4%; 29.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES INFECTIONS
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Pred. No. 40;
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

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Best Local Similarity
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Sequence 13, Application US/08415655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6025480 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747/47418
                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/415,655
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
NEGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Massague, Joan APPLICANT: Lee, Mong-hong
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                                                                                                                                                                                                                                                                                                                                                                                                         UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 332 VAPGVGAVEQTPRKR 346
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CITY: New York
STATE: New York
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STRANDEDNESS: not rele
TOPOLOGY: not relevant
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1185 Avenue of the Americas
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US-08-415-655-15
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Best Local Similarity 30.7
Matches 23; Conservative
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INFORMATION FOR SEQ ID NO:
                                                             TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Massague, APPLICANT: Lee, MONG TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 1747/47418
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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COMPUTER READABLE FORM:
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                 MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: not
                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                              amino acid
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: United States of America
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1185 Avenue of the Americas
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                                   linear
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                                                                                                                                    (212)
              protein
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                                                                                                                                      278-0400
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Query Match Best Local Similarity

17.2%; 30.7%;

Score 62; Pred. No.

DB 4.8;

Length 348;

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US-08-476-900A-29
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MOLECULE TYPE: protein
US-08-404-531B-29
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APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonylurea Patent No. 6031150

TITLE OF INVENTION: and Method of Detecting Persistent Hyperi TITLE OF INVENTION: Infancy
                                                                                  Sequence 29, Application US/08476900A Patent No. 6031150
GENERAL INFORMATION:
APPLICANT: Joseph Bryan, Lydia Ag
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 29, Application US/08404531B Patent No. 5863724
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GENERAL INFORMATION:
GENERAL INFORMATION:
JOSEPH Bryan, Lydia Aguilar Bryan, Daniel Nelson, Pamela
APPLICANT: Thomas, Gilbert Cote, and Robert Gagel
APPLICANT: Thomas, Gilbert Cote, and Robert Gagel
TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonylurea Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: Beardell, Lori Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                      948 KASEPSQGLPRAMSSRDG------LILDEEEEEEEAAESEEDDNLSSVL 990
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STREET: One Liberty Place 46th. Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 -- PGVG--RYSPRSR 69
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                                                                                                                                                                                                                                                                                               3 REDEEKEGSEQALSSRDGAPVQHPLALLPSGSYEEDPQTILDDHLSRVL 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
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and Method of Detecting Persistent Hyperinsulinemic Hypoglycem Infancy
                                                                                                                                                                                                                                                                                                                                                            16.4%;
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                                                                                                                                                                                                                                                                                                                                      Score 59; DB
Pred. No. 84;
7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                       Patent No. 6054313
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 29, Application US/08488546A Patent No. 6054313
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                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,546A
                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                               CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Joseph I
                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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FILING DATE:
                                                                      FILING DATE:
                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                     ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz ADDRESSEE: No. 6054313ris
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: No. 6031150ris
STREET: One Liberty Place 46th. Floor
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Thomas, Gilbert Cote, and Robert Gagel
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15-MARCH-1995
                                                                      07-JUNE-1995
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                                                                                                                                          PC-DOS/MS-DOS
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                08/404,531
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Pred. No. 84;
7; Mismatches 1
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ATTORNEY/AGENT INFORMATION:

CLASSIFICATION:

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Query Match
Best Local Similarity
Thes 18; Conserve
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Best Local Similarity
Watches 18; Conserve
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                                                                                                       US-08-404-531B-9
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NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                     TELEFAX: 215-568-3439 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson, Pamela APPLICANT: Thomas, Gilbert Cote, and Robert Gagel TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonylurea Receptor
                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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LENGTH: 1582 amino aci
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                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/404,531B FILING DATE: 15-MAR-1995
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ZIP: 19103
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                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                      NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER:
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One Liberty Place 46th, Floor
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                 Conservative
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                 16.48;
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                              Score 59;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 59; DB
Pred. No. 84;
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                 Mismatches
                                                 DB 2; Length 1582;
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                 18;
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                                                                                                                                                                                                                                     RESULT
                                                                                                                                                     Patent No. 6054313
GENERAL INFORMATION:
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Matches
                                                              Patent No. 6054313

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                     APPLICANT: JOSEPH DA. APPLICANT: Thomas, G. APPLICANT: Thomas, G. TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: an TITLE OF INVENTION: IN NUMBER OF SEQUENCES: 4
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ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                    948 KASEPSQGLPRAMSSRDG--
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 STREET:
                                                                                                                                                                                                                                                                                                                                                     Local Similarity 36.7 tes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 07-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                             ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz ADDRESSEE: No. 6054313ris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 REDEEKEGSEQALSSRDGAPVQHPLALLPSGSYEEDPQTILDDHLSRVL 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9, Application US/08476900A
5. 6031150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
: One Liberty Place 46th. Floor Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PΑ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.25
                                                                                                                               Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson, Pamela
Thomas, Gilbert Cote, and Robert Gagel
                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-JUN-1995
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: Sequence Encoding Mammali
                                                                                                                                                                                                                                                                                                                                                                    16.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Infancy
49
                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Method of Detecting Persistent Hyperinsulinemic Hypogly
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                                                                                                                                                                                                                                                                                    ----LLLDEEEEEEEAAESEEDDNLSSVL 990
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                                                                                                                                                                                                                                                                                                                                                     Score 59; DB Pred. No. 91; 7; Mismatches
                                                                                                                  Encoding
                                                                                                                  Mammalian
                                                                                                                                                                                                                                                                                                                                                                                    DB 3; Length 1582;
                                                                                                                                                                                                                                                                                                                                                      18;
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                                                                                                                  Sulfonylurea Receptor
                                                                                                                                                                                                                                                                                                                                                      Indels
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US-08-726-320-5
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Best Local Similarity 36.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/08726320 Patent No. 6171815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 215-568-3439
                                                                                                        APPLICATION NUMBER: US/08/726,320 FILING DATE: Filed Herewith PRIOR APPLICATION DATA:
                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Coleman, Roger
TITLE OF INVENTION: NOVEL HUMAN SULFONYLUREA RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     948 KASEPSQGLPRAMSSRDG-----LILDEEEEEEEAAESEEDDNLSSVL 990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTORNEY/AGENT INFORMATION:
              NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                    CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 15-MAR CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08, FILING DATE: 07-JUNE-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 REDEEKEGSEQALSSRDGAPVQHPLALLPSGSYEEDPQTILDDHLSRVL 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH:
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                                                                                                                                                                                                            IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215-568-3100
                                                                                                                                                                                                                                Diskette
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 NUMBER:
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AF-0001 US
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Pred. No. 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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US-08-007-282B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                        TELEX: 248345
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 567 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR., GERALD M.
REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
             HYPOTHETICAL:
                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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LIBRARY: GenBa
CLONE: 784874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                             TYPE: AMINO STRANDEDNESS:
                                                                                                                                                  TELEPHONE: /U3-205-8050
                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
SOFTWARE: PatentI
                                               TOPOLOGY:
                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: UFILING DATE: 19930121
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 22042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                              AMINO ACID
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VA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: BIRCH, STEWART, KOLASCH & BIRCH 8110 Gatehouse Road Suite 500 East
                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CALVERT, JAI .. CALVERT, RICHARD L.
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NO
                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.4%;
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                                                                                                                                                                                                                          28,977
                                                                                                                                                                                                                1644-104P
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: POS/MS-DOS
SOFTWARIK SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,531B
FILING DATE: 15-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Beardell, Lori Y.
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0003
TELEPHONE: 215-568-3100
TELEPHONE: 
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Search completed: June 7, 2001, 02:02:11 Job time: 5404 sec
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US-08-404-531B-28
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Patent No. 5863724
GENERAL INFORMATION:
APPLICANT: Joseph Bryan, Lydia Aguilar Bryan, Daniel Nelson, Pamela
APPLICANT: Thomas, Gilbert Cote, and Robert Gagel
TITLE OF INVENTION: Sequence Encoding Mammalian Sulfonylurea Receptor
                                                                                                                                                                                                                                                                                                                                                                 Query Match 16.1%;
Best Local Similarity 39.1%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 16.1%;
Best Local Similarity 37.5%;
Matches 15; Conservative
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                                            951 EPSQGLPRAMSSRDG------LLLDEDEEEEEAAESEEDDNLSSVL 990
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ADDRESSEE: No. 5863724ris
STREET: One Liberty Place 46th. Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: UZIP: 19103
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                                                                                                                                                                                                                                                  6 EEKEGSEQALSSRDGAPVQHPLALLPSGSYEEDPQTILDDHLSRVL 51
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                                                                                                                                                                                                                                                                                                                                                             Score 58; DB 2; Length 1498;
Pred. No. 1.1e+02;
6; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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## ALIGNMENTS

R:Yamamotto, H.; Kishida, S.; Uochi, T.; Ikeda, S.; Koyama, S.; Asashima, M.; Kikuchi, Mol. Cell. Biol. 18, 2867-2875, 1998
A;Title: Axil, a member of the Axin family, interacts with both glycogen synthase kin A; Reference number: Z16414; MUID: 98226558
A; Accession: T08423
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-838 <7AM>
A; Cross-references: EMBL:AF017757; NID:g3080758; PIDN:AAC40089.1; PID:g3080759
A; Note: interacts with GSK-3beta and beta-catenin
C; Keywords: phosphoprotein; signal transduction A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Residues: 1-832 <IKE>
A.Cross-references: EMBL:AF017756; NID:g2982197; PIDN:AAC40066.1; PID:g2982198
A:Note: GSK-3beta interacting protein
C:Keywords: phosphoprotein; signal transduction N;Alternate names: rAxin (Norway rat)
C;Species: Rattus norwegicus (Norway rat)
C;Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 21-Jul-2000
C;Accession: T08422
R;Ikeda, S.; Yamamoto, H.; Murai, H.; Kishida, S.; Kikuchi, A.
EMBO J. 17, 1371-1384, 1998
A;Reference number: Z16413; MUID:98151361
A;Accession: T08422
A;Accession: T08422 Axin homolog Axil - rat
W; Alternate names: Axil
C; Species: Rattus norvegicus (Norway rat)
C; Date: 05-Nov-1999 #sequence\_revision 05
C; Accession: T08423
C; Accession: T08423 Вp δõ 밁 Š negative regualtor axin [imported] - rat Query Match Best Local ( Matches 457 VGRYSPRSR 465 61 VGRYSPRSR 69 ch 100.0%; 1 Similarity 100.0%; 69; Conservative 0; Score 360; DB 2; Pred. No. 3.9e-32; ); Mismatches 0; 05-Nov-1999 #text\_change 21-Jul-2000 Length Indels 838; 0, Gaps 0

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A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-745',V',747-793 <RES> A;Residues: 1-745',V',747-793 <RES> C;Comment: This subtilisin-like endoproteinase removes paired basic resic C;Comment: This subtilisin-like endoproteinase removes paired basic resic C;Genetics: A;Gene: FUR
                                                                                                                                                         A;Cross-references: GB.X54056; NID:g50996; PIDN:CAA37988.1; PID:g50997 R;Creemers, J.J.W.; Roebroek, A.A.J.; van den Ouweland, A.A.M.; van Duf Mol. Biol. 11, 127-138, 1992 A;Title: Cloning and functional expression of a 4.3 kbp mouse fur cDNA: A;Reference number: 149677 A;Accession: 149677
                                                                                                                                                                                                                                                                                                                                            C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
C;Accession: A23679; I49677
R;Hatsuzawa, K.; Hosaka, M.; Nakagawa, T.; Nagase, M.; Shoda, A.; Murakami, K.;
J, Biol. Chem. 265, 22075-22078, 1990
A;Title: Structure and expression of mouse furin, a yeast Kex2-related protease.
A;Reference number: A23679; MUID:91093035
A;Accession: A23679
                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-793 <HAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R:MOMOI, H.; Yamada, H.; Ueguchi, C.; Mizuno, Gene 134, 119-122, 1993
A;Title: Sequence of a fission yeast gene enc A;Reference number: JT0764; MUID:94063505
A;Accession: JT0764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N; Alternate names: kexin homolog; paired-basic endopeptidase; prohormone-processing
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A;Accession: PN0161
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A; Residues: 1-409 < MOM>
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R;Schmidt, A.; Endo, N.; Rutledge, S.J.; Vogel, R.; Shinar, D.; Rodan, G.A. wol. Endocrinol. 6, 1634-1641, 1992
A;Title: Identification of a new member of the steroid hormone receptor superfamily A;Reference number: A45360; MUID:93078797
A;Accession: A45360
                                                                                                                                                                                                                                                                                              A;Experimental source: osteosarcoma SAOS-2/B10 cells
A;Note: sequence extracted from NCBI backbone (NCBIP:118801)
C;Superfamily: unassigned erbA-related proteins; erbA transforming protein homology
C;Keywords: DNA binding; steroid hormone receptor; transcription regulation; zinc fin
F;72-359/Domain: erbA transforming protein homology <ERBA>
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A45360
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C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;715-735/Domain: transmembrane #status predicted <TMM>F;736-793/Domain: intracellular #status predicted <INT>F;136-793/Domains: hitracellular #status predicted F;153,194,368/Active site: Asp, His, Ser #status predicted F;387,440,553/Binding site: carbohydrate (Asn) (covalent)
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                                                                                    60 MGCDGASCGSLNMECR
                                          54 PGCQSPGVGRYSPRSR 69
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30.3%; Pred. No. 5.4;
Live 10; Mismatches
75
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Pred. No. 5.6;
3; Mismatches
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hypothetical protein homolog MJ0888 - Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000 C;Accession: H64410 R;Bult, C.J; White, O; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G. Reich, C.I; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Grson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O. A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus in the control of the control of the methanococcus in the control of the co
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-206 <BUL>
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A;Accession: H64410
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R;Brown, D.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, June 1997 A;Reference number: Z21796 A;Accession: T38487
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A:Map position: REV819507-818887
C:Superfamily: glyoxalase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec A;Reference number: A69250; MUID:98049343
A;Accession: A69335
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A;Molecule type: DNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C; Superfamily: tr
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A; Residues: 1-563 <KLE>
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C:Accession: A69335
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C; Species: Archaeoglobus fulgidus
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Query Match
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Pred. No. 9.3;
L1; Mismatches
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Score 66;
Pred. No.
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RESULT
C70648
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A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987
A;Accession: C70648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable nuoJ protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: C70648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;144-382/Domain: subtilisin homology <SBT>
F;715-735/Domain: transmembrane #status predicted <TMM>
F;715-735/Domain: intracellular #status predicted <INT>
F;153-794,368/Active site: Asp, His, Ser #status predicted
F;387,440,553/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: kexin; subtilisin homology
C;Keywords: glycoprotein; hydrolase; serine proteinase;
F;1-26/Domain: signal sequence #status predicted <SIG>F;27-793/Product: furin #status predicted <WAT>F;27-714/Domain: extracellular #status predicted <EXT>
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A; Title: Sequence of the cDNA encoding rat A; Reference number: S13106; MUID:91067492
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                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-262 <COL>
A;Cross-references: GB:283867; GB:AL123456; NID:g3261695;
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X55660; NID:g56171; PIDN:CAA39193.1; C;Comment: This subtilisin-like endoproteinase removes paired
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Nucleic Acids Res.
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C; Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                             R;Cole, S.T.; ; Connor, R.;
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A; Residues: 1-793 <MIS>
                                                                                                                                                                                                                                                 A; Status: preliminary; nucleic acid sequence not shown; translation
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A;Note: sequence extracted from NCBI backbone (NCBIN:111148, NCBIP:111150)
C;Keywords: surface antigen
                                                                                                                                                                                                                                                                         A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-907 <HAL>
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C;Species: Theileria annulata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: T49459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: Z25022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-414 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein B14D6.110 [imported] - Neurospora crassa
                                                                                                                                                                                                                                                                                                                                                                            Hall, R.; Hunt, P.D.; Carrington, M.; Simmons, D.; Williamson, J. Biochem. Parasitol. 53, 105-112, 1992
                                                                                                                                   Matches
                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000 Accession: T49459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Species: Neurospora crassa
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180
                                                                  120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 -LSVPRMLRTRGADGLQTPSPGAVS 254
                                40
                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 HLS--RVLKT---PGCQSPGVGRYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11
                                                                                                 4 EDEEKEGSEQALSSRD--GAPVQHP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 EDEEKEGSEQALSSRDGAPVQHPLALLPSGSYEEDPQTILDDHLSRVLKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ω
                                QTILDDHLSRVLKTPGCQSPGVG 62
                                                                DDEEEEEDDKSTSSKNGKGSPKAQPGVSSSSTSSASPTSPTTTLSQTGLGPSGSHAQQDP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EEEEEEEEEEDDDDDGGEEAHASPSLSSSTHQESPPT-SRDHYHHLLVT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RERFERRKTQRELSQERFRPGGHPTPLPNPGVYARHNAVDVAALLPDGSYSE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REDEEKEGSEQALSSRDGAPVQHP-----
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----VGVPGVGVPGVG 192
                                                                                                                                   Conservative
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                                                                                                                                                   17.8%;
26.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
                                                                                                                                                   Score 64;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , J.; Brand
Database,
                                                                                                                                                     Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 64.5; |
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Theileria annulata
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                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura.
base, May 2000
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                                                                                                                                                                     2:
                                                                                                                                   15;
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                                                                                                                                                                  Length 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 414;
                                                                                                   -LALLPSGSY-EEDP 39
                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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A; Status: T31113
                                                                               cyclin cdk inhibitor p57 - mouse
N;Alternate names: CDI p57; cyclin-cyclin-dependent kinase inhibitor C;Species: Mus musculus (house mouse)
C;Date: 09-Mar_1996 #sequence_revision 09-Mar-1996 #text_change 05-Nc
                                                                                                                                                               RESULT
149262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
R;Lee, M.H.; Reynisdottir, I.; Massague, J.
Genes Dev. 9, 639-649, 1995
A;Title: Cloning of p57KIP2, a cyclin-dependent kinase inhibitor with unique domain
                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                           δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-1832 <BAR>
A;Cross-references: EMBL;AF068065; NID:g4063041; PID:g4063042; PIDN:AAC98153.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mucin-like glycoprotein 900 - Cryptosporidium parvum
C;Species: Cryptosporidium parvum
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable metalloproteinase - Chlamydia trachomatis (serotype D,
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change
                                                             C; Accession: I49262
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                                                                                                                                                                                                                                                                                                                      В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: T31113
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A;Experimental source: serotype D, strain UW-3/Cx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tA;Reference number: A71570; MUID:99000809
A;Accession: B71559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Science 282, 754-759, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-619 <ARN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  458 KFRDEQERRYYLERIEAEKQRISL--GIPLK-DLAV----QYNPDPWVLMEESVSDSLKT 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        511 -- VKALGMGRVSPQ 522
                                                                                                                                                                                                                                                                               57 QSPGVGRYSPRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54 PGCQSPGVGRYSPR 67
                                                                                                                                                                                                                                                                                                                                                             8 KEGSEQALSSRDGAPVQHPLALLPSGSYEEDPQT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QIREDEEK-----EGSEQALSSRDGAPVQHPLALLPSGSYEEDPQTILDDHLSRVLKT
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                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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29.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                    8;
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 62.5; DB 2; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
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                                                                                                                                                                                                                                                                                                                                                             -ILDDHLSRVLKT-PGC 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of Cryptosporidium parvum media
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1832;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Result
No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    360
360
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217.5
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139.5
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72
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360
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QIREDEEKEGSEQALSSRDG.....VLKTPGCQSPGVGRYSPRSR 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
FURI_RAT
CLX2_NARJA
ABB1_MOUSE
CDNC_MOUSE
CONC_MOUSE
CONC_HOWAN
DRI]_HUMAN
DRI]_YEAST
ACCB_CRICR
PATA_ANASP
VIEL_MCMAN
MI13_HUMAN
MI13_HUMAN
MI13_HUMAN
MI13_RABIT
ENV_AVISN
PURL_NEIMA
PURL_NEIMA
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AXN1_MOUSE
AXN1_HUMAN
EF1G_SCHPO
FURI_MOUSE
PPAS_HUMAN
Y888_METJA
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AXN2_MOUSE
AXN2_HUMAN
AXN2_BRARE
AXN_XENLA
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7 epstein-bar
4 homo sapien
2 homo sapien
6 oryctolagus
6 avian splee
5 neisseria m
5 neisseria m
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7 cricetus cr
8 anabaena sp
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## ALIGNMENTS

DR DR DR DR DR DR TT	88888888	8888888	4000000	RT RA		RESULT AXN2_RAT ID AXN AC 07- DT 01- DT 01- DT AXI DE AXI DE (AX
EMBL; AF017757; AAC40089.1; HSSP; P49799; 1AGR. InterPro; IPR000342; InterPro; IPR001158; Pfam; PF00615; RGS; 1. Pfam; PF00778; DIX; 1. PROSTTE; PS50132; RGS; 1. PROSTTE; PS50132; RGS; 1. Developmental protein; Phosphorylation. DOMAIN 81 200 RGS. DOMAIN 81 200 GSK-3B BINDING SITE (BY SIMILARITY).	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	-:- SUBCELLULAR LOCATION: CYTOPLASMIC:- TISSUE SPECIFICITY: EXPRESSED IN LUNG AND THYMUS:- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY PP2A:- SIMILARITY: CONTAINS 1 RGS DOMAIN:- SIMILARITY: CONTAINS 1 DIX DOMAIN.	MOI. Cell. Biol. 18:2867-2875(1998).  -I: FUNCTION: INHIBITOR OF THE WIN SIGNALING PATHWAY. DOWN REGULATES BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-CATENIN AND APC BY GSK-3B (BY SIMILARITY).  -I: SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B) AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.  TERNARY COMPLEX.	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  TISSUE-Brain;  MEDLINE=98226558; PubMed=9566905;  MEDLINE=98226558; PubMed=9566905;  Yamanoto H., Kishida S., Uochi T., Ikeda S., Koyama S., Asashima M.,  Kikuchi A.;  "Axil, a member of the Axin family, interacts with both glycogen  "Axil, a member of the Axin family, interacts with both glycogen synthase kinase 3beta and beta-catenin and inhibits axis formation of  Xenopus embryos.";	AXIN2. AXIN2. Rattus norvegicus (Rat). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. MCBI_TaxID=10116;	RAT  AXN2_RAT STANDARD; PRT; 838 AA.  O70240;  O1-CCT-2000 (Rel. 40, Created)  O1-CCT-2000 (Rel. 40, Last sequence update)  O1-CCT-2000 (Rel. 40, Last annotation update)  AXIN 2 (AXIS INHIBITION PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN)

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"Properties of mouse Axin2 and human AXIN2: chromos expression pattern, interaction with Axin and effect and formation.";
Submitted '.....
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-i- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-CATENIN AND APC BY GSK-3B (BY SIMILARITY).

-i- SUBGUIT: INTERACTS WITH GIVOGEN SYNTHASE KINASE-3 BETA (GSK-3B) AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.

TERNARY COMPLEX (BY SIMILARITY).

-i- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

-i- PIM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED RY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AXN2_MOUSE STANDARD; PRT; 840 AA.

088566; Q9QXJ6;
01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
01-0CT-2000 (Rel. 40, Last annotation update)
AXIN 2 (AXIS INHIBITION PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN)
                                       the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb.or send an email to license@isb-sib.ch).
                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collab
between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 280:596-599(1998).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Behrens J., Jerchow B.-A., Wuertele M., Grimm J., Asbrand C., Wirtz R., Kuehl M., Wedlich D., Birchmeier W.; "Functional interaction of an axin homolog, conductin, with b catenin, APC, and GSK3beta.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-98221239; PubMed-9554852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
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SIMILARITY: CONTAINS 1 RGS DOMAIN.
SIMILARITY: CONTAINS 1 DIX DOMAIN.
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 AF073788;
AF205889;
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AAC26047.1;
AAF22800.1;
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Rodentia;
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Pred. No. 8.3
); Mismatches
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No. 8.3e-32;
matches 0;
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http://www.isb-sib.ch/announce/
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; Murinae; Mus
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RESULT 3
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G9Y2T1; Q9UH84;
01-CCT-2000 (Rel. 40, Created)
01-CCT-2000 (Rel. 40, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
01-CCT-2000 (Rel. 40, Last annotation update)
AXIN 2 (AXIS INHIBITION PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN)
                                                                                          SEQUENCE FROM N.A.
TISSUB-Brain, and Lymphoblast;
Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D.,
Jenkins N.A., Warburton D., Costantini F.;
"Properties of mouse Axin2 and human AXIN2: chromos
expression pattern, interaction with Axin and effec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pfam; PF00615; RGS; 1.
pfam; PF00778; DIX; 1.
prints; PR01301; RGSPROTEIN.
                 Mai M., Qian C., Yokomizo A., Smith "Cloning of the human homolog of corchromosome 17q23-q24.";
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HSSP; P49799; 1AGR.
                                                                                 axis formation."
                                                                                                                                                                                                                                               NCBI_TaxID=9606
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                       3enomics
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          OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN
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59; Conservative
                                                                                                                                                                          55:341-344(1999).
                                                                                                                                                                                                                                                                     Metazoa;
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COMPLEX (BY SIMILARITY).
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Primates;
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H -> Y (IN |
S -> P (IN |
F -> S (IN |
G -> A (IN |
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BETA-CATENIN BINDING SITE (BY
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Pred. No. 8.3e-32;
; Mismatches 0;
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                                                                                                 effects
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                                                                                                 on embryonic
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RESULT 4
AXN2_BRARE
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DE AXIN2.
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P57095;
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          SEQUENCE FROM N.A.

MEDLINE-20171051; PubMed-10704853;

Shimizu T., Yamanaka Y., Ryu S.-L.,

Bae Y.-K., Hibi M., Hirano T.;
                                                                                         Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
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Developmental protein; Phosphorylation.
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SIMILARITY: CONTAINS 1 RGS DOMAIN.
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; PS50132; RGS; 1.
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(Rel. 40, Last annotation updat
INHIBITION PROTEIN 2).
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  of Bozozok/Dharma
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DIX.

OPGVCKGQVTKPMSVSSNTRRNEDGL ->
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OPS (IN REF. 2).
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MISSING (IN REF. 2).
P -> S (IN REF. 2).
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O -> H (IN REF. 2).
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BETA-CATENIN BINDING SITE (BY
SIMILARITY).
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BY GSK-3B
                           Hashimoto H., Yabe
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9.7e-29;
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DEPHOSPHORYLATED
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DT 01-OCT-2000

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DE AXIN (AXIS

GN AXIN (AXIS

OS Xenopus lase

OC Eukaryota;

OC Amphibla;

OC Xenopusla;

OC Xenopusla;

OC Xenopusla;

OC MRITANIO

CR AMBLINE-931

RN SEQUENCE FI

RX MEDLINE-931

RA Hedgepeth (
RA HEDLING

RT SENDRO

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Best Local Similarity
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SEQUENCE
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01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last seq
01-OCT-2000 (Rel. 40, Last ann
Hedgepeth C.M., Deardorff M.A., Klein P.S.;
Hedgepeth C.M., Deardorff M.A., Klein P.S.;
Hedgepeth C.M., Deardorff M.A., Klein P.S.;

"Xenopus axin interacts with glycogen synthase kinase-3 be
expressed in the anterior midbrain.";

Mech. Dev. 80:147-151(1999).

-i- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN
BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION
CATENIN AND APC BY GSK-3B (BY SIMILARITY).
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Mech. Dev. 91:293-303(2000).
-i- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES
BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
CATENIN AND APC BY GSK-3B (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-i- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
                                                                                                                                                                                                                                                                  AXIN OR AXN.
Xenopus laevis (African
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-99173782; PubMed-10072781;
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InterPro; IPR001158; -.
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SIMILARITY: CONTAINS 1 RGS DOMAIN.
SIMILARITY: CONTAINS 1 DIX DOMAIN.
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Last annotation updat
PROTEIN) (XAXIN).
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Pred. No. 3.1e-16;
9; Mismatches 11
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BETA-CATENIN BINDING SITE (BY
SIMILARITY).
POLY-SER.
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Best Local :
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AXNI_BRARE STANDARD,
P57094;
P57094;
01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, Last annotation update)
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SEQUENCE
Shimizu T., Yamanaka Y., Ryu S.-L., Hashimoto H., Yabe T.,
Bae Y.-K., Hibi M., Hirano T.;
Booperative roles of Bozozok/Dharma and Nodal-related pro
formation of the dorsail organizer in zebrafish.";
Mech. Dev. 91:293-303(2000).

-i- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN
-i- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN
-i- SUBCELULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
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                                                                                                                                                                                                                                                             MEDLINE-20171051; PubMed=10704853; MEDLINE-20171051; PubMed=10704853;
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Pfam; PF00778; DIX; 1.
PROSITE; PS50132; RGS; 1.
Developmental protein; Phosphorylation.
Developmental Protein; Phosphorylation.
DOMAIN 88 211 RGS.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
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DEVELOPMENTAL STACE: WEAKLY AND UBIQUITOUSLY EXPRESSED THROUGHOUT EARLY DEVELOPMENT, AND HIGHLY EXPRESSED IN THE ANVERIOR MESENCEPHALON ADJACENT TO THE FOREBRAIN-MIDBRAIN BOUNDARY.

PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
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SIMILARITY: CONTAINS 1 RGS DOMAIN.
SIMILARITY: CONTAINS 1 DIX DOMAIN.
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EHVQRVMKTPGCQSPGTGRHSPKSR 499
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BETA-CATENIN BINDING SITE
SIMILARITY).
DIX.
BDA152734C97191E CRC64;
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BINDING SITE (BY
               DEPHOSPHORYLATED
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                                                                                                                                                             A Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W. Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.;

The mouse fused locus encodes Axin, an inhibitor of the Wnt pathway that regulates embryonic axis formation.";

Cell 90:181-192(1997).

-i- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN RE BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF CATENIN AND APC BY GSK-3B (BY SIMILARITY).

-i- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

-i- DEVELOPMENTAL STAGE: EXPRESSED AT STAGE 12 TO 15.

-i- PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATION.
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Best Local S
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AXIN (AXIS INHIBITION PROTEIN).
AXIN OR AXN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AXN_CHICK
042400;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for modified and this statement is not removed.
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pfam; pr00778; DIX; 1.
pR0SITE; pS50132; RGS; 1.
Developmental protein; Phosphorylation.
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InterPro;
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                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97373830;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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SIMILARITY: CONTAINS 1 RGS DOMAIN.
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94351 MW;
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Pred. No. 1e-0
10; Mismatches
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BETA-CATENIN BINDING SITE (BY
SIMILARITY).
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OF BETA-
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Interpro; IPRO00342; -.
Interpro; IPRO01158; -.
Pfam; PF00615; RGS; 1.
Pfam; PF007618; DIX; 1.
PROSITE; PS50132; RGS; 1.
PROSITE; PS50132; RGS; 11
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SEQUENCE
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01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
AXIN 1 PROTEIN (AXIS INHIBITION PROTEIN 1) (RAXIN) (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-98151361; PubMed-9482734; Ikeda S., Kishida S., Yamamoto H., Murai H., Koyama S., Kikuchi "Axin, a negative regulator of the Wnt signaling pathway, forms complex with GSK-3beta and beta-catenin and promotes GSK-3beta-
                                                                                                                                                                                                                                                                                                                                                                                                                             dependent phosphorylation of beta-catenin.", EMBO J. 17:1371-1384(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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                                                                                                                                               FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES BETA-CATERIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-CATENIN AND APC BY GSK-3B (BY SIMILARITY).

SUBUNIT: INTERACTS WITH GSK-3B AND BETA-CATENIN. THE INTERACTION BETW-EEN AXIN AND BETA-CATENIN OCCURS VIA THE ANWADILLO REPEATS CONTAINED IN BETA-CATENIN. TERNARY COMPLEX. ALSO BINDS TO PLAKOGLOBIN (GAMMA-CATENIN), APC, DVL AND PPZA (BY SIMILARITY).

SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS, THYMUS AND LUNG FOLLOWED BY CEREBERUM, CEREBELLUM, HEART, KIDNEY, SKELETAL MUSCLE, SPLEEN AND LIVER.
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                                                 SIMILARITY: CONTAINS 1 RGS DOMAIN. SIMILARITY: CONTAINS 1 DIX DOMAIN.
                                                                                                     PP2A (BY SIMILARITY).
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                                                                                                                             PROBABLY PHOSPHORYLATED BY GSK-3B
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BETA-CATENIN BINDING SIMILARITY).
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01-0CT-2000
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                                                                                      CATENIN AND APC BY GSK-3B (BY SIMILARITY).

SUBUNIT: INTERACTS WITH GSK-3B AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN. TERNARY COMPLEX. ALSO BINDS TO PLAKOGLOBIN (GAMMA-CATENIN), APC, DYL AND PP2A (BY SIMILARITY).

SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: EXPRESSED IN EMBRYONIC STEM CELLS.
DEVELOPMENTAL STAGE: WIDELY EXPRESSED AT ELO.5 TO E16.5 DAY.

DEVELOPMENTAL STAGE: WIDELY EXPRESSED AT ELO.5 TO E16.5 DAY.
   SIMILARITY:
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PF00778; DIX; 1.
TE; PS50132; RGS;
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BETA-CATENIN BINDING
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Best Local Similarity
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015169;

01-0CT-2000 (Rel. 40, Cres

01-0CT-2000 (Rel. 40, Last

01-0CT-2000 (Rel. 40, Last

01-0CT-2000 (Rel. 40, Last

101-0CT-2010 (Rel. 40, Last

101-0CT-2010 (Rel. 40, Last)
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SEQUENCE
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pfam; pF00778; DIX; 1.
pROSITE; pS50132; RGS;
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                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE=97373830; PubMed=9230313;

MEDLINE=97373830; PubMed=9230313;

Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L. III,

Zeng L., Tilghman S.M., Gumbiner B.M., Costantini F.;

Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini f.;

"The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling

pathway that regulates embryonic axis formation.";

Cell 90:181-192(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
  - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              544 RVRMEEEGEDGEMP----SGPMASHKLPSVPAWHHFPPRYVDMGCSGLRDAHEENPESIL
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                                                                 BETA-CATEMIN. AND APC BY GSK-3B.
CATEMIN AND APC BY GSK-3B.
CATEMIN: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA-CATEMIN
AND BETA-CATEMIN. THE INTERACTION BETYBEEN AXIN AND BETA-CATEMIN.
OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATEMIN.
OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATEMIN),
TERNARY COMPLEX. MAY ALSO APC, DVL AND PP2A. SUBCELLULAR LOCATION: CYTO TISSUE SPECIFICITY: UBIQUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGI:1096327; Axin.
                                                                                                                                                                                                                     FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30;
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992 AA;
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40, Last sequence update)
40, Last sequence update)
40, Last annotation update;
BITION PROTEIN 1) (HAXIN) (FRAGMENT).
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     UBIQUITOUSLY EXPRESSED
                               CYTOPLASMIC
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4; Mismatches
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GSK-3B BINDING SITE (BY SIMILARITY).
BETA-CATENIN BINDING SITE (BY
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 139.5; DB Pred. No. 1.3e-07
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70EEB53D387BD26F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           624
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P49799;
         Brown D., Churcher C.M., Wood V., Barrell B.G., Rajandream M.A.; Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLY PLAYS A ROLE IN ANCHORING THE COMPLEX TO
                                                                            Momoi H., Yamada H., Ueguchi C., Mizuno T.; 
"Sequence of a fission yeast gene encoding 
homology to eukaryotic elongation factor-1 
Gene 134:119-122(1993).
                                                                                                                                                                                    Schizosaccharomycetales; schizosaccharomyces.
                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                   Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                 TEF3 OR SPAC29A4.02C.
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                                                                                                                            MEDLINE=94063505;
                                                                                                                                        STRAIN-972;
                                                                                                                                                                         NCBI_TaxID=4896;
                                              STRAIN=972;
                                                                                                                                                    SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                         440 REAEEKLEERLKRVRMEEEGEDGDPSSGPPGPC-HKLPPAPAWHHFPPRLCWTWACAGLR 498
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                                                         EQUENCE FROM N.A.
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99803
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                                                                                                                                                    AND SEQUENCE OF 226-244
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BETA-CATENIN BINDING SITE (BY
SIMILARITY).
DIX.
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Pred.
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                                                                                            a protein with extensive gamma.";
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MBL outstation -
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01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
FURIN PRECURSOR (EC 3.4.21.75) (PAIRED BASIC A
CLEAVING ENZYME) (PACE) (DIBASIC PROCESSING EL
FUR OR PCSK3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; JT0764; JT0764.
InterPro; IPR000521; -.
InterPro; IPR001662; -.
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                                                                                                                                                                                                                                                                                                        TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                        J. Biol. Chem. 265:22075-22078(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                     "Structure and expression of mouse furin, a protesse. Lack of processing of coexpressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hatsuzawa K., Hosaka M., Nakagawa T., Nagase M., Shoda A.,
Murakami K., Nakayama K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-91093035; PubMed-2266110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKDEKKKNAPKPQAERPAKPPKHPLASAPNGSFD 264
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12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246 R -> A (IN REF. 2).
45786 MW; A49CB947A9F66DF0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 72; DB 1; Length 409;
; Pred. No. 1.2;
11; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        793
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                                                                                                                                                                                                                                                                                                                                                                                                                                        yeast Kex2-related prorenin in GH4C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMINO ACID RESIDUE
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EMBL; X54056; (
EMBL; L26489; PIR; A23679; K
                                                                                                                                                                                                                                     DOMAIN
TRANSMEM
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <del>-</del> - <del>-</del> -
                                                                                         SITE
SITE
SITE
SITE
                                                                                                                                                                                                  ACT_SITE
DISULFID
                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                     SEQUENCE
                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; Q99405;
                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                         ACT_SITE
                                                                                                                                                                                                                                                                                           PROPEP
                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00137; PROSITE; PS00138;
                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00136;
                                                                                                                                               CARBOHYD
                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                Hydrolase;
                                                                                                                                                                                                                                                                                                                  ymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: SEEMS TO BE EXPRESSED UBIQUITOUSLY.

DOMAIN: CONTAINS A HOMO B DOMAIN, ALSO KNOWN AS P OR MIDDLE DOMAIN

AND A SUBTILISIN-LIKE CATALYTIC DOMAIN. ESSENTIAL DOMAINS FOR

CATALYTIC ACTIVITY.

DOMAIN: CONTAINS A CYTOPLASMIC DOMAIN RESPONSIBLE FOR ITS TGN

LOCALIZATION AND RECYCLING FROM THE CELL SURFACE.

PMM: THE PROPERFIDE IS AUTOCATALYTICALLY REMOVED THROUGH AN

INTRAMOLECULAR CLEAVAGE PROBABLY IN THE ENDOPLASMIC RETICULUM

(ER). IN THE TGN THE SECOND CLEAVAGE IN THE PROPEPTIDE COULD LEAD

TO THE ACTIVATION OF FURIN.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY SB; ALSO KNOWN AS THE

SUBTILASE FAMILY. HIGH SIMILARITY WITH OTHER FURIN-LIKE ENZYMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANS GOLGI NETWORK. PROPEPTIDE CLEAVAGE IS A PREREQUISITE FOR EXIT OF FURLN MOLECULES OUT OF THE ENDOPLASHIC RETICULUM (ER). SECOND CLEAVAGE IN THE PROPEPTIDE OCCUR IN THE TRANS GOLGI NETWORK (TGN), WHICH IS FOLLOWED BY THE RELEASE OF THE PROPEPTIDE BOUND TO FURIN AND THE ACTIVATION OF FURIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESPECTIVE PRECURSORS.
COFACTOR: CALCIUM-DEPENDENT
ENZYME REGULATION: COULD BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: SEEMS TO BE LOCALIZED INTRACELLULARLY TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROPERTIDE.
                                                                                                                                                                                                                                                                                                                    Calcium.
                                                                                                                                                                                                                                                                                                                                Serine
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108
556
715
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194
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211
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387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAA37988.1; -. AAA37643.1; -.
                                                                                                                                                                                                                                                                                                                                          SUBTILASE_ASP;
SUBTILASE_HIS;
SUBTILASE_SER;
                                                                                                                                                                                                                                                                                                                                  protease;
                                                                              440
553
75
107
761
778
500
                                                     86804
19.78;
                                                     ¥
                                                                                                                                                                                                                                                                                                                                Transmembrane; Glycoprotein; Signal;
 Score 71;
Pred. No.
                                                                                                                N-LINKED (GLCNAC. ...) (POTENTIAL)
N-LINKED (GLCNAC. ...) (POTENTIAL)
N-LINKED (GLCNAC. ...) (POTENTIAL)
CLEAVAGE (SECOND AUTO-).
CLEAVAGE (FIRST AUTO-).
                                                                                                                                                                                                             CHARGE
CHARGE
                                                  CELL SURFACE SIGNAL.
TRANS GOLGI NETWORK SIGNAL.
CELL ATTACHMENT SITE (POTENTIAL).
M -> V (IN REF. 2).
55121C3DE2E1A42D CRC64;
                                                                                                                                                                                                                                                                                        POTENTIAL.
BY SIMILARITY.
                                                                                                                                                                                                                                        CHARGE
                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                  CYS-RICH.
                                                                                                                                                                                                                                                                               FURIN
                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY).
INHIBITED BY THE NOT SECONDLY CLEAVED
                                                                                                                                                                                                             E RELAY SYSTEM
E RELAY SYSTEM
            DB 1; Length 793;
                                                                                                                                                                                                              ХВ)
ХВ)
ХВ)
                                                                                                                                                                                                             Y SIMILARITY).
Y SIMILARITY).
Y SIMILARITY).
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Query Match Best Local S Matches 20

Similarity

Conservative

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Mismatches

27;

Indels

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Gaps

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EKEGSEQALSSRDGAPVQHPLALLPSGSYEEDPQTILDDHLSRVLKTPGC

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RESULT 13
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                InterPro; IPR001628; -.
InterPro; IPR001723; -.
InterPro; IPR003074; -.
InterPro; IPR003074; -.
InterPro; IPR003075; -.
Pfam. nerocons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-OCT-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR BETA (PPAR-BETA)
(PPAR-DELTA) (NUCLEAR HORMONE RECEPTOR 1) (NUC1) (NUC1).
PPARB OR NR1C2 OR PPARD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-93078797; PubMed-1333051;
MEDLINE-93078797; Rutledge S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q0318:
                                                                Receptor: Transcription regulation; Activator; DNA-Nuclear protein; Zinc-finger; Multigene family.
DNA_BIND 74 138 NUCLEAR RECEPTOR-TYPE.
DNA_FING 74 94 C4-TYPE.
ZN_FING 74 94 C4-TYPE.
ZN_FING 11 133 C4-TYPE.
DOMAIN 254 441 AA; 49903 MW; 94FBB2A4B46521E8 CRC
                                                                                                                                                                                                                                     Pfam; PF00104; hormone_rec; 1. pfam; PF00105; zf-C4; 1. PRINTS; PR00047; STROIDER. PRINTS; PR00398; STRDHORMONER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its now way non-profit institutions as its content is in no way use by non-profit institutions as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acids."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rodan G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPAS_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L07592; AAA36469.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification of a new member of the steroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Primates;
                                                                                                                                                                                     PRINTS; PRO1290; PROXISOMPABR.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
                                                                                                                                                                                                                       PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P0337;
MIM; 600409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     672
                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000536;
                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A45360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: RECEPTOR THAT BIND PEROXISOME PROLIFERATORS SUCH AS HYPOLLPIDEMIC DRUGS AND FATTY ACIDS. ONCE ACTIVATED BY A LIGAND, THE RECEPTOR BINDS TO A PROMOTER ELEMENT IN THE GENE FOR ACYL-COA OXIDASE AND ACTIVATES ITS TRANSCRIPTION. IT THEREFORE CONTROLS THE PEROXISOMAL BETA-OXIDATION PATHWAY OF FATTY ACIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBURIT: HETERODIMER WITH THE RETINOID X RECEPTOR. SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NR1 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQTCSRQSQSSRESRPQQQPPALRPEVEMEPRLQAGLASHLPEVLAGLSC 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Endocrinol. 6:1634-1641(1992)
                                                                                                                                                                                                                                                                                                                                                                                                              P03372; 1HCQ.
                                                                                                                                                                                                     PR01288; PROXISOMEPAR. PR01290; PROXISOMPABR.
                                                                                                                                                                                                                                                                                                                                                                                                                                  A45360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
19.0%;
30.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           уd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 Score 68.5; D
Pred. No. 3.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a peroxisome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       441 AA
                , DB
                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d hormone receptor proliferator and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shinar D
                                                                                                                                                                         DNA-binding;
                                                                     SIMILARITY)
CRC64;
                   Length 441
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                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997
01-NOV-1997
01-NOV-1997
FURI_RAT
P23377;
01-NOV-1991
01-NOV-1991
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb.or send an email to license@isb-sib.ch).
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MEDLINE-96337999; pubMede-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,

Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,

Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,

Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Scott J.L., Geoghagen N.S.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 273:1058-1073(1996).
-i- SIMILARITY: WEAK, TO B.SUBTILIS YQGX AND TO M.JANNASCHII MJ0296.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL
                                                                                                                               RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
SEQUENCE 206 AA; 23229 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001279; -.
Pfam; PF00753; lactamase_B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U67532; AAB98892.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y888_METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence jannaschii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rigr; MJ0888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10
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                                                                                                                                                                                                                                      76
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                                                                                                                                                                                                                                                                    2 IREDEE----KEGSEQALSSRDGAPVQHPLALLPSGSYEEDPQTILDDHLSRVLKTPG
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Pfam; PF00082; FEPTILISIN.
PROSITE; PS00136; SUBTILISE_ASP; 1.
PROSITE; PS00137; SUBTILASE_HIS; 1.
PROSITE; PS00138; SUBTILASE_HES; 1.
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CAN BE ANY AMINO ACID AND YOA WILLEBRAND FACTOR FROM THEIR

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COMPLEMENT COMPORENT C3 AND YON WILLEBRAND FACTOR FROM THEIR
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STRAIN-WISTAR; TISSUE-Liver;
MEDLINE-91067492; PubMed-2251148;
                                                                                                                                                                                                                                                   Interpro; IPR000209; ...
Interpro; IPR0002884; ...
Pfam; PF01483; P; 1.
Pfam; PF00082; Peptidase_S8; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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MEROPS; S08.071;
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PIR; S13106; KXRTF.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY.

COMAIN: CONTAINS A CYTOPLASMIC DOMAIN RESPONSIBLE FOR ITS TO DOMAIN: CONTAINS A CYTOPLASMIC DOMAIN RESPONSIBLE FOR ITS TO DOMAIN: CONTAINS A CYTOPLASMIC BROW THE CELL SURFACE.

LOCALIZATION AND RECYCLING FROM THE CEMOVED THROUGH AN INTERPOLECULAR CLEAVAGE PROBABLY IN THE ENDOPLASMIC RETICULL (ER). IN THE TGN THE SECOND CLEAVAGE IN THE PROPEPTIDE COULT OTHE ACTIVATION OF FURIN.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8; ALSO KNOWN AS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROPEPTIDE.

SUBCELLULAR LOCATION: SEEMS TO BE LOCALIZED INTRACELLULARLY TO THE TRANS GOLGI NETWORK. PROPEPTIDE CLEAVAGE IS A PREREQUISITE FOR EXIT OF FURIN MOLECULES OUT OF THE ENDOPLASMIC RETICULUM (ER).

SECOND CLEAVAGE IN THE PROPEPTIDE OCCUR IN THE TRANS GOLGI NETWORK (TGN), WHICH IS FOLLOWED BY THE RELEASE OF THE PROPEPTIDE BOUND TO FURIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: SEEMS TO BE EXPRESSED URIQUITOUSLY.

DEVELOPMENTAL STAGE: EXPRESSED ATT E7 DAY IN ENDODERN AND MESODERN,
UNIFORMLY EXPRESSED UNTIL E10, WHEN EXPRESSION IS HIGHER IN HEART
AND LIVER PRIMORDIA. IN MID-AND LATE-GESTATIONAL STAGES, WIDELY
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COFACTOR: CALCIUM-DEPENDENT (BY SIMILARITY).

ENZYME REGULATION: COULD BE INHIBITED BY THE NOT SECONDLY CLEAVED
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POTENTIAL.
BY SIMILARITY.
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                                                                                           Glycoprotein; Signal;
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THE PROPEPTIDE COULD 1
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O15169 homo sapien
O9ptp2 xenopus lae
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O2576 archaeoglob
O90w8 leishmania
O93464 carassius a
P95172 mycobacteri
O99577 neurospora
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01-AUG-1998 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Axil, a member of the Axin family, interacts with both glycogen synthase kinase 3beta and beta-catenin and inhibits axis formation of Xenopus embryos.";
Mol. Cell. Biol. 18:2867-2875(1998).
EMBL; AF017757; AAC40089.1; -.
EMBL; P49799; 1AGR.
INTERPRO; IPR001342; -.
INTERPRO; IPR001342; -.
PFAM; PF00615; RGS; 1.
PFAM; PF00615; RGS; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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PRODOM; PD003639; -; 1.
SEQUENCE 838 AA; 92947 MW; 45B825C13BA07F37 CRC64;
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MEDLINE-98226558; PubMed-9566905;
Yamamoto H., Kishida S., Uochi T., Ikeda S., Koyama S.,
Kikuchi A.;
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Pred. No. 5.5e-34;
Mismatches 0;
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INTERPRO; IPR001342; -.
INTERPRO; IPR001158; -.
PFAM; PF00615; RGS; 1.
PFAM; PF00778; DIX; 1.
PRODOM; PD001580; -; 1.
PRODOM; PD003639; -; 1.
SEQUENCE 840 AA; 92934
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Q9QXJ6;
01-MAY-2000
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Science 280:596-599(1998).
EMBL; AF073788; AAC26047.1; -.
HSSP; P49799; lAGR.
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                                                                                                 Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G., Jenkins N.A., Warburton D., Costantini F.; "Properties of mouse Axin2 and human AXIN2: chromosomal location, expression pattern, interaction with Axin and effects on embryoniaxis formation".
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                    axis formation.";
Submitted (NOV-1999) to the
EMBL; AF205889; AAF22800.1;
HSSP; P49799; 1AGR.
                                                                                                                                                     SEQUENCE FROM N.A. Zhang T., Fagotto F., Jenkins N.A., Warburt
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Birchmeier W.;
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Sciurognathi;
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Homo sapiens (Human).
'hervota; Metazoa; Chordata; (heria; Primates;
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01-MAY-2000
01-MAY-2000
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FPAM; PF00615; RGS; 1.
PFAM; PF00778; DIX; 1.
PRINTS; PR01301; RGSPROTEIN.
SEQUENCE 840 AA; 92896 MW;
Q9Y2T1
Q9Y2T1;
01-NOV-1999
01-NOV-1999
01-OCT-2000
CONDUCTIN.
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"Properties of mouse Axin2 and human Axin2: chromosomal location, expression pattern, interaction with Axin and effects on embryonic axis formation.",
submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF205888; AAF22799.1;
HSSP; P49799, 1AGR.
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PFAM; PF00778; DIX; 1.
PRINTS; PR01301; RGSPRC
SEQUENCE 777 AA; 868
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Pred. No. 5.5e-34;
Mismatches 0;
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Best Local S
Matches 62
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"Cloning of the human homolog of

chromosome 1723-724.";

Genomics 55:341-344(1999).

EMBL; AF078165; AAD20976.1; -

HSSP; P49799; lAGR
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INTERPRO; IPR001158; -.
PFAM; PF00615; RG; 1.
PFAM; PF00778; DIX; 1.
SEQUENCE 843 AA; 9355;
                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE-99173782; PubMed-10072781;

Hedgepeth C.M., Deardorff M.A., Klein P.S.;

"Xenopus axin interacts with glycogen synthase kinase-3

"Xenopus axin interior midbrain.";

expressed in the anterior midbrain.";

Mech. Dev. 80:147-151(1999).

EMBL; AF097313; AAC71036.1; -.

HSSP; P49799; IAGR.
                                                                                                                                                                                                                                                                                                                                             Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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Q9YGY0;
Q1-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-OCT-2000 (TrEMBLrel. 15,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
                                                                                                                              PRODOM; PD001580; -; 1.
PRODOM; PD003639; -; 1.
SEQUENCE 842 AA; 94459 MW;
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INTERPRO; IPR001158; -.
PFAM; PF00615; RGS; 1.
PFAM; PF00778; DIX; 1.
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                                                                                                                                                                                                                                                                                                                                     Xenopodinae;
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DHLSRVLKTPGCQSPGVGRYSPRSR 69
                       EEEGDDGDVSSGPSV-ISHK---LPSGPPMHHFNSRYSETGCVGMQIRDAHEENPESILD 474
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                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93557
                                                                                43.98;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 332; DB 4; I
Pred. No. 1.1e-30;
Pred. No. 1.3e-30;
                                                                               Score 158; DB 1
Pred. No. 3e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                BDA152734C97191E CRC64;
                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               842
                                                                                             DB 13;
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                                              -SYEEDPQTILD 44
                                                                                             842;
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DR RTT RAY OR RTT RAY OR                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
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Best Local :
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HSSP; P49799; 1AGC.
INTERPRO; IPR000342; -
INTERPRO; IPR001158; -
PFAM; PF00615; RGS; 1.
PFAM; PF00778; DIX; 1.
PR0DOM; PD001580; -; 1.
PRODOM; PD003639; -; 1.
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01-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1998
01-OCT-2000
                   rkeda S., Yamamoto H., Murai H., Kishida S., Kikuchi A.;
"Axin, a negative regulator of the Wnt signaling pathway,
complex with GSK-3beta and beta-catenin and promotes GSK-
dependent phosphorylation of beta-catenin.";
EMBO J. 17:1371-1384(1998).
EMBL, AF01756; AAC40066.1; -.
HSSP; P49799; lAGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             070239
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Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perr
III Lee J.J., Tilghman S.M., Gumbhiner B.M., Costantini F.
"The mouse Fused locus encodes Axin, an inhibitor of the
pathway that regulates embryonic axis formation.";
Cell 90:181-192(1997).
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                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-98151361; PubMed-9482734;
                                                                                                                                                                                                                                                          NCBI_TaxID-10116
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IPR000342;
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Pred. No. 7.7e-09;
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; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.
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ni F.;
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Best Local Similarity
Matches 30; Conserv
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Best Local 9
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01-JAN-1998
01-OCT-2000
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PRODOM; PD003639; -; 1.
SEQUENCE 832 AA; 92856 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERPRO; IPRO01158; -. PFAM; PF00615; RGS; 1. PFAM; PF00778; DIX; 1.
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035625;
015169;
015169;
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01-JAN-1998
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Mammalia; Eutheria; Rodentia;
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Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perr
III Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.
"The mouse Fused locus encodes Axin, an inhibitor of the
pathway that regulates embryonic axis formation.";
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INTERPRO; IPR000342; ...
INTERPRO; IPR001158; ...
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                                                                                                                                                                    P49799;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              992 AA; 109917 MW;
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35.3%; Pred. No. 4.4e-08;
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Pred. No. 5.
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Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                           992;
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                  20
                                                           Query Match
Best Local S
Matches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local
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Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L.,

III Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.;

III Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.;

"The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling

"The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling

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"The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling

"The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling

"The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling

"The Maxing India Axing I
                                                                                                                                                                     Submitted (APR-1999) to the EMB: EMBL; AF140243; AAF22574.1; -. INTERPRO; IPR000342; -. INTERPRO; IPR00158; -. PPAM; PF00778; DIX; 1. PPAM; PF001301; RGSPROTEIN. PRINTS; PR01301; RGSPROTEIN. SEQUENCE 706 AA; 79196 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AXIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00615; RGS; 1. PFAM; PF00778; DIX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERPRO; IPRO00342; ...
INTERPRO; IPRO01158; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09PTP2;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2000 (TrEMBLrel. 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR01301; RGSPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9PTP2
                                                                                                                                                                                                                                                                                                                                                    TISSUE=OVARY; Itoh K., Antipova A., Ratcliffe M., "Dishevelled transduces a signal by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AXIN-RELATED PROTEIN.
                                                                                                                                                                                                                                                                                                                             complex.";
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopodinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         499 DAHEENPESILDEHVORVLRTTGROSPGPGHRSPDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 GSYEEDPQTILDDHLSRVLKTPGCQSPGVGRYSPRS 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 REDEEK-----
33;
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                                                                     28;
                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             900 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99803 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.5%;
                                                                                         31.2%;
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                                                                         13;
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Last sequence update)
Last annotation update)
                                                                     Score 112.5;
Pred. No. 5.5e
13; Mismatches
                                                                                                                                                                                                                                                                                                             EMBL/GenBank/DDBJ databases
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Pred. No. 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EE5F990B11FC7B3B
                                                                                                                                                                                 C3D0AF0D9540F162 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                           Sokol S.;
displacing GSK3 from axin-GSK3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .5e-05;
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                                                                                                  .5e-05;
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                                                                                                                       DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
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                                                                              Indels
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Q9JL71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 19.4
Best Local Similarity 32.4
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9JL71
Q9JL71;
                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q918W3;
01-OCT-2000
                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, TEASHIRT 2 (FRAGMENT).
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"Alteration of a single amino acid in activated receptor-alpha (PPAR alpha) phenotype.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=20267232; PubMed=10809235;
Takada I., Yu R.T., Xu H.E., Lambert M.H., Montana V.G., Kliewer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
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EMBL; AF163810; AAF80480.1; -.
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                                                                                                                                                                           gene teashirt."
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-10090;
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                                                                                                                                                                                                               Vertebrate orthologues of
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                                                                                                      Dev. 91:445-448(2000).
AF207880; AAF64095.1;
1098 10
1098 AA;
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                                    1098
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Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66
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   121367 MW;
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Last sequence update)
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Pred. No. 3.2;
12; Mismatches
                                                                                                         .
                                                                                                                                                                                                            Kerridge S.,
e Drosophila
                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EB6E0C39554C76CD CRC64;
   42BA01C7DB2BAFEB CRC64;
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029576;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
01-MAY-2000 (TREMBLREL. 13, Last annotation update)
Q9U0V8 PRELIMINARY; PRT; 679 AA. Q9U0V8; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAY-2000 (TrEMBLrel. 13, Last annotation update) HYPOTHETICAL 73.8 KDA PROTEIN. L7836.04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
EMBL; AE001057; AAB90557.1; -.
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PROSITE; PS00037; MYB_1; UNKNOWN_1.
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TIGR; AF0681; -.
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OC Eushamania major.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-FRIEDLIN;
RA Gliver K., Harris D., Ivens A.C., Lawson D., Quail M.,
RA Gliver K., Harris D., Ivens A.C., Lawson D., Quail M.,
RA Rajandream M.A., Barrell B.G.;
RR Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN-FRIEDLIN;
RA SEQUENCE FROM N.A.
RC STRAIN-FRIEDLIN;
RA Smith D.F.;
Genome Res. 8:135-145(1998).
DR RT "A physical map of the Leishmania major Friedlin genome.";
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Tomato endo-1,4-B-	R14372		501		۳	0
Leishmania antigen	W70219		151		۲.	9
Deduced sequence e	P81771		3210	٠	52	8
Sequence of clone	P93285		3080	٠	52	7
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A. thaliana enviro	Y77930	21	704		N	ພ
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Bacillus subtilis	W11328	18	329		52.5	õ
Simian immunodefic	B01778	21	158		2	ő
Human IKAP protein	Y01084	20	1332		53	æ
Lipoprotein D-MAGE	Y06590	20	446		53	7
CLYTA-MAGE-1-His f	Y06592	20	445		53	õ
Tumour rejection a	W81548	20	309		53	Ğ
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Arabidopsis thalia	G47039	21	699		ω.	ŭ
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Arabidopsis thalia	G43722	21	594			'n

## ALIGNMENTS

PPT d d P Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour; therapy; cytoplasmic degradation; blockade; Wnt signalling pathway; Mingless signalling pathway; Adenomatous Polyposis Coli; APC; tumour suppressor. W93570; Tumor-suppressing protein conductin diagnosis of tumors 17-JUN-1999 (first entry) WPI; 1999-214706/18. N-PSDB; X23370. Behrens J, Birchmeier 02-SEP-1997; 01-SEP-1998; 11-MAR-1999. WO9911780-A2. Homo sapiens. Human conductin protein. W93570 standard; Protein; 840 (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN 97DE-1038205. 98WO-DE02621. Σ ₹ used for treatment and

55.55.55

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W93570 W93569 W96264 W96265 Y90851 B01769 G13112 G13111 G13111 G13110 G45799

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                                                                                                                                                                                                                                                                                                                                                                       Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour; therapy; cytoplasmic degradation; blockade; Wnt signalling pathway; Wingless signalling pathway; Adenomatous Polyposis Coli; APC;
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                                                                                              DELBRUECK CENT MOLEKULARE MEDIZIN MAX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         840 AA;
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                                                                         Birchmeier
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                                                                                                                  97DE-1038205
                                                                                                                                      98WO-DE02621.
                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                              Location/Qualifiers 78..200
                                                                                                                                                                                                                                                                                 343..396
                                                                                                                                                                                                                                                   397..465
                                                                                                                                                                                                                                                                                          /note= "Regulator of described in
                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                      /note-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                                         Σ
                                                                                                                                                                                                                              "Beta-catenin
claim 14"
                                                                                                                                                                                                                                                                      "GSK 3-beta binding region as described
                                                                                                                                                                                                  "Dishevilled claim 15"
                                                                                                                                                                                                                                                           claim 13"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 276; DB 20; Pred. No. 2.7e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                            homology region
                                                                                                                                                                                                                                                                                          G protein signalling domain as claim 12"
                                                                                                                                                                                                                                          binding
                        used
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                         treatment and
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Nucleic acids encoding mutant and wild type Axin and coligonucleotides derived from them are useful for detecting mutations in the Axin gene and for determining whether a subject is clikely to develop cancer (including breast, colorectal, castrointestinal, esophageal, carcinomas or melanomas). The wild cype Axin and homologues of Axin are useful for treating subjects who are likely to develop cancer (thyroid carcinomas). The nucleic acids are also useful for diagnosing cancer and for detecting mutations in cancerous cells. Wild type Axin, its antisense molecule and identified compounds form pharmaceutical compositions in the treatment of cancer. The compositions are also useful for treating cancer by inhibiting tumorigenesis (by inducing degradation of beta-catenin). The nucleic acid encoding Axin, acts through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel human conductin protein which has anti-tumour activity. Detecting the presence or amount of conductin, at protein or nucleic acid levels, is used to diagnose tumours, while agents that (re)activate conductin are used for tumour therapy. Conductin binds to beta-catenin and induces its cytoplasmic degradation, resulting in blockade of the Wntr.Wingless signalling pathway in vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC) fragments and, in conjunction with APC, acts as a tumour suppressor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                  Newly isolated nucleic acid encoding "axis inhibition" (Axin) - useful for detecting, diagnosing and treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            beta-catenin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Axin; cancer; breast cancer; colorectal cancer;
gastrointestinal cancer; esophageal cancer; car
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human axin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-JUN-1999
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                                                                                                                                                                                                                       Disclosure; Figure 11; 95pp; English.
                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                              Constantini F,
                                                                                                                                                                                                                                                                                                                                                                        (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                      09-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnosis; treatment; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                        10-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  840 AA;
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Pred. No. 2.7e-29;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thyroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               carcinoma; melanoma;
inoma; tumorigenesis;
                       (by inducing degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 840;
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                                                                                                                                                                                                                                                        protein cancer
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                                                                                                    who are likely to develop cancer (thyroid carcinomas). The nucleic acids are also useful for diagnosing cancer and for detecting mutations in cancerous cells. Wild type Axin, its antisense molecule and identified compounds form pharmaceutical compositions in the treatment of cancer. The compositions are also useful for treating cancer by inhibiting tumorigenesis (by inducing degradation of beta-catenin). The nucleic acid encoding Axin acts through negative regulation of the Wnt pathway in the Nieuwkoop Center.
                                                                                                                                                                                                            nutations in the Axin year and the present colorectal, likely to develop cancer (including breast, colorectal, gastrointestinal, esophageal, carcinomas or melanomas). The wild type Axin and homologues of Axin are useful for treating subjects type Axin and homologues of Axin are useful for treating subjects type Axin and homologues of Axin are useful for treating subjects.
                                                                                                                                                                                                                                                                         Nucleic acids encoding mutant and wild type Axin and oligonucleotides derived from them are useful for detecting mutations in the Axin gene and for determining whether a subject is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;
diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
                                                                                                                                                                                                                                                                                                                                    Claim 8; Figure 8; 95pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09902179-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   negative regulation of the Wnt pathway in the Nieuwkoop Center.
                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                 Newly isolated nucleic acid encoding "axis inhibition" protein (Axin) - useful for detecting, diagnosing and treating cancer
                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-120510/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        beta-catenin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W96265 standard; Protein; 992 AA
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    34;
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   Conservative
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                  68.8%;
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Pred. No. 1.3e-17;
9; Mismatches 8
              Score 190; DB 20
Pred. No. 2e-17;
    Mismatches
                                DB 20;
    8
                                Length 992;
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RESULT
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                                             condered arrangement of R groups (defining as side chains), excluding specific tabulated arrangements (tables given in the specification).

(I), and related enzymes, are used to produce a wide range of terpenoids (e.g. cyclic, acylic, optionally hydroxylated), useful e.g. as components of signal transduction pathways, precursors of steroid hormones and bile acids, as photoreceptors and as co-factor side chains. Some synthases with little or no catalytic activity (and nucleic acids encoding them) are used as controls in the analysis of products formed by enzymatic synthesis; as nutrient supplements; for affinity purification of isoprenoids; or to develop immunological reagents or nucleic acids for monitoring expression of terpene synthase or inheritance of the gene in plant breeding programs. The new synthases was produce novel terpene products. A38910 to A38938 and y90831 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-SEP-1998;
22-APR-1999;
23-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthase; protein co-ordinate data; active site; modification; terpenoid; 3-dimensional coordinate; alpha carbon atom; plant; terpene synthase; isoprenoid; breeding programme; fragrance; flav pheromone; defensive agent; pigment; antitumour; steroid hormone; signal transduction pathway; bile acid; affinity purification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Castor bean casbene synthase protein sequence SEQ ID NO:42.
                                                                                                                                                                                                                                                                                                                                                The present invention describes an isolated terpene synthase (I) comprising a region with at least 20% identity to region 265-535 of a 548 amino acid (aa) sequence (Ia), given in ¥90831. (I) contains nine alpha-carbon atoms (alphaC) that have interatomic distances, between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chappell J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAR-2000
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                                                                                                                                                                                                                                                                                                               each other, within tabulated ranges, have a centre point (within a sphere of radius 2.3 Angstrom ) within tabulated ranges, and have an
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 106; Page 406-407; 450pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel terpene synthase enzymes, useful for producing terpene hydrocarbons, e.g. fragrances or antitumor agents, are derived known enzymes by specific amino acid alterations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Manna KR,
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99US-0150262.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Starks CM;
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Sequence

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                                               Query Match
Best Local Similarity
Matches 15; Conser
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Best Local Similarity
                                                                                                                                          The present sequence is the Pol protein from the simian immunodeficiency virus found in the red capped mangabey and designated SIVrcm. This virus is related to the HIV viruses that cause AIDS in humans. Knowing the sequence of the Pol protein and its gene is useful as it enables screening for the virus to take place in humans and animals (there is a possibility that this virus undergoes cross-species transmission), allows vaccines to be produced and aids research into the origin of these viruses. This latter is important if an AIDS vaccine is to be found.
                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                        New polypeptide, useful for producing antibodies and for diagnosis simian viral infection in humans comprises complete genome of new simian immunodeficiency virus isolate -
                                                                                                                                                                                                                                                                                                                                            WPI; 2000-423454/36.
N-PSDB; A51008.
B01775, B01776.
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                                                                                                                                                                                                                                                              Disclosure; Page 152-156; 173pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Simian immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Red capped monkey; simian immunodeficiency virus; SIV; SIVrcm; vaccination; Pol protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Simian immunodeficiency virus SIVrcm Pol protein #1.
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                                                                                                                                                                                                                                                                                                                                                                                                            Hahn ВН,
                                                                                                                                                                                                                                                                                                                                                                                                                                      (UABR-) UAB RES FOUND.
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936 latnklqnqiskiqnfrvyyregrdqlwrgpakliwkgegavviqeetgdlkvvprrkak 995
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              LTLGHFKEQLSKKGNYRYYFKKASDEFACG------AVFEEIWDDETVLPMYEGR 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14;
                                                                                                                                                                                                                                                                                                                                                                                                            Shaw GM, Gao F,
                                                                                                                      1018 AA;
                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein; 1018
                                                                 20.5%;
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                                                                 Score 56.5;
Pred. No. 43;
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Pred. No. 5.4;
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                                                   Mismatches
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                                                                             DB 21;
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hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
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29 - OCT - 1999;
                                                                                                                             G45799 standard; Protein; 975
                                                                                                           G45799;
                             Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                  Arabidopsis thaliana protein fragment SEQ ID NO: 57544.
          Arabidopsis thaliana
                                                                                        18-OCT-2000
                                                                                                                                                                               130
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                                                                                                                                                                                                                   ch 20.1%;
l similarity 33.3%;
l3; Conservative
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99US-0152363.
99US-015376.
99US-015376.
99US-0154018.
99US-01544018.
99US-0155139.
99US-0156458.
99US-0156458.
99US-0157753.
99US-0157865.
99US-0158022.
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99US-0160767.
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99US-0160814.
99US-0160814.
99US-0160814.
99US-0161406.
99US-016136.
                                                                                         (first entry)
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; Pred. No. 19;
8; Mismatches
                                                                                                                                 AA.
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23-JUN-1999;
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01-JUL-1999;
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99US-0140353.
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99US-0140695.
99US-0141842.
99US-0142055.
99US-0142055.
99US-0142055.
99US-0142055.
99US-0142055.
99US-014306.
99US-0144005.
99US-0144086.
99US-0144333.
99US-0144333.
99US-0144333.
99US-0144088.
99US-0145088.
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99US-014508.
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99US-014514.
99US-014518.
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99US-014638.
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AUG-1999; AUG-1999; AUG-1999; AUG-1999; SEP-1999; SEP-1999; SEP-1999; SEP-1999; SEP-1999;	AUG-1999; AUG-1999; AUG-1999; AUG-1999; AUG-1999; AUG-1999; AUG-1999; AUG-1999;	AUG-1999; AUG-1999; AUG-1999; AUG-1999; AUG-1999; AUG-1999; AUG-1999; AUG-1999; AUG-1999; AUG-1999; AUG-1999; AUG-1999;	JUL-1999; JUL-19	-JUL-1999 -JUL-1999
AUG-1999 99US-011 AUG-1999 99US-011 AUG-1999 99US-011 AUG-1999 99US-011 AUG-1999 99US-011 SEP-1999 99US-011 SEP-1999 99US-011 SEP-1999 99US-011 SEP-1999 99US-011 SEP-1999 99US-011 SEP-1999 99US-011	AUG-1999; 99US-01 AUG-1999; 99US-01 AUG-1999; 99US-01 AUG-1999; 99US-01 AUG-1999; 99US-01 AUG-1999; 99US-01 AUG-1999; 99US-01 AUG-1999; 99US-01 AUG-1999; 99US-01	AUG-1999 99US-011 AUG-1999 99US-011 AUG-1999 99US-011 AUG-1999 99US-011 AUG-1999 99US-011 AUG-1999 99US-011 AUG-1999 99US-011 AUG-1999 99US-011 AUG-1999 99US-011 AUG-1999 99US-011 AUG-1999 99US-011 AUG-1999 99US-011 AUG-1999 99US-011 AUG-1999 99US-011 AUG-1999 99US-011 AUG-1999 99US-011 AUG-1999 99US-011 AUG-1999 99US-011 AUG-1999 99US-011	JUL 1999 99US-011 JUL 1999 99US-011 JUL 1999 99US-011 JUL 1999 99US-011 JUL 1999 99US-011 JUL 1999 99US-011 JUL 1999 99US-011 JUL 1999 99US-011 JUL 1999 99US-011 JUL 1999 99US-011 JUL 1999 99US-011 JUL 1999 99US-011 JUL 1999 99US-011 JUL 1999 99US-011 JUL 1999 99US-011 JUL 1999 99US-011 JUL 1999 99US-011 JUL 1999 99US-011 JUL 1999 99US-011 JUL 1999 99US-011	-JUL-1999; 99US-01: -JUL-1
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RESULT 11
W04271
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Query Match
Best Local
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22-SEP-1999;
23-SEP-1999;
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28-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                    13-OCT-1999
                                                         Neutral protease; npr gene; alkaline protease; apr gene; insecticidal toxic protein; ITP; crystal protein; delta endotoxin; insecticide; bioinsecticide; biological control agent.
                                                                               B.t. neutral protease
                                                                                                       W04271;
                                                                                                                   W04271 standard; Protein; 566 AA.
                                   W09630526-A2
                                              Bacillus thuringiensis var. kurstaki strain
                                                                                            15-DEC-1996
            29-MAR-1996;
                       03-OCT-1996
                                                                                                                                                                         Local
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                                                                                                                                                                     l Similarity
16; Conserv
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                                                                                            (first entry)
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99US-0155139.
99US-0155486.
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9908-0159331
9908-015937
9908-0159638
9908-0159584
9908-0160741
9908-0160767
9908-0160767
9908-0160770
9908-0160814
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99US-0159294.
99US-0159295.
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99US-0161993.
99US-0162142.
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99US-0156596
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99US-0158369
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99US-0161920
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99US-0161404.
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 95US-0415823.
            96WO-US04310.
                                                                                                                                                                            20.1%;
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Pred. No. 56;
7; Mismatches
                                                                                                                                                                                  DB
                                                EG2371 (NRRL B-18209)
                                                                                                                                                                       15;
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RESULT 12
G43722
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A neutral protease (W04271) and an alkaline protease (W04270) were identified as being the respective products of the npr gene (T38353) and apr gene (T38352) of Bacillus thuringiensis var. (Rurstaki strain EG2371. Proteases have been implicated in the decline of insecticidal activity of crystal proteins in B.t. bioinsecticides. Genetic disablement of the npr and apr genes, by deletion of specific sequences, has allowed the prodn. of B.t. constructs having reduced proteolytic activity and therefore useful for enhanced prodn. of B.t. toxin protein. The B.t. toxins recovered from these B.t. constructs exhibit improved stability with respect to insecticidal activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disabled Bacillus thuringiensis apr and npr genes - encoding neutral and alkaline protease incapable of degrading insecticidal toxic protein (ITP), therefore increasing ITP prodn. and stability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1996-455371/45.
N-PSDB; T38353.
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
16-APR-1999;
19-APR-1999;
21-APR-1999;
23-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ECOG-) ECOGEN INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                      25-FEB-1999;
05-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana protein fragment SEQ ID NO: 54682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                 25-FEB-2000;
                                                                                                                                                                                                                                                                                                                         06-SEP-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                             termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72
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                                                                                                                                                                                                                                                                                     2000EP-0301439
                      990S-0126264
990S-0126785
990S-0127462
990S-0128234
990S-0128714
990S-0128714
990S-0130077
990S-01300449
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99US-0123548.
99US-0125788.
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        9908-0130510
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; pred. No. 39;
5; Mismatches
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99US-0144333 99US-0144333 99US-0144334 99US-0144335 99US-0144352 99US-0144632	2000	222	င့်ငှင့်	99US-0142055 99US-0142390	99US-0141842. 99US-0142154	200	99US-0140354 99US-0140695	99US-0139899. 99US-0140353.	99US-0139763. 99US-0139817.	990S-0139463. 990S-0139750.	990S-0139461. 990S-0139462.	99US-0139459. 99US-0139460.	99US-0139457.	99US-0139455. 99US-0139456.	99US-0139492. 99US-0139454.	99US-0139452. 99US-0139453.	99US-0138847. 99US-0139119.	ėė	25	9	ėĖ	Ė	20	22	ė	20	01	20	ġ	22	20	222	99US-0130891. 99US-0131449.
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13-OCT-1999 13-OCT-1999 14-OCT-1999 14-OCT-1999 14-OCT-1999 14-OCT-1999 14-OCT-1999	07-OCT-1999; 99US-0158 08-OCT-1999; 99US-0158 112-OCT-1999; 99US-0158 113-OCT-1999; 99US-0158	04-OCT-1999; 99US-0157 05-OCT-1999; 99US-0157 06-OCT-1999; 99US-0157	24-SEP-1999; 99US-0158 28-SEP-1999; 99US-0158 29-SEP-1999; 99US-0158	R 22-SEP-1999; 99US-0159 R 23-SEP-1999; 99US-0159	R 16-SEP-1999; 99US-0154	R 13-SEP-1999; 99US-0153 R 13-SEP-1999; 99US-0153	R 01-SEP-1999; 99US-0151	R 30-AUG-1999; 99US-0151 R 31-AUG-1999; 99US-0151	R 27-AUG-1999; 99US-0151 R 27-AUG-1999; 99US-0151	R 26-AUG-1999; 99US-0150 R 27-AUG-1999; 99US-0151	R 23-AUG-1999; 99US-0149 R 25-AUG-1999; 99US-0150	R 20-AUG-1999; 99US-0149 R 23-AUG-1999; 99US-0149	R 20-AUG-1999; 99US-0149 R 20-AUG-1999; 99US-0149	R 17-AUG-1999; 99US-0149 R 18-AUG-1999; 99US-0149	R 13-AUG-1999; 99US-0149 R 16-AUG-1999; 99US-0149	R 12-AUG-1999; 99US-0148 R 13-AUG-1999; 99US-0148	R 10-AUG-1999; 99US-014E R 11-AUG-1999; 99US-014E	R 09-AUG-1999; 99US-0147 R 09-AUG-1999; 99US-0147	R 06-AUG-1999; 99US-0147	R 05-AUG-1999; 990S-0147	R 04-AUG-1999; 99US-0147	R 03-AUG-1999; 99US-0147	R 02-AUG-1999; 99US-0146	R 28-JUL-1999; 99US-0145	R 27-JUL-1999; 99US-0145	R 27-JUL-1999; 99US-0145	R 26-JUL-1999; 99US-0145	R 23-JUL-1999; 99US-0145	R 22-JUL-1999; 99US-0145 R 23-JUL-1999; 99US-0145	22-JUL-1999; 99US-0145	22-JUL-1999; 99US-0145 22-JUL-1999; 99US-0145	21-JUL-1999; 99US-0145 21-JUL-1999; 99US-0145	1999; 99US-0144 1999; 99US-0144

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RESULT
G43721
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Best Local
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18-OCT-1999;
21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
22-OCT-1999;
22-OCT-1999;
22-OCT-1999;
25-OCT-1999;
25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
25 FEB-1999

05 MAR 1999

09 MAR 1999

23 MAR 1999

25 MAR 1999

26 MAR 1999

01 APR 1999

01 APR 1999

16 APR 1999

16 APR 1999

21 APR 1999

23 APR 1999

23 APR 1999

23 APR 1999

23 APR 1999

24 APR 1999

25 APR 1999

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30 APR 1999

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30 APR 1999

30 APR 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G43721 standard;
                                                                                                                                                                                                                                                                                                                                                 protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                G43721;
                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana protein fragment SEQ ID NO:
                                                                                                                                                                                                                                                                              06-SEP-2000
                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                         18-OCT-2000
                                                                                                                                                                                                                                                        25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 19.7%;
1 Similarity 34.8%;
16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                         2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0159638
99US-0159584
99US-0160741
99US-0160767
99US-0160768
99US-0160814
99US-0160981
99US-0160981
99US-0161404
99US-0161406
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99US-0161360
99US-0161360
99US-0161361
99US-0161361
99US-0161392
99US-0161392
 990S-0121825.
990S-0123548.
990S-0125788.
990S-0126785.
990S-0126785.
990S-01267462.
990S-0128734.
990S-0128814.
990S-0130077.
990S-0130049.
990S-0130449.
990S-0132485.
990S-0132485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein; 615 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 54.5; DI
; Pred. No. 42;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
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          04-JUN-1999;
07-JUN-1999;
08-JUN-1999;
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21-MAY-1999;
24-MAY-1999;
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14-MAY-1999;
18-MAY-1999;
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07-MAY-1999;
11-MAY-1999;
14-MAY-1999;
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16-JUN-1999;
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27-MAY-1999;
        18-JUN-1999;
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10-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-JUN-1999;
          990S-0132487
990S-013428
990S-0134286
990S-0134286
990S-0134211
990S-0134211
990S-0134211
990S-0134768
990S-0135353
990S-0136021
990S-0136021
990S-0136021
990S-0136282
990S-0137528
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Matches 16
25-FEB-1999
05-MAR-1999
09-MAR-1999
23-MAR-1999
24-MAR-1999
01-APR-1999
01-APR-1999
01-APR-1999
16-APR-1999
16-APR-1999
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11-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana protein fragment SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            termination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; Protein; 699
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16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence
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990S-0160980

990S-0160989

990S-0161406

990S-0161406

990S-0161406

990S-0161350

990S-0161361

990S-0161920

990S-0161922

990S-0161922

990S-0161922
990S-0121825

990S-012548

990S-0125788

990S-0126765

990S-0128234

990S-0128234

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990S-0130077

990S-013049

990S-013049

990S-013048

990S-013048

990S-0132486

990S-0134218

990S-0134218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 54.5; DI
; Pred. No. 44;
5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
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22-JUL-1999
23-JUL-1999
23-JUL-1999
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24-JUL-1999
27-JUL-1999
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27-JUL-1999
28-JUL-1999
29-AUG-1999
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990S-0145192.
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26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                                   Peptide(s) corresp. to HIV-2 amino acid sequences - used in diagnosis in vaccines and in prodn. of antibodies for diagnosis
                                                                                                                                          The amino acid sequence is that of a polymerase from the ROD HIV-2 isolate, it is encoded by nucleotides 1829-4936. See also R20596-R20596-R20508 and R22745-R22749.
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                                                                                                                   Sequence
                                                                                                                                                                                           Disclosure; Page 13; 30pp; English.
                                                                                                                                                                                                                                                        WPI; 1992-041067/05.
N-PSDB; Q20616.
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                                                                                                                                                                                                                                                                                                                      (INSP ) INST PASTEUR.
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vative 12; Mismatches 16; Indels 1
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STATE:
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ALIGNMENTS

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TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kraus, Guenter
APPLICANT: Wong-Staal, Flossie
APPLICANT: Talbott, Randy
APPLICANT: Poeschla, Eric
TITLE OF INVENTION: Isolation of No. 5883081el HIV-2 Proviruses
CORRESPONDENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1055 amino acids
LOCATION: 1..1055
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   San Francisco
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                                                                                            Sequence 4, Application US/08415823 Patent No. 5759538
                                                                               Patent No. 5759538 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (213) 977-100 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: The Regents of the University of California TITLE OF INVENTION: Isolation of Novel HIV-2 Proviruse: NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1055 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Berliner, Robert
REGISTRATION NUMBER: 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 201 N. Figueroa Street, 5th Floor CITY: Los Angeles STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
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                                APPLICANT: Tan, Yuping
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1055 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                             Conservative
                                                                 Donovan, William P.
                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (213) 977-1001
                                                                                                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    977-1003
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                                                                                                                                                                                                                                                                            19.9%;
   BACILLUS THURINGIENSIS APT AND NPT PROTEASE GENES AND ALKALINE PROTEASE DEFICIENT AND NEUTRAL PROTEASE DEFICIENT B.T. STRAINS
                                                                                                                                                                                                                                                                                                                                                        /note= "pol protein encoded by HIV-2KR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT/US96/11445
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5555-399C1
                                                                                                                                                                                                                                                                              Score 55;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                              5:
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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-415-823-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
US-09-086-662-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 566 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dono APPLICANT: Tan,
                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 KGDYKLGEKSAQDSFKVKQVKKDAVTDSTVVRMQQVYEG 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/415,823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Panitch Schwarze Jacobs & Nadel, P.C. ADDRESSEE: A.S. Nadel STREET: 1601 Market Street, 36th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                     CITY: Philadelphia
                                                                             APPLICATION NUMBER: FILING DATE:
                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                   COUNTRY:
STRANDEDNESS:
                                                                                                                                         FILING DATE:
                                                                                                                                                         APPLICATION NUMBER:
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15; Conserv
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                  amino
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1601 Market Street,
                                                                                                                                                                                                                                                                                                      Pennsylvania
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Donovan, William P.
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                  acid
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 single
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                                                                                                                                                                                                                                                                                                                                                                                                                BACILLUS THURINGIENSIS APT AND DPT
PROTEASE GENES AND ALKALINE PROTEASE DEFICIENT AND NEUTRAL
PROTEASE DEFICIENT B.T. STRAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schwarze Jacobs & Nadel,
                                                                                                                                                            US/09/086,662
                                                                                                 08/415,823
                                                                 4:
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Pred. No. 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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linear

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TOPOLOGY:
; MOLECULE TYP
US-09-086-662-4
                                                                                                                                                                                                                              ; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-465-167A-24
RESULT 6
US-08-993-118-10
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US-08-465-167A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
SOFTWARE: DAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,167A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/103,623
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
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Matches 15; Conserv
                                                                                                                                           Matches
                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24, Application US/08465167A Patent No. 5750395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Livingston, Brian D.
APPLICANT: Sette, Alessandro D.
                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-5/6-0300
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sette, Alessandro D.

APPLICANT: Sidney, John C.

TITLE OF INVENTION: DNA ENCODING MAGE-1 C-TERMINAL
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES (as amended)
                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                     212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 KGNYRYYFKKASDEFACGAVFEEIWDDETVLPM---YEG 48
                                                                                                    34 EEIWDDETVLPMYEGR 49
                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Parmelee, Steven W. REGISTRATION NUMBER: 31,990 REFERENCE/DOCKET NUMBER: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 KGDYKLGEKSAQDSFKVKQVKKDAVTDSTVVRMQQVYEG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 206-467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98111
                                                                   EEIWEELSVMEVYDGR 227
                                                                                                                                                                                                                                                                                                 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.7%;
                                                                                                                                                          19.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                              14137-60-1
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Pred. No. 11;
                                                                                                                                                           Score 53; I
Pred. No. 8
                                                                                                                                           Mismatches
                                                                                                                                                                            DB 1;
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                                                                                                                                           2
                                                                                                                                                                          Length 309;
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Query Match
Best Local Similarity
Best B; Conserv
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US-08-845-528C-10
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                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                            Sequence 10,
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                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/8
FILING DATE: April 25, 1997
ATTORNEY/AGENT INFORMATION:
NAME: MATY ANNE Schofield
                                                                                                                    APPLICANT: LUCAS, SO, APPLICANT: DE SMET, C APPLICANT: BOON-FALLE TITLE OF INVENTION: I TITLE OF INVENTION: T TITLE OF INVENTION: T TITLE OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: LU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM PS/2
COMPUTER: FOR COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,118
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TITLE OF INVENTION:
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APPLICANT: BOON-FALLEUR, Thierry
                                                                                                    CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                212 EEIWEELSVMEVYDGR 227
                                STREET: 805 Third Avenue CITY: New York City STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                              34 EEIWDDETVLPMYEGR 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acids STRANDEDNESS: sine
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STATE: New York
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COUNTRY: USA
ZIP: 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                             Application US/08845528C
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805 Third Avenue
                                                                                                                                             BOON-FALLEUR, Thierry
IVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING FOR TUMOR
IVENTION: REJECTION ANTIGEN PRECURSOR MAGE-C1 AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DE SMET,
                                                                                                                                                                                                  LUCAS, Sophie;
ne SMET, Charles;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SS: single stranded
linear
                                                                                    Felfe & Lynch
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                                                                                                                     THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                us/08/845,528
25, 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-971-244-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                         TELEFAX: (650) 343-4342 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cohen, Lucy
APPLICANT: Baeuerle, Patrick
TITLE OF INVENTION: IKAP Proteins, Nucleic Acids and Methods
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1332 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Mary Anne Schofield
REGISTRATION NUMBER: 36,669
REFERENCE/DOCKET NUMBER: LUD 5455
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,528C
FILING DATE: April 25, 1997
CLASSIFICATION: 4335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 EEIWDDETVLPMYEGR 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.2%;
Local Similarity 50.0%;
mes 8; Conservation
                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM FS
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acids
STRANDEDNESS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
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                  protein
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Pred. No. 8
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                                                                                                                                                                                                                                                                                                                      Version #1.30
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                                                                                                              US-08-432-016-3
                                                                                                                             RESULT
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                                                                             Sequence 3, Application US/08432016 Patent No. 5968768
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Best Local Similarity
                                                                                                                                                                                                                                         Matches
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                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (650) 343-43 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1332 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/286,891
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cohen, Lucy
APPLICANT: Baeuerle, Patrick
TITLE OF INVENTION: IKAP Proteins, Nucleic Acids and Methods
 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                            321 QLWTVGNYHWYLKQSLSFSTCGKSKIVSLMWDPVT 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          321 QLWTVGNYHWYLKQSLSFSTCGKSKIVSLMWDPVT 355
                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                       TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                        9 QLSKKGNYRYYFKKASDEFACG--AVFEEIWDDET 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSEE: SCIENCE & TECHNOLOGY LAW GROUP
I: 75 DENISE DRIVE
HILLSBORUGH
CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                   amino acid
HAYNES, BARTON F.
ARUFFO, ALEJANDRO
PATEL, DHAVALKUMAR
BOWEN, MICHAEL A.
                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                        linear
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50) 343-4342
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34.3%;
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Pred. No. 53;
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Pred. No. 53;
                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                       Length 1332
                                                                                                                                                                                                                                           Indels
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MARQUARDT,

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US-08-684-594-3
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GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,016
FILING DATE: 01-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/333,350
FILING DATE: 02-NOV-1994
                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (703) 816-41
NFORMATION FOR SEQ ID NO:
              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 02-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                      TITLE OF INVENTION: CD6 LIGAND NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MARQUAR
                                                   STATE: VIRGINIA COUNTRY: U.S.A. ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                             52 YKDRLSLSENYTLSIKNARISDEKRFVCMLVTEDDVSEEPTVVKVFK 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32.
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS
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                                                                                                     CITY: ARLINGTON
                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                6 FKEQLSKKGNYRYYFKKA--SDE--FACGAVFE-EIWDDETVLPMYE 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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1100 NORTH GLEBE ROAD
                                                                                                                 E: NIXON & VANDERHYE P.C.
1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       477 amino acids
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                                                                                                                                                                                                                      PATEL, DHAVALKUMAR
BOWEN, MICHAEL A.
                                                                                                                                                                                                                                                          ARUFFO,
                                                                                                                                                                                                                                                          HAYNES, BARTON F. ARUFFO, ALEJANDRO
                                                                                                                                                                                                          MARQUARDT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US 08/143,903
                                                                                                                                                                                                          HANS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 52.5;
Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1579-95
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Query Match
Best Local Similarity
Matches 16; Conserve
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; TOPOLOGY: Linear
; MOLECULE TYPE: protein
US-08-684-594-3
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SEQUENCE CHARACTERISTICS:
LENGTH: 477 amin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08854585 Patent No. 6114140
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas K. and
                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703),816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/143,903
FILING DATE: 02-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
               ATTORNEY/AGENT INFORMATION:
NAME: BOTUN, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 276
                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Density Enhanced Protein Tyrosine Phosphatase NUMBER OF SEQUENCES: 6
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                                                                                                                          PRIOR APPLICATION DATA:
TELECOMMUNICATION INFORMATION:
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                                                                                       APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 YKDRLSLSENYTLSIKNARISDEKRFVCMLVTEDDVSEEPTVVKVFK 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 0: FILING DATE: 02-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/432,016 FILING DATE: 01-MAY-1995
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                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                STREET: 233 S
                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 FKEQLSKKGNYRYYFKKA--SDE--FACGAVFE-EIWDDETVLPMYE 47
                                                                                                                                                                                                                                                                                                60606
                                                                                                                                                                                                                                                                                                                             Illinois
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PatentIn Release #1.0, Version #1.30
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Pred. No. 1
                 27866/31954
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RESULT 1
5223423-4
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GALLO,
                                Patent No. ,5223423
                                                                                                                                                                                      Matches
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GENERAL INFORMATION:
APPLICANT: Tooks, Nicholas K. and stman, Arne
TITLE OF INVENTION: Density Enhanced Protein Tyrosine
                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                     TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1337 amino acid
                                                                                                                     1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05512
FILING DATE:
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CORRESPONDENCE ADDRESS:
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 APPLICANT: FRANCHINI, GENOVEFFA; WONG-STAAL, FLOSSIE;
O, ROBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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CITY: Chicago
STATE: Illinoi
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TYPE: amino acid
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Pred. No.
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Pred. No.
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US-07-687-466B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : TITLE OF INVENTION: CHARACTERIZATION OF REPLICATION COMPETENT :HUMAN IMMUNODEFICIENCY TYPE 2 PROVIRAL CLONE HIV-2 SBL/ISY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/07687466B Patent No. 5328999
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Best Local Similarity
Matches 13; Conserv
                                                                    Matches
                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin L. Bastian
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bennett, APPLICANT: Fischer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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 282
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                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                        TYPE:
                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 34
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                  TORNEY/AGENT. Kevin L.
NAME: Bastian, Kevin L.
34,774
                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US FILING DATE: 19910418 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 03-31-1989
                                                                                  Local
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                                 7 KEQLSKKGNYRYYFKKASDEFACGAVFE 34
KEYLNGKSNLE-KFKKDADSFICGLMPE 308
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California
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25.5%;
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Endo-1,4-Beta-Glucanase Genes
                                                                                    46.48;
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                                                                                    Score 51.5;
Pred. No. 2
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                                                                                      26;
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Search completed: June Job time: 5406 sec

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Post-processing: Minimum Match 0%
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   Score
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Gapop 10.0 , Gapext 0.5
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   DB
   T08423
A49840
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JC5763
JC5763
JC576407
T19802
T16600
T43171
T743171
E64233
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Query Ma Best Loo Matches	RESULT 2 T08422 T08422 negative regualtor axin [imponed of the property of the	Query M Best Lo Matches Qy 1	RESULT 1 T08423 Axin homolog N;Alternate C;Species: R C;Date: 05-N C;Accession: R;Yamamoto, Mol. Cell. B A;Title: Axi A;Reference A;Accession: A;Status: pr A;Molecule t A;Residues: A A;Cross-refe A;Note: inte C;Keywords:		33 33 33 33 33 33 33 33 33 34 44 44 44 4
atc	RESULT 2 T08422 T08422 T08422 Respectes: Rattus norvegicus C; Species: Rattus norvegicus C; Date: 05-Nov-1999 #sequence C; Accession: T08422 C; Accession: \$131-1384, 1998 R; Ikeda, \$5; Yamamoto, H.; Mu EMBO J. 17, 1371-1384, 1998 A; Title: Axin, a negative reg A; Reference number: Z16413; M A; Accession: T08422 A; Status: preliminary; transl A; Molecule type: mRNA A; Residues: 1-832 - XIKE> A; Coss-references: EMBL:AF01 A; Note: GSK-3beta Interacting C; Keywords: phosphoprotein; s	T L SO WA	Phirelling		
h Similarity 33; Conserva	ualtor axin [imp names: rAxin rattus norvegicus ov-1999 #sequenc r08422 Yamamoto, H.; M 1371-1384, 1998 1371-1384, 1998 n, a negative re number: Z16413; r08422 eliminary; trans ype: mRNA 1-832 < IKE> rences: EMBL:AFO 3beta interactin; phosphoprotein;	h Similarity 51; Conservat LGHFKEQLSKKGNY 	Axil - rat names: Axil attus norvegicus (No) ov-1999 #sequence_rev T08423 H.; Kishida, S.; Uoc) iol. 18, 2867-2875, 1 l, a member of the An number: Z16414; MUID: T08423 eliminary; translated ype: mRNA 1-838 <yam> 1-838 <yam> raccs: EMBL:AF01775; raccs: with GSK-3beta phosphoprotein; signa</yam></yam>		19.7 19.7 19.6 19.6 19.4 19.4 19.4 19.4 19.4 19.4
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Score 190; DB 2; Ler Pred. No. 1e-15; 10; Mismatches 8; :	- rat ay rat) sion 05-Nov-1999 H.; Kishida, S.; r of the Wnt sign 8151361 from GB/EMBL/DDBJ NID:g2982197; PI ein transduction	Score 276; DB 2; L Pred. No. 1.9e-26; 0; Mismatches 0; 0; SDEFACGAVEEIWDDETVLPM 	way rat) vision 05-Nov-199 vision 05-Nov-199 ii, T.; Ikeda, S. 1998 cin family, inter 198226558 from GB/EMBL/DD d from GB/EMBL/DD cand beta-catenin and beta-catenin	ALIGNMENTS	RDHY75 HYBSU \$25541 \$25541 \$42923 00VZF1 B35390 00VZF1 F72159 \$33086 T728510 T7355 B75212 D71021 D71021 T01135
Length 832; Indels 0; Gaps 0;	9 #text_change 21-Jul-2000 ; Kikuchi, A. gnaling pathway, forms a complex wit BJ PIDN:AAC40066.1; PID:g2982198	Length 838; Indels 0; Gaps 0; MYEGRIL 51         MYEGRIL 831	<pre>9 #text_change 21-Jul-2000 ; Koyama, S.; Asashima, M.; Kikuchi, acts with both glycogen synthase kin BJ PIDN:AAC40089.1; PID:g3080759</pre>		dihydrofolate redubacillolysin (EC 3) heat shock protein glucose-6-phosphat infected cell prot F1 protein vacci replication protei replication protei f2 protein vacci f30R protein var G9R protein var G9R protein protei g37K myristylprotei amidophosphorlbosy hypothetical prote GTP-binding regula hypothetical prote

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dishevelled protein 3 - human C;Species: Homo sapiens (man) C;Date: 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000 C;Accession: JC5763 R;Bui, T.D.; Beier, D.R.; Jonssen, M.; Smith, K.; Dorrington, S.M.; Kaklamanis, Blochem. Biophys. Res. Commun. 239, 510-516, 1997 A;Title: CDNA cloning of a human dishevelled DVL-3 gene, mapping to 3q27, and ex A;Reference number: JC5763; MUID:98008870 A;Accession: JC5763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: dsh
A;Cross·references: FlyBase:FBgn0000499
C;Superfamily: GLGF domain homology
F;258-333/Domain: GLGF domain homology <GLG2>
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C;Species: Drosophila melanogaster
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1998
C;Accession: A49840
dishevelled homolog C; Species: Xenopus 1
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C;Superfamily: GLGF domain homology
F;255-331/Domain: GLGF domain homology <GLG4>
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C;Genetics:
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A; Residues: 1-623 <KLI>
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A; Residues: 1-716 <BUI>
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VTLGQFKELLTKKGSYRYYFKKVSDEFDCGVVFEEVREDEAILPVFEEKII 825
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                                                                                                                                           VTLADFKGVL-QRPSYKFFFKSMDDDF--GVVKEEISDDNAKLPCFNGRVV
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       African clawed frog
evis (African clawed frog)
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                                                                                                                                                                                                                              Score 95.5; DB 2;
Pred. No. 0.00052;
Wismatches 16;
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C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change C;Accession: I51691  
R;Sokol, S.Y; Klingensmith, J.; Perrimon, N.; Itoh, K. Development 121, 1637-1647, 1995  
A;Title: Dorsalizing and neuralizing properties of Xdsh, a mater A;Reference number: I51691; MUID:95324391
                                                                                                                                                                                                                                                                            ferrichrome-iron receptor 1 - Synechocystis sp. (strain PCC 6803)

N;Alternate names: protein.sll1409

C;Species: Synechocystis sp.

A;Variety: PCC 6803

C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000

C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
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C;Superfamily: GLGF domain homology
F;260-336/Domain: GLGF domain homology <GLG4>
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                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
S74447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Keywords: NADP; oxidoreductase F;3-125/Domain: type I dihydrofolate reductase homology <DFR> F;30,34,64,70/Binding site: substrate (Glu, Phe, Asn, Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Lai, P.H.; Pan, Y.C.E.; Gleisner, J.M.; Peterson, D.L.; WILLIAMS, Biochemistry 21, 3284-3294, 1982
A;Title: Structure of dihydrofolate reductase: primary sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dihydrofolate reductase (EC 1.5.1.3) - bovine C;Species: Bos primigenius taurus (cattle) C;Date: 15-Oct.1982 #sequence_revision 15-Oct.1982 C;Accession: A00388
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A;Status: nucleic acid sequence not shown;
A;Molecule type: DNA
A;Residues: 1-863 <KAN>
                                                                                                                                                                              C;Accession: S74447
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; V DNA Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: liver C; Superfamily: type I dihydrofolate reductase; type I dihydrofolate
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                                                                                                                                                        DNA Res. 3, 109-13
A; Title: Sequence
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                                                                           A; Reference number: S74322; MUID: 97061201
A; Accession: S74447
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Local Similarity 34.18;
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                                                                                                                                                           analysis of the genome of the
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                                                           translation not shown
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                                                                                                                                                                unicellular cyanobacterium Synechocys
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                                                                                                                                                                                                                                            E.; Nakamura,
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R;Bentley, D.

R;Bentley, D.

R;Bentley to the EMBL Data Library, September 1995

A;Description: The sequence of C. elegans cosmid K09F5.

A;Reference number: Z18544

A;Recession: T16600

A;Recession: T16600

A;Recession: Preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1616 <ABNN

A;Residues: 1-1616 <ABNN

A;Residues: 1-1616 <ABNN

A;Residues: SMBL:U37430; NID:g1019963; PID:g1945496; PIDN:AAB52675.1; GSPDB:GNOG

A;Cross-references: EMBL:U37430; NID:g1019963; PID:g1945496; PIDN:AAB52675.1; GSPDB:GNOG

A:Experimental source: Strain Bristol N2; clone K09F5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Map position: 1
A:Introns: 33/3; 124/1; 265/1; 298/2; 328/3
C:Superfamily: Caenorhabditis elegans hypothetical protein C37A5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:D90899; GB:AB001339; NID:g1651650; PIDN:BAA16599.1; PID:g165167
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
                    A;Map position: X
A;Introns: 291/3; 386/3; 1448/3; 1531/1
C;Superfamily: vitellogenin
                                                                                                                                                                                                                                                                                                                                                                                                               vitellogenin vit-1 - Caenorhabdit
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-336 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, A; Reference number: Z19180 A; Accession: T19802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
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A;Start codon: GTG
C;Superfamily: ferrichrome-iron receptor 1;
C;Keywords: iron transport
                                                                                                    A; Gene: CESP: vit-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein C37A5.9 - Caenorhabditis elegans
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Best Local S
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 FKEQLSKKGNYRYYFKKASDEFACGAVFEEI-----WDDETVLPMYEG
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ilarity 29.4%;
Conservative 1;
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    Caenorhabditis elegans

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28.0%;
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membrane transport protein (glnQ) homolog MG303 - Mycoplasma genitalium
C;Species: Mycoplasma genitalium
C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 07-Dec-1999
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                                                                             E64233
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submitted to the EMBL Data Library, May 1998
A;Description: Mig-5, a gene that controls cell fate a;Reference number: Z22326
A;Accession: T43171
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-666 <GUO>
A;Cross-references: EMBL:AF063244; PIDN:AAC16434.1
C;Genetics:
A;Gene: mig-5
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                                                                                                                                                                                                                                                                                                                                                           hypothetical protein T05C12.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T24507 R;Burton, J.
                                                                                                                                                       A;Gene: CESP:T05C12.6
A;Map position: 2
A;Introns: 13/3; 63/2; 114/3; 140/1; 299/2; 340/2; 449/1; 624/1
                                                                                                                                                                                                       A;Cross-references: EMBL:266500; PIDN:CAA91307.1; A;Experimental source: clone T05C12 C;Genetics:
                                                                                                                                                                                                                                                                                      A; Reference number: Z19901
A; Accession: T24507
A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, October 1995 A; Reference number: Z19901
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                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-672 <WIL>
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                                                                       Matches
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2 TLGHFKEQLSKKGNYRYYFKK 22
|||:|| :| :| |:| |:
37 TLGNFKNSFTKRG-YKYYAKE 56
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                                                                       Conservative
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Pred.
                                                                   Score 57.5; D
Pred. No. 27;
5; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                             from GB/EMBL/DDBJ
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                                                                                                     Length 672;
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T-kininogen I precursor - rat
N.Alternate names: 73K protein; LMW kinin
N.Contains: bradykinin; T-kinin
C.Species: Rattus norvegicus (Norway rat)
C;Date: 17-Mar-1987 #sequence_revision 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: mRNA A;Residues: 1-1238 <KUR>
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A;Title: The minimal gene complement of Mycoplasma genitalium A;Reference number: A64200; MUID:96026346
A;Accession: E64233
                                                                                                                                                                                                                                                                                                                                                                                                                                             F;29-1238/Product: HPTP beta-like tyrosine phosphatase #status predicted F;267-347/Domain: fibronectin type III repeat homology <3FR> F;267-348/Domain: protein-tyrosine-phosphatase homology <PTP> F;966-1188/Domain: protein-tyrosine-phosphatase homology <PTP> F;1140/Active site: Cys (phosphocysteine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: protein-tyrosine-phosphatase, receptor type C;Keywords: phosphoprotein F;1-28/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:D45212; NID:g1208432; PIDN:BAA08146.1; PID:g1208433 C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: E64233
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J
                                                                                                                                                                                                                                                                                                                                                                                                                 F;1140/Active site: Cys (phosphocysteine intermediate) *scalus prodicted F;1146/Binding site: substrate phosphate (Arg) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: S68700; A; Accession: S68700
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R;Kuramochi, S.; Matsuda, S
FEBS Lett. 378, 7-14, 1996
A;Title: Molecular cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HPTP beta-like tyrosine phosphatase precursor - mouse C;Species: Mus musculus (house mouse) C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change
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Best Local (
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                                                                                                                                                                                                                                                                                                          Local Similarity
nes 16; Conserv
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                                                                                                                                                                                                               KSKLIRVENFEAYFKKQQADSNCG--FAEEYEDLKLIGISLPKYTAEI 963
                                                                                                                                                                                                                                                          KEQLSKKGNYRYYFKKASDEFACGAVFEEIWDDETV---
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, MUID:96140699
                                                                          LMW kininogen
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Pred. No.
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A;Experimental source: strain Sprague-Dawley
R;Kageyama, R.; Kitamura, N.; Ohkubo, H.; Nakanishi, S.
J. Biol. Chem. 262, 2345-2351, 1987
A;Title: Differing utilization of homologous transcription
A;Reference number: A25488; MUID:87137465
A;Accession: B25488
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A;Residues: 330-420,'r',422-429,'P' <KAN>
R;Anderson, K.P.; Croyle, M.L.; Lingrel, J.B.
Gene 81, 119-128, 1989
A;Title: Primary structure of a gene encoding
A;Reference number: JQ0027; MUID:90034172
A;Accession: JQ0027
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Jpn. J. Cancer Res. 81, 63-68, 1990
A;Title: Identification of a protein increasing
A;Reference number: PL0193; MUID:90216390
A;Accession: PL0193
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A;Title: Purification and characterization of :
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A;Title: Differing expression patterns and A;Reference number: A92625; MUID:87137443
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A;Residues: 1-430 <FUR>
A;Cross-references: GB:M11883; NID:g205084; PIDN:AAA41489.1; PID:g205085
A;Cross-references: GB:M11883; NID:g205084; PIDN:AAA41489.1; PID:g205085
A;Cross-references: GB:M11883; NID:g205084; PIDN:AAA41489.1; PID:g205085
A;Cross-references: GB:M11883; NID:g205084; PIDN:AAA41489.1; PID:g205085
A;Cross-references: GB:M11883; NID:g205084; PIDN:AAA41489.1; PID:g205085
A;Cross-references: GB:M11883; NID:g205084; PIDN:AAA41489.1; PID:g205085
A;Cross-references: GB:M11883; NID:g205084; PIDN:AAA41489.1; PID:g205085
A;Cross-references: GB:M11883; NID:g205084; PIDN:AAA41489.1; PID:g205085
A;Cross-references: GB:M11883; NID:g205084; PIDN:AAA41489.1; PID:g205085
A;Cross-references: GB:M11883; NID:g205084; PIDN:AAA41489.1; PID:g205085
A;Cross-references: GB:M11883; NID:g205084; PIDN:AAA41489.1; PID:g205085
A;Cross-references: GB:M11883; NID:g205084; PIDN:AAA41489.1; NID:g205085
A;Cross-references: GB:M11883; PIDN:g205085
A;Cross-references: GB:M
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A;Introns: 65/3; 102/3; 130/1; 187/3; 223/2; 252/1; 309/3; 345/3; 374/3; C;Superfamily: kininogen; cystatin homology C;Keywords: acute phase; bradykinin; cysteine proteinase inhibitor; duplif;1-18/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                        A; Molecule type: protein
A; Residues: 376-430 (EN2)
R; Sierra, F.; Walter, R.; Vautravers, P.; Guigo
Arch. Biochem. Biophys. 322, 333-338, 1995
A; Title: Identification of several isoforms of
A; Reference number: S68034; MUID:96032652
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A;Title: Purification and characterization of two kinds of log.
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A; Residues: 'E'; 20-48; 376-430 <ENJ>
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A; Residues: 375-430 <KIT>
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                                                                                                                                      C; Genetics:
A; Introns: 65/3;
                                                                                                                                                                                                                                     d of an Arg or Lys, it is probably not released from
C;Comment: The T-kininogens are produced in response
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A; Residues: 1-48 < KAG>
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A; Residues: 340-430 <SIE>
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A; Residues: 1-60, 'E', 62-113, 'R', 115-165, 'F', 167-178, 'TKI', 182-211, 'F', 213-256, 'S', 258
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C;Accession: B38475; J00974

R:Tristem, M: Hill, F:; Karpas, A.
J. Gen. Virol. 72, 721-724, 1991

A;Title: Nucleotide sequence of a Guinea-Bissau-derived human immunodeficiency virus typ A;Reference number: A38475; MUID:91170959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;141-252/Domain: cystatin homology <CY2>
F;263-374/Domain: cystatin homology <CY3>
F;263-374/Domain: cystatin homology <CY3>
F;378-386/Product: bradykinin #status predicted <BDY>
F;137/Modified site: pyrolidone carboxylic acid (Gln) (in mature form) #status experimen F;82,126,168,204,326/Binding site: carbohydrate (Asn) (covalent) #status predicted F;83-94,107-125,141-144,205-217,228-247,263-266,327-339,350-369/Disulfide bonds: #status
                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: pol polyprotein
C;Keywords: AIDS; aspartic proteinase; endonuclease; hydrolase; immunodeficiency; nucleof;85-183/product: retropepsin #status predicted <RTP>
F;109/Active site: Asp (shared with dimeric partner) #status predicted
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A;Residues: 1-1034 <TRI>
A;Residues: 1-1034 <TRI>
C;Comment: The cleavage sites of this polyprotein have not been determined.
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N;Contains: endonuclease (EC 3.1...); retropepsin (EC 3.4.23.16); RNA-directed DNA poly
C;Species: human immunodeficiency virus type 2, HIV-2
A;Note: host Homo saplens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 31-Jan-1997
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-I- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-CATENIN AND APC BY GSK-3B (BY SIMILARITY).

-I- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B) AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                       use by non-profit institutions as lone modified and this statement is not remove entitles requires a license agreement (ST) or send an email to license@isb-sib.ch).
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between the Swiss Institute of Bioinformatics and the EMBL outst
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Jenkins N.A., Warburton D., Costantini
"Properties of mouse Axin2 and human A)
expression pattern, interaction with Ay
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                                                                              AF073788;
                                                                 AF205889;
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F.;
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QY2T1; Q9UH84;
Q1-QCT-2000 (Rel. 40, Created)
Q1-QCT-2000 (Rel. 40, Last seque)
Q1-QCT-2000 (Rel. 40, Last annot)
AXIN 2 (AXIS INHIBITION PROTEIN)
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                                            <del>-</del> <del>-</del> <del>-</del> <del>-</del>
                                                                                                                                                                                              SUDMITTED (NOV-1999) to the EMBL/GenBank/DDBJ databases.

-I: FUNCTION: INHIBITOR OF THE WAT SIGNALING PATHWAY. DOWN REGULATES
-BETA-CATENIN, PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-CATENIN AND APC BY GSK-3B (BY SIMILARITY).

-[- SUBUNIT: INTERACTS WITH GLYCOGEN SYNTHASE-3 BETA (GSK-3B)
-AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.
                                                                                                                                                                                                                                                                                                                                                             Zhang T., Fagotto F., Hsu W., Zeng L., Gilbert D., Copeland N.G., Jenkins N.A., Warburton D., Costantini F.; "Properties of mouse Axin2 and human AXIN2: chromosomal location, expression pattern, interaction with Axin and effects on embryoni
                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Brain, and Lymphoblast; Zhang T., Fagotto F., Hsu W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome 17q23-q24.";
Genomics 55:341-344(1999).
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Mai M., Qian C., Yokomizo A., Smit
"Cloning of the human homolog of c
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SIMILARITY: CONTAINS 1
SIMILARITY: CONTAINS 1
                                                                                                                         SUBCELLULAR LOCATION: CYTOPLASMIC.
TISSUE SPECIFICITY: EXPRESSED IN B
                                                                                                                                                                      OCCURS VIA THE ARMADILLO REPEATS CONTAINED TERNARY COMPLEX (BY SIMILARITY).
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stazoa; Chordata; Craniata; Vertebrata;
+horia: Primates; Catarrhini; Hominidae;
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ON PROTEIN 2) (CONDUCTIN) (AXIN-LIKE PROTEIN)
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pred. No. 3.3
); Mismatches
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H -> Y (IN REF. 2).
S -> P (IN REF. 2).
F -> S (IN REF. 2).
G -> A (IN REF. 2).
A07D5EFB25DE7277 C
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BY GSK-3B
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No. 3.3e-27;
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MEDLINE-20171051; PubMed-10704853;

MEDLINE-20171051; PubMed-10704853;

A Shimizu T., Yamanaka Y., Ryu S.-L., Hashimoto H., Yabe T., Hi
A Bae Y.-K., Hibi M., Hirano T.;

"Cooperative roles of Bozozok/Dharma and Nodal-related protei
formation of the dorsal organizer in zebrafish.";

L Mech. Dev. 91:293-303(2000).

C -!- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN RE
BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF
C CATENIN AND APC BY GSK-3B (BY SIMILARITY).

C -!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

C -!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

C -PDM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLAT

PODA (BY SIMILARITY).

C -!- SIMILARITY: CONTAINS 1 DIX DOMAIN.
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P57095;
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Eukaryota; Metazoa; Chordata;
Actinopterygil; Neopterygil; T
                                                                                                                                                                                                                                                                                                                01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
AXIN 2 (AXIS INHIBITION PROTEIN 2).
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PROSITE; PS50132; RGS; 1.

Developmental protein; Phosphorylation.

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DOMAIN 327 413 GSK-3B BINI

DOMAIN 413 476 BETA-CATEN
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_Cyprinidae; Rasborinae; Danio.
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P -> S (IN REF. 2).
Q -> H (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pathway that regulates embryonic axis formation."; Cell 90:181-192(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97373830; PubMed=9230313;
Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J.,
Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.
"The mouse Fused locus encodes Axin, an inhibitor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus.
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Pfam; PF00778; DIX; 1.
PROSITE; PS50132; RGS;
Developmental protein;
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                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY). DEVELOPMENTAL STAGE: EXPRESSED AT STAGE 12 TO 15. PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPI PP2A (BY SIMILARITY).

SIMILARITY: CONTAINS 1 RGS DOMAIN.
SIMILARITY: CONTAINS 1 DIX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLAT CATENIN AND APC BY GSK-3B (BY SIMILARITY).
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POLY-SER.
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Best Local Similarity
                                                                                                                                       use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE
                         InterPro; IPR00
InterPro; IPR00
Pfam; PF00615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hedgepeth C.M., Deardorff M.A., Klein P.S.;
"Xenopus axin interacts with glycogen synthase kinase-3 bet expressed in the anterior midbrain.";
Mech. Dev. 80:147-151(1999).
-i- FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN BETA-CATENIN. PROBABLY FACILITATE THE DHOGDUDOWN TARROWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last seq
01-0CT-2000 (Rel. 40, Last ann
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01-0CT-2000
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DOMAIN 88 211
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InterPro; IPR001158;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AXIN (AXIS INHIBITION
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                                                                                            EMBL; AF097313; AAC71036.1; HSSP; P49799; lAGR.
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MEDLINE=99173782; PubMed=10072781;
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SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
DEVELOPMENTAL STAGE: WEAKLY AND UBIQUITOUSLY EXPRESSED THROUGHOUT EARLY DEVELOPMENT, AND HIGHLY EXPRESSED IN THE ANTERIOR MESENCEPHALON ADJACENT TO THE FOREBRAIN-MIDBRAIN BOUNDARY.
PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED BY
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SIMILARITY: CONTAINS 1 RGS DOMAIN.
SIMILARITY: CONTAINS 1 DIX DOMAIN.
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                                                   IPR001158;
                                                                          IPR000342; -.
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841 /
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     RGS;
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94931
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PROTEIN) (XAXIN).
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DIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 197; DB 1; 1
Pred. No. 3.2e-17;
0; Mismatches 7;
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Best Local
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Developmental
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DOMAIN
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
AXIN 1 (AXIS INHIBITION PROTEIN 1) (HAXIN) (FRAGMENT).
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015169;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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01-OCT-2000
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HSSP; P49799; 11
                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: CYTOPLASMIC.
TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED
PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATENIN AND APC BY GSK-3B.
SUBUNT: INTERACTS WITH GLYCOGEN SYNTHASE KINASE-3 BETA (GSK-3B)
AND BETA-CATENIN. THE INTERACTION BETWEEN AXIN AND BETA-CATENIN
OCCURS VIA THE ARMADILLO REPEATS CONTAINED IN BETA-CATENIN.
TERNARY COMPLEX. MAY ALSO BINDS TO PLAKOGLOBIN (GAMMA-CATENIN),
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 1 RGS DOMAIN. SIMILARITY: CONTAINS 1 DIX DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J.J., Tilghman S.M., Gumbiner B.M., Costantini F.; mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling
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34; Conservative
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94459
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Phosphorylation
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; Pred. NO. 5.7e
9; Mismatches
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BETA-CATENIN BINDING SITE (BY SIMILARITY).
DIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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.7e-17
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N OF BETA-
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InterPro; IPR000342; -.
InterPro; IPR001158; -.
Pfam; PF00615; RGS; 1.
Pfam; PF00778; DIX; 1.
PROSITE; PS50132; RGS; 1
Developmental protein; P
NON\_TER

Developmental

1.
Phosphorylation

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Axin, a negative regulator of the Wnt signaling pathway, forms a

complex with 65K-3beta and beta-catenin and promotes GSK-3beta-

complex with 65K-3beta and beta-catenin.*;

complex with 65K-3beta and promotes GSK-3beta-

complex with 65K-3beta and promotes GSK-3beta-

complex with 65K-3beta and promotes GSK-3beta-

complex min probably facilitate the phosphorylation of Beta-

catenin and Apc by GSK-3b and Beta-Catenin. The interaction of Between axin and Beta-catenin occurs via the Armadillo Repeats

contained in Beta-catenin. Ternary complex. Also Binds to

plakoglobin (GAMMA-CATENIN). APC, DVI AND PP2A (BY SIMILARITY).

complex minds and beta-catenin. Ternary complex. Also Binds to

plakoglobin (GAMMA-CATENIN). APC, DVI AND PP2A (BY SIMILARITY).

complex minds for the first probable of the followed by Cerebbum, Cerebellum, Heart, Kidney, Skelftal Muscle,

followed by Cerebbum, Cerebellum, Heart, Kidney, Skelftal Muscle,

followed by Cerebbum, Cerebellum, Heart, Kidney, Skelftal Muscle,
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Best Local :
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01-OCT-2000 (Rel. 4
01-OCT-2000 (Rel. 4
AXIN 1 PROTEIN (AXI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
SEQUENCE
                                                                 InterPro; IPR000342; -.
InterPro; IPR001158; -.
Pfam; PF00615; RGS; 1.
Pfam; PF00778; DIX; 1.
                                                                                                                                         EMBL; AF017756; AAC40066.1; ALT_INIT. HSSP; P49799; lagr.
                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and formatics are the statement in the statement in the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          070239
PROSITE; PS50132; RGS; 1.
Developmental protein; Phosphorylation.
NON_TER 1 1 1
DOMAIN 154 277 RGS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                SIMILARITY: CONTAINS 1 RGS DOMAIN. SIMILARITY: CONTAINS 1 DIX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                  PP2A (BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                         SPLEEN AND LIVER
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el. 40, Last sequence update)
el. 40, Last annotation update)
el. 40, Last annotation (FRAGMENT).
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99803
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470
540
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66.7%;
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Pred. No. 2e-16;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSK-3B BINDING SITE (BY SIMILARITY).
BETA-CATENIN BINDING SITE (BY
SIMILARITY).
DIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EE5F990B11FC7B3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           893
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                                                                                                                                                                                                                                                                                               collaboration
                                                                                                                                                                                                                                                                                outstation
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RESULT
AXN1_MC
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Best Local
Pfam; PF00615; RGS; 1.
Pfam; PF00778; DIX; 1.
PROSITE; PS50132; RGS; 1.
PROVELOPMENTAL PROTEIN; FINANCA_TER 1 1 1
DOMAIN 10 18
DOMAIN 217 340
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DOMAIN
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SEQUENCE
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01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
AXIN 1 (AXIS INHIBITION PROTEIN 1) (FUSED PROTEIN) (FRAGMENT).
AXIN1 OR AXIN OR FU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOUSE
                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F. "The mouse Fused locus encodes Axin, an inhibitor of pathway that regulates embryonic axis formation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                        MGD; MGI:1096327; Axin.
InterPro; IPR000342; -.
InterPro; IPR001158; -.
                                                                                                                            MGD; MGI:1096327; A
Interpro
                                                                                                                                                      EMBL; AF009011;
HSSP; P49799; 11
                                                                                                                                                                                                   or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pathway that regulates embryonic axis cell 90:181-192(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS 1 AND MEDLINE-97373830; Pubmed-9230313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AXN1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          836 VTLGQFKELLTKKGSYRYYFKKVSDEFDCGVVFEEVREDEAILPVFEEKII
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                                                                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS 1 RGS DOMAIN. SIMILARITY: CONTAINS 1 DIX DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                    CATENIN AND APC BY GSK-3B (BY SIMILARITY).

SUBUNIT: INTERACTS WITH GSK-3B AND BETA-CATENIN. THE INTERACTION
BETMEEN AXIN AND BETA-CATENIN OCCURS VIA THE ARMADILLO REPEATS
CONTAINED IN BETA-CATENIN. TERNARY COMPLEX. ALSO BINDS TO
PLAKOGLOBIN (GAMMA-CATENIN), APC, DYL AND PP2A (BY SIMILARITY).

SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY)
ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE
PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: EXPRESSED IN EMBRYONIC STEM CELLS.
DEVELOPMENTAL STAGE: WIDELY EXPRESSED AT E10.5 TO E16.5 DAY
PTM: PROBABLY PHOSPHORYLATED BY GSK-3B AND DEPHOSPHORYLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: INHIBITOR OF THE WNT SIGNALING PATHWAY. DOWN REGULATES BETA-CATENIN. PROBABLY FACILITATE THE PHOSPHORYLATION OF BETA-
                                                                                                                                                                                                    an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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499
811
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Rodentia;
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893
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                                              1.
Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                   agreement (See http://www.isb-sib.ch/announce/
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Pred. No. 2.6e-16;
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BETA-CATENIN BINDING SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                outstation
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Best Local S
Matches 34
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01-OCT-2000 ()
01-OCT-2000 ()
AXIN 1 (AXIS
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                          DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                 Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BRARE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARSPLIC
                                                                                                                                                                                                                                                                                                                                                              Shimizu T., Yamanaka Y., Ryu
Bae Y.-K., Hibi M., Hirano T
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-20171051; PubMed-10704853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AXN1_BRARE
                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        935
                                                                             DOMAIN
                                                                                               PROSITE;
                                                                                                           Ptam;
                                                                    DOMAIN
                                                                                      Developmental
                                                                                                                            InterPro; IPR000342; -. InterPro; IPR001158; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 1 RGS DOMAIN. SIMILARITY: CONTAINS 1 DIX DOMAIN.
                                                                                                                                                                                                                                                                 PP2A (BY SIMILARITY). SIMILARITY: CONTAINS
                                                                                             PF00615; RGS; 1.
PF00778; DIX; 1.
TE; PS50132; RGS; 1
                                                                                                                                                         AB032262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 66.7
34; Conservative
                                                      ental protein; Phosphorylation.
92 214 RGS:
351 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             860
992 AA;
                           753
835
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562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 40, Created)
(Rel. 40, Last sequence up
(Rel. 40, Last annotation
INHIBITION PROTEIN 1).
                                                                                                                                                                                                                                                                                                                                                                         Yamanaka Y., Ryu S.-L.,
                                                                                                                                                 1AGR
                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                         BAA92439.1;
                             835
94351
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                              ME:
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Pred.
                                               GSK-3B BINDING
BETA-CATENIN BI
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSK-3B BINDING SITE (BY SIMILARITY).
BETA-CATENIN BINDING SITE (BY
SIMILARITY).
DIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISSING (IN ISOFORM); 70EEB53D387BD26F
                    DIX.
; 1C62FCF1F5937C87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190;
No. 2.
                                                                                                                                                                                                                                                                                                                                                                          Hashimoto H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
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2.9e-16;
les 8;
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A
                                                           BINDING
                                                                    SITE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRC64;
Length 835
                                                                                                                                                                                                                                                                                                                                                                           Yabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                           SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Ostariophysi;
                                                                                                                                                                                                                   restrictions
                                                                                                                                                                                                                                                                                                                                                                         Η.,
                                                                                                                                                                                                                                                                                                                                                       proteins in
                                                            (BY
                                                                                                                                                                                                                             EMBL
                                                                                                                                                                                                                                                                                                                 N REGULATES
OF BETA-
                                                                                                                                                                                                                               a collaboration -
                                                                                                                                                                                                                                                                                                                                                                           Hirata T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                                                                          the
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Query Match

.4%;

Score

DB

1;

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RESULT 11

RESULT 11

DSH_DDD

DSH_DD

AC P5114-AC

P5114-AC

P5114-AC

DF 01-OC

DF 01-OC

DF 01-OC

DF 01-OC

DF 01-OC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSH_DROME
P51140;
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arumeres, Diptera; Pterygota; Neoptera; Endopterygota; Diptera; Ephydroidea; Drosophilidae; Drosophila.
FlyBase; F
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klingensmith J., Nusse R., Perrimon N., "The Drosophila segment polarity gene diprotein required for response to the wingenes Dev. 8:118-130(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ephydroidea; Dro
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yanagawa S.-I., van Leeuwen F., Wodar
"The dishevelled protein is modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell polarity and cell identity bevelopment 120:347-360(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Theisen H., Purcell J., Bennett M., Kanse "Dishevelled is required during wingless cell polarity and cell identity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEGMENT
                     EMBL; 126974; AAA16535.1;
EMBL; U02491; AAA20216.1;
FlyBase; FBgn0000499; dsh
                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95262901; PubMed=7744250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94200163; PubMed=8149913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94116855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                        entities requires a
                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                         OBSERVED IN BRAIN LOBES.

PTM: PHOSPHORYLATED. WG SIGNALING GENERATES HYPERPHOSPHORYLATED FORMS. OF DSH WHICH ARE THE ACTIVE FORMS.

SIMILARITY: BELONGS TO THE DSH FAMILY.

SIMILARITY: CONTAINS 1 DEP DOMAIN.

SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION. REQUIRED TO ESTABLISH COHERENT ARRAYS OF POLARIZED CELLS AND SEGMENTS IN EMBRYOS. PLAYS A ROLE IN WINGLESS (WG) SIGNALING, POSSIBLY THROUGH THE RECEPTION OF THE WG SIGNAL BY TARGET CELLS AND SUBSEQUENT REDISTRIBUTION OF ARM PROTEIN IN RESPONSE TO THAT SIGNAL IN EMBRYOS. THIS SIGNAL SEEMS TO BE REQUIRED TO ESTABLISH PLANAR CELL POLARITY AND IDENTITY.

SUBCELLULAR LOCATION: CYTOPLASMIC. ASSOCIATED WITH THE MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WHEN HYPERPHOSPHORYLATED.
TISSUE SPECIFICITY: FOUND IN EGG CHAMBERS OF THE OVARY AND UBIQUITOUSLY THROUGHOUT EMBRYOGENESIS AND IN DISCS. EXPRESSING SEEN IN SALIVARY GLANDS, MUSCLES OR VENTRAL GANGLIA BUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLARITY PROTEIN DISHEVELLED.
                                                                                                                                s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9:1087-1097(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34, Last sequence update)
40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=8288125;
                                                                                                                                                                                                                rmatics Institute. There are no restrictions institutions as long as its content is in
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wodarz A., Klingensmith J. ified by wingless signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene dishevelled
the wingless sign
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kansagara
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ches 9;
                                                                                                                                                                (See
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signaling
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                                                                                                                                                                http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brachycera; Muscomorpha;
                                                                                                                                                                                           Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lled encodes signal.";
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establish both
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXPRESSION
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InterPro; IPR001158; -.

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RESULT 12
DVL2_HUMAN
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Best Local S
Matches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00610; DEP; 1.
Pfam; PF00778; DIX; 1.
Pfam; PF00595; PDZ; 1.
PROSITE; PS50186; DEP; 1.
PROSITE; PS50106; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY 2000 (Rel. 39, Created)
30-MAY 2000 (Rel. 39, Last sequence update)
01-OCT 2000 (Rel. 40, Last annotation update)
SEGMENT POLARITY PROTEIN DISHEVELLED HOMOLOG (DSH HOMOLOG 2).
                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                            EMBL; AF006012; AAB65243.1; HSSP; P31016; 1BFE. MIM; 602151; -
                                                                                                                                                                                                                                      <del>:</del>
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., SUBCELLULAR LOCATION, MEDLINE-97336056; PubMed-9192851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             014641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DVL2_HUMAN
                                                                                                                                                                                                                                                                       Genomics 42:302-310(1997).
                                                                                                                                                                                                                                                                                                           Semenov M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                 interPro;
                                                                                                                                                                                                                                                            ÷
                                                                                                                                                                                                                                                                                     family."
                                                                                                                                                                                                                                                                                             Human dishevelled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35 VTLRDFKLVLNKQNNNYKYFFKSMDADF--GVVKEEIADDSTILPCFNGRVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE DSH FAMILY. SIMILARITY: CONTAINS 1 DEP DOMAIN. SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
                                                                                                                                                                                                                                    FUNCTION: MAY PLAY A ROLE IN THE SIGNAL TRANSDUCTION PATHWAY MEDIATED BY MULTIPLE WNT GENES.
SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                         PTM: PHOSPHORYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 39.7%;
Similarity 46.2%;
24; Conservative 1
; IPR000591; -.; IPR001158; -.; IPR001478; -.
00610; DEP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR001478;
                                                                                                                                                                                                                                                                                                            Snyder M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                              genes constitute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68845
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1.
Phosphorylation;
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POLY-GLN.
POLY-GLN.
POLY-SER.
POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 109.5; DB 1
Pred. No. 2.6e-06;
0; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D -> N (IN REF. 2).
T -> I (IN REF. 2).
S -> F (IN REF. 2).
; OBA253CE4COB71F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        736
                                                                                                                                                                                                                                                                                              DHR-containing multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Segmentation polarity protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ξ
                                                                                                                                                                                                                                                                                                                                 AND PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                              DVL-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
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Q60838;
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
Q1-QCT-2000 (Rel. 40, Last annotation update)
SEGMENT POLARITY PROTEIN DISHEVELLED HOMOLOG
(DSH HOMOLOG 2).
                    HSSP; P31016; 1BFE.
MGD; MGI:106613; Dv12.
InterPro; IPR000591; -.
InterPro; IPR001158; -.
InterPro; IPR001478; -.
Pfam; PF00610; DEP; 1.
Pfam; PF00778; DIX; 1.
Pfam; PF00778; DIX; 1.
Pfam; PF00595; PDZ; 1.
PROSITE; PS50186; DEP; 1.
PROSITE; PS50186; DEP; 1.
                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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DVL2_MOUSE
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PROSITE; PS50186; DEP;
PROSITE; PS50106; PDZ;
                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - FUNCTION: MAY PLAY A ROLE IN THE SIGNAL TRANSDUCTI
MEDIATED BY MULTIPLE WHT GENES.
- IS SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
- ITISSUE SPECIFICITY: UBIQUITOUS.
- IS SIMILARITY: BELONGS TO THE DSH FAMILY.
- IS SIMILARITY: CONTAINS 1 DEP DOMAIN.
- IS SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BALB/C; TISSUE-Brain; MEDLINE-97042042; PubMed-8887313;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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HSSP; P31016;
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Pred. No. 2.8e-05;
B; Mismatches 20
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          C TISSUE-Bone marrow;

C MEDLINE-BOTH MAY PUBMED-9039502;

A Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayasi Y.,

A Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;

Prediction of the coding sequences of unidentified human genes. VI.

The coding sequences of 80 new genes (KIAAO201-KIAAO280) deduced by

The coding sequences of 80 new genes (KIAAO201-KIAAO280) deduced by

The coding sequences of 80 new genes (KIAAO201-KIAAO280) deduced by

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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation updat
SEGMENT POLARITY PROTEIN DISHEVELLED HOMOLO
                                                                                                                                                                                                                                                                                                                                "cDNA characterization and chromosomal mapping of the Drosophila dishevelled polarity gene.", hum. Mol. Genet. 5:953-958(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-98008870; PubMed=9344861;
Bui T.D., Beier D.R., Jonssen M., Smith K., Dorrington S.M.,
Bui T.D., Kearney L., Regan R., Sussman D.J., Harris A.L.;
Raklamanis L., Kearney L., Regan R., Sussman D.J., Harris A.L.;
"cDNA cloning of a human dishevelled DVL-3 gene, mapping to 3q27,
expression in human breast and colon carcinomas.";
Biochem. Biophys. Res. Commun. 239:510-516(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                Pizzuti A., Amati F., Calabrese G., Mari A., Giardino L., Ratti A., Penso D., Calza L., P. Novelli G., Dallapiccola B.;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
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Pizzuti A., Amati
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                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00778; DIX; Pfam; PF00595; PDZ;
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                       JU-MAY-2000 (Rel. 39, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
SEGMENT POLARITY PROTEIN DISHEVELLED HOMOLOG DVL-3 (DISHEVELLED-3)
(DSH HOMOLOG 3).
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L; AF006013; AAB65244.1; -...
L; U49262; AAB87447.1; -...
L; D86963; BAA13199.1; -...
P; P31016; 1BFE.
    musculus
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sen the Swiss Institute of Bioinformatics and the EN
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S -> I (IN REF. 3).
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HSSP; P31016; 1BFE.
MGD; MGI:108100; Dv13.
InterPro; IPR000591; -
InterPro; IPR001158; -
InterPro; IPR001478; -
Pfam; PF00510; DEP; 1.
Pfam; PF00778; DIX; 1.
Pfam; PF00595; PDZ; 1.
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SEQUENCE
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Dev. Dyn. 207:253-262(1996).

-I FUNCTION: MAY PLAY A ROLE IN THE SIGNAL TRANSDUCTION PATHWAY MEDIATED BY MULTIPLE WNT GENES.

-I- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

-I TISSUE SPECIFICITY: UBIQUITOUS.

-I- SIMILARITY: BELONGS TO THE DSH FAMILY.

-I- SIMILARITY: CONTAINS 1 DEP DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-Brain;
MEDLINE-97081279; PubMed-8922524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tsang M., Lijam N., Yang Y., Beier D.R., Wynshaw-Boris A., Sussman D.J.;
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DOMAIN 249 321
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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015169 homo sapien
070239 rattus norv
035625 mus musculu
09ptp2 xenopus lae
09yz9 drosophila
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09ug5 rattus norv
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O62090 caenorhabdi
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PFAM; PF00615; RGS; 1.
PFAM; PF00778; DIX; 1.
PF0DOM; PD0001580; -; 1.
PRODOM; PD0001580; -; 1.
PRODOM; PD0003639; -; 1.
SEQUENCE 838 AA; 92947
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01-AUG-1998 (
01-OCT-2000 (
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Mol. Cell. Biol. 18:2867-2875(1998).
EMBL; AF017757; AAC40089.1; -.
HSSP; P49799; LAGR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-98226558; PubMed-9566905;
Yamamoto H., Kishida S., Uochi T.,
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                                                                                                                           Score 276; DB 11;
Pred. No. 4.7e-26;
Mismatches 0;
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INTERPRO; IPR001158; -.
PFAM; PF00615; RGS; 1.
PFAM; PF00778; DIX; 1.
PRADDM; PD001580; -; 1.
PRODDM; PD003639; -; 1.
SEQUENCE 840 AA; 92934 MW; //
                                                                                                                                                     Jenkins N.A., Warburton D., Costantini "Properties of mouse Axin2 and human AX expression pattern, interaction with Ax axis formation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9QXJ6;
Q9QXJ6;
01-MAY-2000
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01-NOV-1998
01-OCT-2000
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EMBL; AF
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Science 280:596-590/1000
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Mammalia; Eutheria;
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                                                                                                                                   Submitted (NOV-1999) to the EMBL; AF205889; AAF22800.1;
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                  PRINTS;
                                                                        HSSP; P49799; 1AGR.
INTERPRO; IPR000342; -.
INTERPRO; IPR001158; -.
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SEQUENCE
                                      PFAM;
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Local Similarity 100.0%;
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              PF00615; RGS; 1.
PF00778; DIX; 1.
S; PR01301; RGSPR
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AF073788; AAC26047.1; -.
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Pred. No. 4.7e-26;
Mismatches 0;
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Sciurognathi; Muridae;
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01-MAY-2000
01-MAY-2000
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"Properties of mouse Axin2 and human AXIN2: chromosomal expression pattern, interaction with Axin and effects on axis formation.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF205888; AAF22799.1;
HSSP; P49799; 1AGR.
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Q9Y2T1;
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SEQUENCE
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Mammalia; Eutheria;
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                                                         "Cloning of the human homolog chromosome 17q23-q24."; Genomics 55:341-344(1999). EMBL; AF078165; AADZ0976.1; -HSSP; P49799; 1AGR.
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Metazoa; Chordata;
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                                                                                                                                                         MEDLINE=99168905; PubMed=10049590; Mai M., Qian C., Yokomizo A., Smit
                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                   CONDUCTIN.
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01-NOV-1999
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INTERPRO; IPR001158; -.
PFAM; PF00615; RGS; 1.
PFAM; PF00778; DIX; 1.
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  INTERPRO; IPRO00342; -.
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Pred. No. 1.4e-25;
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l; Mismatches
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Catarrhini; Hominidae;
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MEDLINE-99173782; PubMed-10072781;
MEDLINE-99173782; PubMed-10072781;
MEDLINE-9917382; PubMed-10072782;
PubMed-10072782; PubMed-10072782;
MEDLINE-9917382; PubMed-10072782; PubMed-10072782; PubMed-10072782; PubMed-10072782; PubMed
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                                                                                                                                                                                        AAAAN.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                                                                                                            AXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF009012; AAC60245.1; HSSP; P49799; 1AGR. INTERPRO; IPR000342; -. INTERPRO; IPR001158; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zeng L., Fagotto F., Zhang T., Hsu W., Vasicek T.J., Perry W.L., III Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini F.; "The mouse Fused locus encodes Axin, an inhibitor of the Wnt signathway that regulates embryonic axis formation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE-97373830; PubMed-9230313;
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                                                                                                                                                          NCBI_TaxID=8355;
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PRODOM; PD003639; -; 1.
SEQUENCE 841 AA; 94931 MW;
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93557 MW;
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Pred. No. 1.5e-25;
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Pred. No. 3.1e-16;
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Best Local Similarity
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MeCh. Dev. 80:147-131(1999).

EMBL; AR097313; AAC71036.1; -.
HSSP; P49799; 1AGR.
INTEREPRO; IPRO00342; -.
INTEREPRO; IPRO00342; -.
INTEREPRO; IPRO01158; -.
PFAM; PF00615; RGS; 1.
PFAM; PF00778; DIX; 1.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
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EMBL, AF0096674; AAC51624.1; -.
HSSP; P49799; LAGR.
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PRODOM; PD003639; -; 1.
SEQUENCE 842 AA; 94459 MW;
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III Lee J.J., Tilghman S.M., Gumbiner B.M., Costantini
"The mouse Fused locus encodes Axin, an inhibitor of t
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Pred. No. 1.9e-15;
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Pred. No. 5.6e-16;
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      Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                           Indels
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O35625,
01-JAN-1998 (TrEMBLrel. 0
01-JAN-1998 (TrEMBLrel. 0
01-OCT-2000 (TrEMBLrel. 1
                                                                                                                                    MGD; MGI:1096327; Axin.
INTERPRO; IPR000342; -.
INTERPRO; IPR001158; -.
PFAM; PF00615; RGS; 1.
PFAM; PF00778; DIX; 1.
                                                                                                                                                                                                                                           "The
                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
   935
                                                                                                      SEQUENCE
                                                                                                                             PRINTS;
                                                                                                                                                                                                          EMBL; AF009011;
                                                                                                                                                                                                                     pathway that regulates embryonic axis formation."; Cell 90:181-192(1997).
                                                                                                                                                                                                                                                              MEDLINE=97373830; PubMed=9; Zeng L., Fagotto F., Zhang
                                                                                                                                                                                                                                                     III Lee J.J., Tilghman S.M.,
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                             AXIN.
                                                                                                                                                                                                                                                                                                                                                                     AXIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRODOM; PD001580; -; 1.
PRODOM; PD003639; -; 1.
SEQUENCE 832 AA; 92856 MW; B489504C7E594347 CRC64;
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INTERPRO; IPRO01158; -.
PFAM; PF00615; RGS; 1.
PFAM; PF00778; DIX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ikeda S., Yamamoto H., Murai H., Kishida S., Kikuchi A.;
"Axin, a negative regulator of the Wnt signaling pathway, forms complex with GSK-3beta and beta-catenin and promotes GSK-3beta-dependent phosphorylation of beta-catenin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-98151361; PubMed-9482734;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBC J. 17:1371-1384(1998).
EMBL; AF017756; AAC40066.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     775
                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia;
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VTLGQFKELLTKKGSYRYYFKKVSDEFDCGVVFEEVREDEPVLPVFEEKII
                                                                                                                                                                                                                                           mouse Fused locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P49799;
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33; Conser
                                                                                                                           PR01301; RGSPROTEIN.
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                                                                                                                                                                                                          AAC53285.1;
                                                                                                                                                                                                                                                                            PubMed=9230313;
                                                                                                      109917 MW;
                                                        68.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                      hang T., Hsu W., Vasicek T.J., Perry W.L., S.M., Gumbiner B.M., Costantini F.; encodes Axin, an inhibitor of the Wnt signaling
                                                                                                                                                                                                                                                                                                                                                                               15,
                                            Score 190;
Pred. No. 2.
9; Mismatche
                                                                                                                                                                                                                                                                                                                                                                          Created)
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Pred. No. 2.3e-15;
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.8e-15;
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RESULT 11

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Q9PTP2
ID Q9PTP2;
AC Q9PTP2;
AC Q9PTP2;
DT Q1-MAY-2000 (
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                      Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Bubayani A., An H.-J., Andrews-Pfannkoch C.R., Miklos, G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Devis, B.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Deup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Hostin R.J., Harvey D., Heiman T.J., Hennandez J.R., Houck J.,
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Best Local
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STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSH PROTEIN
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Battachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=OVARY;
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"Dishevelled transduces
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E 706 AA; 79196 MW;
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Harvey D., Heiman T.J., Hernandez buston K.A., Howland T.J., Wei M.-
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es a signal by
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displacing GSK3 from axin-GSK3
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Matches 21
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INTERPRO; IPR000591; -.
INTERPRO; IPR001158; -.
INTERPRO; IPR001478; -.
PFAM; PF00595; PDZ; 1.
PFAM; PF00610; DEP; 1.
PFAM; PF00778; DIX; 1.
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Q9NL46;
01-OCT-2000
01-OCT-2000
01-OCT-2000
                                                                                                                                                                                                                                                                   Imai K., Takada N., Satoh N., Satou Y.;
"An essential role of beta-catenin in the endoderm specification ascidian embryo.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB031541; BAA92183.1;
EMBL; AB031541; BAA92183.1;
BAA92183.1;
BAA92183.1;
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Eukaryota; Metazoa;
Cionidae; Ciona.
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                            LTLGHFKEQLSKK-GNYRYYFKKASDEFACGAVFEEIWDDETVLPMYEGRIL
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Similarity 41.2%;
21; Conservative
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illarity 46.2%;
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68917 MW; OBA24ED350666CF5 CRC64;
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Pred. No. 0.00
L4; Mismatches
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Pred. No. 1.7e-05;
0; Mismatches 15
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00014;
es 13;
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Matches 15; Conservative
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INTERPRO; IPRO01158; -.
INTERPRO; IPRO01478; -.
PFAM; PF00630; PDZ; 1.
PFAM; PF00610; DEP; 1.
PFAM; PF00778; DIX; 1.
SEQUENCE 695 AA; 7544;
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Q9QUG5;
01-MAY-2000 (
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01-NOV-1999
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                                                                                                                                              SEQUENCE FROM N.A.

MEDLINB-99174088; PubMed-10073940;

Hamada F., Tomoyasu Y., Takatsu Y., Nakamura M., Nagai S.,

Fujita F., Shibuya H., Toyoshima K., Ueno N., Akiyama T.;

"Negative regulation of Wingless signaling by D-axin, a Dro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            De Lange R.P.J., Burr K., Clark J.S., Negri C.D., Brosnan M.J., St Clair D.M., Shaw D.J., Dominiczak A.F.;
"Does Dishevelled-1 determine sensitivity to cerebral ischaemic in a rat model of stroke?";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF143546; AAD33897.2; -.
EMBL; AF143545; AAD33896.2; -.
HSSP, P31016; 1BE9.
                                                              PFAM; PF00778; SEQUENCE 743
                                                                                  homolog of axin.";
Science 283:1739-1742(1999).
EMBL; AF086811; AAD24886.1;
INTERPRO; IPR000342; .
INTERPRO; IPR001158; .
                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopteryda; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                 Q9XYC1
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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NCBI_TaxID=7227;
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(TrEMBLrel. 12,
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Score 85; DB
Pred. No. 0.02
14; Mismatches
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                       Length 743;
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1: gb_bal:*
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3: gb_ba3:*
4: gb_in1:*
5: gb_in2:*
June 6, 2001, 18:46:26 ; Search time 4956.99 Seconds (without alignments) 8404.839 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

11 490.	c 10 698.	9 850.	c 8 95	7 1359.	6 1571.2	5 1944.	4 2389.	3 2645	2 282	1 282	Result No. Score
17.4	24.7	30.1	33.8	48.1	55.6	68.8	84.6	93.6	100.0	100.0	Query
91041	84263	3485	91041	2104	2538	3072	3216	3016	2825	2825	Length DB
69	85	œ	69	89	88	88	94	94	94	9	
AC024114	AC004805	AB032263	AC024114	AK025718	AF205888	AF078165	AF017757	AF205889	AF073788	A98521	ID
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Query Match  100.0%; Score 2825; DB 9; Length 2825;  Best Local Similarity 100.0%; Pred. No. 0;  Matches 2825; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Qy 1 cagccyttcycyatygatttcygygcacccygagycygcygagycytccycaaagy 60	SOURCE unidentified.  ORGANISM unidentified unclassified.  REFERENCE 1 (bases 1 to 2825) AUTHORS CONDUCTINE PROTEIN AND A RELATED AGENT FOR DIAGNOSING AND TREATING TIMER TOWNOR ILLNESSES  JOURNAL PACETER WALTER (DE); BEHRENS JUERGEN (DE) FEATURES BIRCHMEIER WALTER (DE); BEHRENS JUERGEN (DE) FEATURES LOCATION/Qualifiers  SOURCE //Organism="unidentified" //db_xref="taxon:32644" BASE COUNT 703 a 815 c 813 g 494 t	ALIGNMENTS  RESULT 1 A98521 LOCUS A98521 2825 bp DNA PAT 26-JAN-2000 DEFINITION Sequence 6 from Patent WO9911780. ACCESSION A98521 VERSION A98521.1 GI:6781607	27 1623 3.9 2.121 6 ARF40243 ARF40243 Xenopus I 27 162 5.7 162 9 A98525 ARF40243 Xenopus I 27 162 5.7 162 9 A98525 ARF40243 ARF40243 Xenopus I 27 162 5.7 162 9 ARF40243 ARF40243 Xenopus I 28 153 5.4 153 9 ARF40243 ARF40243 ARF40243 Xenopus I 28 153 5.4 153 9 ARF40243 ARF4025 Sequence 10 2.9 1.9 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0	401.8 14.2 3411 88 AF009674 378.6 13.4 1863 85 AB052751 369 13.1 369 9 A9822 337.6 12.0 3761 94 AF009011 316 11.2 3156 8 AF009012 312.2 11.1 3460 94 AF017756 265 9.4 2529 8 AF097313 256.6 9.4 2529 8 AF097313 256.6 9.1 3066 8 AB032262 209.4 7.4 323786 91 HS415C1 209.4 7.4 39170 85 AC005202 209.4 7.4 133069 70 AC026836 209.4 7.4 133069 70 AC026836 209.4 7.4 187272 74 AC069076
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Mus musculus
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Behrens,J., Jerchow,B.-A.
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Zhang, T., Fagotto, F., Hsu, W., Zeng, L., Gilbert, D., Copeland, N.G., Jenkins, N.A., Warburton, D. and Costantini, F. Properties of mouse Axin2 and human AXIN2: chromosomal location, expression pattern, interaction with Axin and effects on embryonic
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KCVDTLDFWFACNGFROMNLKDTKTLRVAKAIYKY I ENNSVYSKOLKPATKTY IRDG
IKKOOIGSVMFDOAOTELQAVMEENAYQYFLTSDIYLEYVRSGGENTAYMSNGGLGSL
KVLCGYLPTLNEEEEWTCADLKCKLSPTVVGLSSKTLRATASVRSTETAENGFRSFKR
SDPVNPYHVGSGYVFAPATSANDSELSSDALTDDSMSMTDSSVDCVPPYRMGSKKOLQ
REMHRSVKANGOVSLCHFPFRTHRLPKEMTPVEPAPAFABELISRLEKLKLELESRHSLE
ERLQQIREDEEKEGSEQALSSRDCAPVQHPLALLPSGSYEEDPQTILDDHLSRVLKTP
GCQSPGVGRYSPRSRSPDHHHOHYHHQQCHTLLPTGGKLPPVAACPLLGGKSSLTKOT
TKHVHHHYIHHHAVPKTKEEIEAEATGRVRCLCPGGTDYYCYSKCKSHPKAPEPLPGE
QFCGSRGGTLFKRAKGTEPGLALSARDGGMSSAAGAPQLFGEEGDSQDVWQWMLES
ERQSKSKPHSAQSIRKSYPLESARAAPGERVSRHLLGASGHSRSVARAHPFTQDPAM
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1487 1327	aggggtctgagccctgagctcacgggatggagcaccggtccagcaccccctggccc 	1428 1268
1427 1267	tggaaagccgccatagtctggaggagcggctgcagcagatccgggaggatgaagaaagg 	1368 1208
1367 1207	tggaacctgcttcgccgccgagctcatctccaggctggagaactgaaactggagc 	1308 1148
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1247 1087	accycatygygaytaayaaacayctccayayayayatycatcycaytytyaayyccaaty	1188 1028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (08-AUG-1997) Blochemistry, Hiroshima University, School
of Medicine, 1-2-3 Kasumi, Minami-ku, Hiroshima, Hiroshima 734,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Axil, a member of the Axin family, interacts with both glycogen synthase kinase 3beta and beta-catenin and inhibits axis formation of Xenopus embryos
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Yamamoto, H., Ikeda, S., Murai, H., Kishida, S. and Kikuchi, A.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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1. Cell. Biol. 18 (5), 2867-2875 (1998)
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 860
                               KCVDTLDEWFACNGFROMNLKDTKTLRVAKAIYKRYIENNSVVSKOLKPATKTYIRDG
IKKQQIGSVWAFDQAQTEIQAVWEENAYQVELTSDIYLEVYRSGCENTAVWSNGGLGSL
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ERLQQIREDEEKEGSEDALSSRDAPAPVHPLALLPSGSYEEDPQTILDDHLSRVLKTP
GCQSPGYKYSPRSRSPDHHHHHQCHALLPSGSYEEDPQTILDGRSSFTLKGTK
HVHHHYIHHHAVPKTKEEIEAEATQRVRCLCPGGTDYYCYSKCKSHSKPPEPLPGEQF
CGSRGGTLPKRNTKGTEPGLALPAREGGMSAAAPQLPEEEGDRSQDVAQWMLESER
QSKSKPHSTOSIRKSVPLESARAPPGEBVSRHHLLGAGGHPRSAARAHPFTQDPAMPP
LTPPNTLAQLEEACRRLAEVSKPQKQRCCVASQQRDRNHPATGQAGPTSFSNPSLASE
DHKEPKRRLASYHALQASELITTYFFGGEEIPYRRMLKAQSLTLGHFKEQLSKKGNYRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 3216 bp mRNA ROD 24-APR-1998 norvegicus GSK-3beta interacting protein. Axil mRNA, cor
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YFKKASDEFACGAVFEEIWDDETVLPMYEGRILGKVERID® 914 c 872 g 570 t
                                                                                                                                                                                                                                                                /translation="mssavlvtllpdpsssfredaprppvpgeegetppcqpsvgkvq
strpmpvssnarrnedglgepegraspdspltrwtkslhsllgdqdgavlfrtflere
                                                                                                                                                                                                                                                                                                                                                                                                                 /organism-"Rattus norvegicus"
/db_xref⊳"taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                        /protein_id="AAC40089.1"
/db_xref="GI:3080759"
                                                                                                                                                                                                                                                                                                                                             /product-"Axil"
                                                                                                                                                                                                                                                                                                                                                                                 'note="GSK-3beta interacting protein; Axin like protein"
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Mag	י לו לה י	tch 84.6%; Score 2389.2; DB 94; Length 3216; al Similarity 93.7%; Pred. No. 0; 2525; Conservative 0; Mismatches 163; Indels 8; Gaps	,
Оγ	131 1	tgagaggaactggaagaagaaaaggaggaggagggaaaaaagcaaaaccaaatccaaa 19 	_ 0
Qy	191	o Gr	0
Q D	61 251	TCAGTGAGACGCTCTCCCTCACCATGAGTAGCGCTGTGTTAGTGACTCTCCTTCCAGAT 12 ccagcagcagcagcttccgcgaggatgctccgcgggcccccggttccgggagaagaaggggag 31	0 0
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F 2	241	CCTARIGOTAGGOGGARTGAGATGGGCTGGGGGAGCCGGAGGGGGGGGGGCTCCCCCGAT 43 	0 0
Qγ	431	ccctttgaccaggtggaccaagtctttacactccttgttgggtgaccaggatggtgca 49	0
Вb	301	TCCCCTCTGACCAGGTGGACCAAGTCTTTGCACTCCTTGTTGGGGGACCAAGATGGTGCA 36	0
do V	<b>491</b> 361	tacctcttccggactttcctggagagggagaaatgtgtgggatacgctggacttctggttt 55	0 0
Qγ	551	cttgtaatgggttcaggcagatgaacctgaaggataccaaaactttgcgagtggccaaa 61	0
В	421	CTGCAATGGGTTCAGGCAGATGAACTTGAAGGATACCAAAACTTTGCGAGTGGCCAAA 48	0
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Db	601	CGCAGACGGAGATTCAGGCGGTGATGGAGGAAAATGCCTATCAGGTGTTCTTGACT 66	0
Qγ	791	totgacatttacotggaatatgtgaggagtgggggggaaaacacagottacatgagtaac 85	0
В	661	CTGACATATACCTCGAATATGTGAGGAGTGGGGGAGAAAACACAGCTTACATGAGCAAT 72	0
Dy Qy	851 721	99999act9999agcctaaaggtcttatgtggctacctccccaccttgaatgaa	0 0
γ	911	agtggacgtgtgccgacctcaagtgcaaactctcacccacc	0
Db	781	GTGGACATGTGCCGACCTGAAGTGCAAACTTTCACCCACC	0
Qy	971	cgggccaccgcgagtgtgagatccacggaaacagctgaaaacggattcagg 10 	30
Ъ	841	AAACTCTCCGGGCCACAGCGAGCGTGAGATCCACAGAAACGGCTGAAAACGGATTCAGA 90	0
D Qy	1031 901	tccttcaagagaagcgacccagtcaatccttatcacgtaggttccggctatgtctttgca 10	90
Qy	1091	ccagccaccagcgccaacgacagcgagttatccagcgacgcactgaccgacgattccatg 11	50

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CACCACCACCACCACCACCACCACCCCGCCGTCCCTAAGACCAAGGAGGAGATCGAGGCAGAA
                                                                                                                 CGGTCACAGGATGTCTGGCAGTGGATGTTGGAGAGTGAGCGTCAGAGCAAGTCCAAGCCC
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                                                                               2 (bases 1 to 3072)
Mai,M., Qian,C., Smith,D.I. and Liu,W.
Direct Submission
Submitted (15-JUL-1998) Lab Medicine and
200 First Street SW, Rochester, MN 55905,
                                                                                                                                           Mai,M., Qian,C., Yokomizo,A., S
Cloning of the human homolog of
to chromosome 17q23-q24
Genomics 55 (3), 341-344 (1999)
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AF078165.1 G
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Eukaryota; Metazoa; Chordata; Craniata; Ve
Mammalia; Eutheria; Primates; Catarrhini;
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1709	2 tttcgactggggggaagctgcccccgtggctgcttgccccctccttg	Оу 166	
53	7 GCTCCCGCTCCCCGGACCACCACCACCACCACCATTCGCAGTACCACTCCCTGC	14	
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1 9	/ ATCACATAGGTTCTGGCTATGTCTTTGCACCAGCCACCAGCGCCAACGACAGTGAGATAT	٠ .	
<u> </u>	2 atcacgtaggttccggctatgtctttgcaccagccaccagcgccaacgacagcgagttat		
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876	TITTCGCCAACCGTGGTTGGCTTGTCCAGCAAAACTCTGAGGGCCACGGCGAGTGTGAGGT		
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut Mammalia; Eutheria; Primates; Catarrhin; Hominidae; HC 1 (bases 1 to 2538)
Zhang, T., Fagotto, F., Hsu, W., Zeng, L., Gilbert, D., Cope Jenkins, N.A., Warburton, D. and Costantini, Properties of mouse Axin2 and human AXIN2: chromosomal expression pattern, interaction with Axin and effects of
                                                             Homo sapiens
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(AXIN2) mRNA, complete
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Direct Submission
Submitted (16-NOV-1999) Genetics & Development,
University, 701 W168th St. HHSC 1416, New York,
Location/Qualifiers
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PNTLAHLEEACRRLAEVSKPEKQRCCVASQQRDRNHSATVQTGATPFSNESLAFEDHK
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653 <sub>.</sub>	ctttgcgagtggccaaagcaatctataagaggtacattgagaacaacagcgttgtctcca 	594 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'-& 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        University of Tokyo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnai@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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Mammalia; Eutheria; Primates;
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/note="cloning vector pME18SFL3"
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/cell_type="hepatoma"
/clone="HEP10566"
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                                                                                                                                                                                                                         ACO24114 191041 bp DNA Mus musculus chromosome 11 clone SEQUENCE, 30 unordered pieces.
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AC024114.8 GI:11094615
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Direct Submitssion
Direct Submitssion
Submitted (24-FEB-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Raylor Plaza, Houston, TX 77030, USA
Raylor Plaza, Houston, TX 77030, USA
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On Nov 4, 2000 this sequence version replaced gl:9929587
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NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Chemistry: Dye-primer Bodipy: 95% of reads
Chemistry: Dye-terminator Big Dye: 5% of reads
Chemistry: Dye-terminator Big Dye: 5% of reads
Chemistry: Dye-terminator Big Dye: 5% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 158769 bases at least Q40
Consensus quality: 172780 bases at least Q30
Consensus quality: 179030 bases at least O20
Estimated insert size: 180377; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 3.2x in Q20 bases; sum-of-contigs estimation
 113342
120172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Baylor College of Medicine Center code: BCM
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33864
47739
47839
59612
59712
67898
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77930
78030
86606
86706
                86605: contig

86705: gap of

93904: contig

94004: gap of

104236: contig

104336: gap of

113241: gap of

120171: gap of

120271: gap of

120271: gap of

120599: contig

120599: contig

131969: gap of

131869: contig

131969: gap of

131969: contig

130304: gap of

146106: gap of

150788: gap of

150888: gap of

150925: contig

150888: gap of

150925: contig

150925: contig
                                                                                                                                                                                                                                                                                                                                                                                                                          59711: gap of unknown length 67897: contig of 8186 bp in le 67997: gap of unknown length 77929: contig of 9932 bp in le 78029: gap of unknown length 86605: contig of 8576 bp in le
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19444:
33763:
33863:
47738:
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                                                   f unknown length g of 4682 bp in 1. f unknown length g of 6037 bp in 1. f unknown length
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g of 8905 bp in l
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 of 4145
unknown
of 3041
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of 7325
unknown
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BASE COUNT
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nes 955; Conserv
                                                                                                                                                                                                                                                                                                             agcagcttccgcgaggatgctccgcgggcccccggttccgggagaagaaggggagacccca
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                               aatgggttcaggcagatgaacctgaaggataccaaaactttgcgagtggccaaagcaatc
                                                                                                               ttgaccaggtggaccaagtctttacactccttgttgggtgaccaggatggtgcatacctc 496
                                                                                                                                              CCGTGTCAGCCTAGTGTGGGCAAGGTCCAGTCCACCAAACCTATGCCCGTTTCCTCTAAT 111491
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                                                                                                                                                                                                                               AGCAGCTTCCGCGAGGATGCTCCGCGGCCCCCGGTTCCGGGAGAAGAAGGGGGAGACCCCA 111551
tataagaggtacattgagaacaacagcgttgtctccaagcagctgaagcccgccaccaag
                     AATGGGTTCAGGCAGATGAACCTGAAGGATACCAAAACTTTGCGAGTGGCCAAAGCAATC
                                                                                                      TTGACCAGGTGGACCAAGTCTTTACACTCCTTGTTGGGTGACCAGGATGGTGCATACCTC
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/db_xref="taxon:10090"
/chromosome="11"
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43523 c 42989 g 51816
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Shimizu,T., Yamanaka,Y., Ryu,S.L., Hashimoto,H., Yabe,
Hirata,T., Bae,Y.K., Hibi,M. and Hirano,T.
Cooperative roles of Bozozok/Dharma and Nodal-related
the formation of the dorsal organizer in zebrafish
Mech. Dev. 91 (1-2), 293-303 (2000)
                                                                                                                                                                                                                                                                          Hirano, Biomedical research center, Osaka Univ. Med. scool. Department of Molecular Oncology; 2-2, Yamadaoka, Suita, Os 565-0871, Japan (E-mail:hirano@molonc.med.osaka-u.ac.jp, URL:http://www.med.osaka-u.ac.jp/pub/molonc/www/index.html, Tel:81-6-879-3880, Fax:81-6-879-3889)
                                                                                                                                                                                                                                                                                                                                2 (bases I to 3403)
Hirano, T., Hibi, M. and Shimizu, T.

Birect Submission
Submitted (09-SEP-1999) to the DDBJ/EMBL/GenBank databases. Toshio
Submitted (09-SEP-1999) to center, Osaka Univ. Med. scool,
Submitted (09-Sep-1999) to the DDBJ/EMBL/GenBank databases. Toshio
Submitted (09-Sep-1999) to the DDBJ/EMBL/GenBank databases. Toshio
Submitted (09-Sep-1999) to the DDBJ/EMBL/GenBank databases. Toshio
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/gene="axin2"
297. .2735
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                                                                                                                                                                                                              /db_xref="taxon:7955"
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Query Match
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Matches 1561; Conser COUNT 1015 1046 746 655 686 626 535 566 475 506 415 446 386 966 775 908 595 355 316 986 926 326 CAGTAGCTTCAGAGAAGATGACCCACGTCCACGGTCCCAGGGGAAGAGGGTGAGACGAC tgaccaggatggtgcatacctcttccggactttcctggagaggggagaaatgtgtggatac CTCTGCAATGTTTGATCAGGCTCAAATGGAGATCCAGACGGCTATGGAGGAGAATGCCTA gcgggcctcccccgattcccctttgaccaggtggaccaagtctttacactccttgttggg ggttggcttgtccagcaaaactcttcgggccaccgcgagtgtgagatccacggaaacagc agcttacatgagtaacggggggactggggagcctaaaggtcttatgtggctacctccccac CAGCGCATCCCCGGACTCCCCTCTTGCCCGGTGGACCAAATCTTTGCATTTTCTTCTCGG GGCTGATCTTCGTTGCTCCACGGCCAGGGGGGTGAGGATGGACTTGGGGGAACCTGAGGG ATGCCACCATCCCAGCAAACTGGCCATGATGAGACCGAAGGATCCTGTCAAGACCATTAT accgtgtcagcctagtgt------AGTGGGTCTGTCTGCCAAAACACTACGGTCACCACC---TCTTCGTGCTGTGGAAGCACT TTTAAATGAAGAAGAAGAGTGGAGTTGTAATGACTTTAAAGCCAAAGCTTTGGCCACTGT CAGTCATGTGAATCCCAATGGTCTAGGAGGTCTAAAGCTGGTGTGCGGATACTTGCCGAC Conservative ø RRSDPGNPNRFTSGYSFAPATSANDSEVSSDALTDDSMSMTDSSVDAIPPYKLGSKKQ
LQREMQRNMRMMGOVSLPPFPRTRRPPKEMTYVEPAAFRAQLIARLERLKREGETMSS
LEERLQQIQEEEERDESBMSSSSASHSLPLLPPGTCEEDPQAILDEHLSRVLKTPGCQ
SPGLLRHSPRSBSPEQRPLPRGGLSTRROSSSMNGYVPAKTFISRQSTKHIHHYIHH
HAGPKSKEQIEVEATQRVQCLCHGTSECCTAPYIRSRSLGRDQCASPAEVALGHSSTL
SKRLCKSGEEVENEGLENSLLQLPADSTDRSQNVMQWILESDROTKHKPHSTQNVKKS
HSLEPTRTHTWGGGGSSGHLRAHQPAHFFVQDFAMPPLPPNTLAQLEEARRRLEVES
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NYEGKILGKVDRMD 30.1%; G 0 Score 850.2; DB 8; Pred. No. 9.3e-192; 0; Mismatches 828; 864 g **~** -gggcaaggtccagtccaccaa Indels Length 3485; 114; Gaps 1074 1014 1045 985 894 925 834 865 805 654 474 505 445 385 315 774 685 594 565 10;

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Muzny, D., Arenson, A.D., Adams, C., Brundage, E., Bunac, C., Muzny, D., Arenson, A.D., Adams, C., Di, W., Dhig, Y., Dugan, S., Carvelli, K., Chacko, J., Chen, J., Di, W., Dhig, Y., Dugan, S., Durbin, J., Forcum, J., Ganesh, R., Garcia, C., Goodman, M., Durbin, J., Haywood, M., Hernandez, J., Jackson, L., Jin, S., Gorrell, J.H., Haywood, M., Hernandez, J., Jackson, L., Lichtarge, O., Kampal, R., Karpathy, S., Kovar, C., Heal, B., Li, Y., Lichtarge, O., Liu, W., Logan, O., Lu, J., Ly, T., Martinez, C., Oswal, G., Perez, L., Rashid, N.D., Rowland, K., Savage, L., Scherer, S.E., Shen, H., Simon, M., Stovall, K., Timms, K.M., Todd, J., Vo, Q., Williamson, A., Worley, K.C., Yu, W., Chinault, C., Nelson, D. and Gibbs, R.A.
  Worley, K.C.
Direct Submission
                                                 Worley, K.C.
Direct Submission
Submitted (06-JUN-1998) Molecular and Human Genetics, Baylor Submitted (Medicine, One Baylor Plaza, Houston, TX 77030, US3 (bases 1 to 184263)
                                                                                                                                                                                                              Worley, K.C., Yu, W.,
Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Worley, K.C.
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         ccaccaagacctacatacgagatggcatcaagaagcaacagatcggctcggtcatgtttg
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AGACCCCACCGTGTCAGCCAGGGGTGGGCCAAGGGCCAGGTCACCAAACCCATGCCTGTCT
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complement(40374. .40
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\_family="AluSx"

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'rpt\_family-"(TA)n" 13730. .24033

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/rpt\_family="MER45" complement(21627. . .

.21702)

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rpt\_family="MIR" 1967. 32000

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complement(21413. .21449)
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family-"AluSq"

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/rpt\_family="Alusp"

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.17678

family-"AluSx" .18006

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/rpt\_family="AluJ"
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/rpt\_family="L2"

.17473)

\_family="L1PA9"

.15996

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/rpt\_family="AluSx"
complement(34112..34294)
/rpt\_family="FRAM"

/rpt\_family="LTR16C" complement(33298. .3 complement(31308. .31532) complement (30648. .31228)

family="MIR"
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complement(34460...34767) /rpt\_family-"Alusg" 35143...35452

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family-"AluJb"

complement(25689. .25985) /rpt\_family="AluSx" complement(26521. .26812) /rpt\_family="AluSg"

complement(24840...25146)
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complement(25147...25299) /rpt\_family="Alusx"
complement(24676. .24839)
/rpt\_family="AluJo"

/rpt\_family="AluJo"
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complement(30127...30432)
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complement(30433...30589)
/rpt\_family="MLT1A2"

complement(29910. .30126) /rpt\_family="MLT1A2" complement(27279. .27602)
/rpt\_family="Alusx"

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Metzker, M.L., Lewis, L.R., Hume, J., Edwards, C., Harris, C., Dederich, D., Thomas, S., Okwuonu, G., Carlock, C., Garner, T., Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J., Buhay, C., Bunac, C., Burkett, C., Chacko, J., Chen, G., Chen, Z., Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S., Fernandez, C., Ferraguto, D., Forcum-Tansey, J., Gill, R., Gorrell, J.H., Gunaratne, P., Haller, G., Hernandez, J., Hogues, M., Hosak, H., Hou, X., Huber, J., Jackson, L., Jia, Y., Kelly, J., Kelly, S., Kovar, C., Liu, J., Liu, W., Loulseged, H., Lozado, R. J., Marrin, S., Massey, E., McLeod, M.P., Mei, G., Moore, S., Morgan, M., Morris, S., Neal, D., Nelson, A., Nguyen, R., Nguyen, N., Oguh, M., Parish, B., Perez, L., Reiter, D., Say, J., Shen, H., Vasquez, L., Watlington, S., Muzny, D. M., Rives, M., Scherer, S., Sodergren, E., Weinstock, G., Morrley, K., and Gibbs, R.
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Direct Submission
Submitted (24-FFB-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                   Baylor
On Nov
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              Center project name: MACA Center clone name: RP23-278J12 Sequencing vector: M13; L08821
                                                                                                  Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------ Project Information
Chemistry:
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  Dye-primer Bodipy: 95% of reads
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NOTE: Estimated insert size may differ from sequence length (see http://www.bgsc.bcm.tmc.edu/docs/Genbank_draft_data.) NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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be preserved.
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Consensus quality: 158769 bases at least Q40
Consensus quality: 172780 bases at least Q30
Consensus quality: 179030 bases at least Q20
Estimated insert size: 180377; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 3.2x in Q20 bases; sum-of-contigs estimation
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Best Local Similarity
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                                                                                                                                                                                     12
                                                                                                                                                                                                                      ggcaagagcttcctgaccaaaacagacgacgaagcacgttcaccaccaccactacatccaccac 1771
                                                                                                                                                                                                                                                                                                                                                                                                                       ataccettetttegactgg-gggcaagetgeeecegtggetgettgeeceettetttgga 1711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acagcccacggtcccgctcccccgaccaccaccagcaccaccaccatcagcagtgtc 1652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acgaccacctctccagggtcctcaagacccccggctgtcaatcccctggtgtgggtcgct 1592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCACCCCTGGCCCTACCCTCCGGCAGCTATGAAGAGGACCCACAAACCATTTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                agcacccctggccctcctaccctccggcagctatgaagaggacccacaaaccattttgg 1532
                                                                                                                                                                                                                                                                                                                                                               GGCAAGAGCTTCCTGACCAAACAGACGACGAAGCACGTTCACCACCACCACCACCACCAC
                                                                                                                                                                                                                                                                                                                                                                                                            ATACCCTTCTTCCGACTGGCGGCCAAGCTGCCCCCGTGGCTTGCCCCCCTCCTTGGA 31364
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATAGCCCACGGTCCCGCTCCCCCGACCACCACCAGCACCACCACCATCAGCAGTGTC 31304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACGACCACCTCTCCAGGGTCCTCAAGACCCCCGGCTGTCAATCCCCTGGTGTGGGTCGCT 31244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                504;
Two dominant mutations in
transposon insertions
Genetics (1997) In press
                                Eukaryota; Metazoa; Chordata; Crani Mammalla; Eutheria; Primates; Catax 1 (bases 1 to 3411)
Vasicek, T.J., Zeng, L., Guan, X.-J., Tilghman, S.M.
                                                                                                                                         Homo sapiens
AF009674
                                                                                          Homo sapiens
                                                                                                                            AF009674.1
                                                                                                                                                             AF009674
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188273
188373
189635
189735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .191041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="RP23-278J12"
43523 c 42989 g 51816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188272: contig of 1118 t
188372: gap of unknown I
189534: contig of 1262 t
189734: gap of unknown I
191041: contig of 1307 t
                                                                                                                              GI:2252819
                                                                                                                                                  3411
axin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.48;
                                                                                                                                                  (AXIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 490.6; DB 69 Pred. No. 2.4e-106;
                                                                                                                                                  mRNA
) mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                        the
                                                                                                                                                                                                                         31573
                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                        mouse
                                                                                                                                                  partial
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bp in length
length
                                              Zhang, T.,
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                       gene
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                                              Costantini, F. and
                        are
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                         result of
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BASE CO
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MEDLINE
REFERENCE
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Best Local Sim
Matches 1297;
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503
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                                                                                                                                                                                           tocttgttgggtgaccaggatggtgcatacctcttccggactttcctggagagggagaaa 523
                      aacctgaaggataccaaaactttgcgagtggccaaagcaatctataagaggtaca---tt 631
                                                                                                       tgtgtggatacgctggacttctggtttgcttgtaatgggttcaggcagatg------
                                                                                                                                                                                                                                                          GAGCCTGAGGGCAGTGCCTCCCCCACCCACCATACTTGAAGTGGGCTGAGTCACTGCAT
                                                                                                                                                                                                                                                                                gagcccgaggggcgggcctccccccgattccccctttgaccaggtggaccaagtctttacac 463
GACTCGAACGAGGAGAAGAGGCTGAAGCTGGCGAGAGCCATCTACCGAAAGTACATTCTT
                                                                                   TGTGCCGACTTGCTGGACTTCTGGTTTGCCTGCACTGGCTTCAGGAAGCTGGAGCCCTGT
                                                                                                                                                                         TCCCTGCTGGATGACCAAGATGGGATAAGCCTGTTCAGGACTTTCCTGAAGCAGGAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zeng, L., Fagotto, F., Zhang, T., Hsu, W., Vasicek, T.J., Perry, W. 3rd, Lee, J.J., Tilghman, S.M., Gumbiner, B.M. and Costantini, F. The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling pathway that regulates embryonic axis formation Cell 90 (1), 181-192 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (22-JUN-1997) Biological Technology, Millennium Pharmaceuticals, Inc., 640 Memorial Drive, Cambridge, MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vasicek,T.J.,
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                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FREEPOSNEEKREKLARAIYRKYILDNIGIVSROTKPATKSFIKGCIMKQLIDPAM
FDQAOTTSIQATMEENTYDSFLKSDIYLEYTRIGSESPKYCSDOSSGSGTGKGISGYLD
TLNEDEWKCDODMDEDDGRDAPPGRLPQKILLETPAPRYSSSRYYSEGREFRYSG
REPVNPYYVNAGYALAPATSANDSEQOSLSSDADTLSLTDSSVDGIPPYRIRKOHRRE
MQESAQVNGRVPLIPHITRTYKVPKEVRVEOOKAEELLHRLEAVQRTREAEEKLEERL
KRVRHEEEGEDODPSSGPGPOHELTPAPAMHHFPPRLCWTWACAGLRDAHEENPESI
LDEHVQRVLRTTGRQSPGFOHENSPDSGHVAKMPVALGGAASGHGKHVPKSGAKLDAAG
LHHHRIYHHIYHHSTARREGVYBAEATRAQSSFAWGLEPHSHGARSRGYSESVGAAP
NASDGLAHSGRKYGVACKRANKKAESGKSASTEVPGASEDAEKNOKINGNIIDEGEELS
RHRRTGHGSSGTRKPOPHENSRPLSLEHPWAGPOLKTSVOPSHLFIQDPTMFPHPAPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLTQLEEARRRLEEEEKRASRAPSKQRYVQEVMRRGRACVRPACAPVLHVVPAVSDME
LSETETRSQRKVGGGSAQPCDSIVVAYVFCGEPLPYKTILVRGRAVTLGQFKELLTKKG
SYRXYFKKVSDEFDCGVVFEEVREDEAVLPVFEEKIIGKVEKVD*
1 1010 c 1066 g 582 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAC51624.1"
/db_xref="G1:2252820"
/db_xref="G1:2252820"
/translation="GPSRHHRARDRLIHEGAVSTDVLGCSAHCSLTQSPKMNIQEQG
FPLDLGASFTEDAPRPPVPGEEGELVSTDPRPASYSFCSGKGVGIKGETSTATPRRSD
LDLGYEPEGSASPTPPYLKWAESLHSLLDDQDGISLFRTFLKQEGCADLLDFWFACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     may inhibit embryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Fused mutation due
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="ubiquitously expressed in
adults"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="axin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <1. .3411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="contains RGS domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene-"AXIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="AXIN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                function may inhibit embryonic axis formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             map="16p13.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /chromosome="16"
                                                                                                                                                                                                                                                                                                                                                             14.2%; 52.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tilghman,S.M.,
                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                           Score 401.8; DB 88; Pred. No. 4.9e-85; O; Mismatches 1052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to
to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the classical dominant mouse tail kink an iap insertion in the Axin gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Costantini, F.,
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1612 ccccgaccaccaccaccaccaccaccatcagcagtgtcatacccttcttto	1552 ceteaagaceceeggetgteaateceetggtgtgggtegetacageceaeggte 	ggacgaccacctc           CGGGATGCACACG	1441gccctgagctcacgggatggagcaccggtccagcacccctggcc	1382 agtetggaggageggetgeageagateegggaggatgaagaaaaggagggtel	1322 ttcgccgccgagctcatctcccaggctggagaaactgaaactggagctggaaag	1262 cctcattttccgagaacccaccgcctgcccaaggagatgacgcctgtggaacc 	1202 aagaaacagctccagagagagatgcatcgcagtgtgaaggccaatggccaagtc	1142 gattccatgtccatgacggacagtagcgtagatggagtccctccttaccgcatg	1082 gtctttgcaccagccaccagcgccaacgacagcgagttatccagcgacgcactgic	1022. ggattcaggtccttcaagagaagcgacccagtcaatccttatcacgtaggttcci	983gccaccgcgagtgtgagatccacggaaacagctg1323 cTGCTCCTGGAGACAGCTGCCCCGAGGGTCTCCTCCAGTAGACGGTACAGCGA	926 gacctcaagtgcaaactctcacccaccgtggttggcttgtccagcaaaactctt	866 ctaaaggtcttatgtggctacctccccáccttgaatgaagaagaggagtggacc 	catgagtaacgggggact              TGTAGTGACCAGAGCTCTGGGTC	752 gcagtgatggaggaaaatgcctaccaggtgttcttgacttctgacatttacctgll	692 ggcatcaagaagcaacagatcggctcggtcatgtttgaccaggcacagaccgac 	563 GATAACAATGGCATCGTGTCCCGGCAGACCAAGCCAGCCA
6 H	gtcccgctc 16	വ	0 - 0	G t	Ga	$\alpha - \alpha$	G — G	> — №	ctgaccgac 11    AGCGATGCA 11	G t	G - G	0 - 0	> — a	1 0	+T C	gagatccag 751           GAAATCCAG 682	ATAAAGGC 622

2782	D1D2D2120E2DEE2DD1120EE2D1D2120E2CD1120D2120E2T10EE2D1EEDEE	1	?	-
2689	GAGGTTCGAGAGGCCGTCCTGCCCGTCTTTGAGGAGAAGATCATCGGCAAAGTG	2630	ъ	
2722	gagatetgggaegaegagaegagtgeteeecatgtaegaaggeaggateetgggeaaagtg	2663	Qy	
2629	aattacaggtattatttcaagaaggcgagtgacgaarttgcctgcggagcagtrttcgag 	2603 2570	Фр	
2569	TIGETGAGGGGCCGCGCTGTCACCCTGGGCCAGTTCAAGGAGCTGCTGACCAAAAAAGGC	N	Db	
2602	atyctyaayyctcaaaycttyaccctygyccacttcaayyaycaqctcaycaaaaayyya	2543	Оу	
2542 2509	caggccagtgagctggttgtcacctactttttctgtggagaagaaattccatacaggagg	2483 2450	Qy da	
2449	ATGGAGCTCTCCGAGACAGACAAGATCGCAGAGGAAGGTGGGCGGCGGGAGTGCCCAG	2390	Db	
2482	ccaagcctggctccagaagatcacaaagagccaaagaaactggcaagtgtccacgcgctc		Ωу	
2422 2389	gacaggaaccactcggctgctggtcaggcaggagcctcacccttcgccaac	2372 2330	Qy bb	
2329	AGAGAGCCAGCCGAGCACCCTCCAAGCAGAGGTATGTGCAGGAGGTTATGCGGCGGGGA	2270	ф	
2371	aag	2330	Qy	
2269	CAGCTCCCAACCCCTAACCCAGCTGGAGGAGGCGCCGACGTCTGGAGGAGAAA		Db	
2329	accccacccaacactttggcacagctagaggaagcctgccgcaggctggcagaggtgtcg		Q <sub>V</sub>	
2269	cactcccgctcagtggcccgggctcacccatttaccaggacctcgcaatgcctccctt	2210	dd Yo	
2149	CCACAGCCCCATGAGAACTCCAGACCYTTGTCCCTTGAGCACCCCTGGGCCGGCCCTCAG	2090	Db	
2209	tctgcccgtgcggccccaggagaacgagtcagccggcaccatctgttgggggccagcga	2150	Qy	
21 <b>4</b> 9 2089	cggcagagcaagtccaagccccatagtgcccaaagcataagaaaga	2090 2036	. Qy	
2089	cttcctggggaagaaggagaccggtcacaggatgtctggcagtggatgttggagagtgag	2030 1976	Qy db	
1975	GCGTGCAAAAGAAATGCCAAGAAGGCTGAGTCGGGGAAGAGCGCCAGCACCGAGGTGCCA	91	Db .	
2029		1970	0	
1969 1915	gagcagttttgtggcagcagaggtggtaccttgccaaaacggaatgcaaaagggcaccgaa	1910	ρ <sub>b</sub>	
1856	GCTTCGCCTGGGGCCTGGAACCACACACACGCATGGGGCAAGGTCCCGAGGCTACTCAGAGA	1797	DЬ	
1909		1850	Qy	
1796	AAGGAGCAGGTGGAGGCCGAGGCCACCCGCAGGGCCCAGAGCA	1754	Db	
1849		1790	Qy	
1789 1753	acagacgacgaagcacgttcaccaccactacatccaccaccacgccgtccccaagacc 	1732 1694	Qy Db	
1693		1634	Db	
1731	gggcaagctgcccccgtggctgcttgccccctccttggaggcaagagcttcctgaccaa	1672	QΥ	

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BASE COUNT
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AUTHORS
TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takahashi,M. and Furukawa,Y.
Identification of 3' UTR of Axin2
Published Only in DataBase (2000) In pres
2 (bases 1 to 1863)
Nakamura,Y., Furukawa,Y. and Takahashi,M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (16-DEC-2000) to the DDBJ/EMBL/GenBank databases. Yoichi Furukawa, Institute of Medical Science, Human Genome Center; 4-6-1 Shirokanedai, Minato-Ku, Tokyo 108-1639, Japan (E-mail:furukawa@ims.u-tokyo.ac.jp, Tel:81-35449-5373,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Fax:81-35449-5406)
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/gene="Axin2"
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SLAPEDHKEPKKLAGVHALQASELVVTYFFCGEEIPYRRMLKAQSLTLGHFKEQLSKK
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/db_xref="GI:11967904"
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Patent: WO 9911780-A 7 11-MAR-1999;
BIRCHMEIER WALTER (DE); BEHRENS JUERGEN
Location/Qualifiers
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Birchmeier, W. and Behre
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/db_xref="taxon:32644"
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N AND A RELATED AGENT FOR DIAGNOSING AND TREATING
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                                    tccttgttgggtgaccaggatggtgcatacctcttccggactttcctggagagggagaaa 523
                                                                                                  GAGCCCGAGGGCAGTGCCTCCCCCACCCCACCATATTTGAGGTGGGCTGAGTCACTGCAT
                   Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

1 (bases 1 to 3761)

Zeng,L., Fagotto,F., Zhang,T., Hsu,W., Vasicek,T.J., Perry,W.L.

Zeng,L., Fagotto,F., Zhang,T., Gumbiner,B.M. and Costantini,F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zeng, L., Fagotto, F., Zhang, T., Hsu, W., Vasicek, T.J., Perry, W.L. 3rd, Lee, J.J., Tilghman, S.M., Gumbiner, B.M. and Costantini, F. The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling pathway that regulates embryonic axis formation Cell 90 (1), 181-192 (1997)
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KQRYVQAVMQRGRTCVRPACAPVLSVVPAVSDLELSETETKSQRKAGGGSAPPCDSIV
VGYYFCGEPIPYRTLVRGRAVTLGQFKELLTKKGSYRYYFKKVSDEFDCGVVFEEVRE
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GHVAKTAVLGGTASGHCKHVPKLGLKLDTAGLHHHRHVHHHVHHNSARPKEQMEAEVA
RRVQSSFSWGPETHGHAKPRSYSENAGTTLSAGDLPFGGKTSAPSKRNTKKAESGKNA
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YILDSNGIVSRQTKPATKSFIKDCVMKQQIDPAMFDQAQTEIQSTMEENTYPSFLKSD
IYLEYTRTGSESPKVCSDQSSGSGTGKGMSGYLPTLNEDEEWKCDQDADEDDGRDPLP
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EQQSLSSDADTLSLTDSSVDGIPPYRIRKQHRREMQESIQVNGRVPLPHIPRTYRMPK
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/db_xref="GI:2252816"
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/product="Axin"
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/function="may
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/chromosome="17"
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Vector pShuttle DN	Anti-sense strand	Nucleotide sequenc	Epstein Barr virus	Human colon cancer	Nucleotide sequenc	FLGA insert stabil	Human adenosine Al	Sequence encoding	Genomic DNA sequen	Quelling deficient	Moraxella catarrha	Mouse neural Mena+	Trichoderma reesei	Plant microsatelli	Murine RGS protein	Modified FL-specif	-	Ras-binding protei	Human gene express	DNA encoding a hum	Macaque mucosal ad	cDNA encoding a re	Human regulator of	colon car		Human netrin-1 cDN	Mammalian Ena (Men	Nucleotide sequenc	Gene encoding a su	Wheat phytochelati	clone G11	Genomic DNA encodi	Mouse RATH1.1 DNA.

## ALIGNMENTS

x23369;

X23369 standard; cDNA; 2825

ВP

Human conductin DNA. 17-JUN-1999 (first entry)

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Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour; therapy; cytoplasmic degradation; blockade; Wnt signalling pathway; Wingless signalling pathway; Adenomatous Polyposis Coli; APC; tumour suppressor; ss.
                                                                                                                                          Key
misc_feature
                                     protein_bind
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                                                                                                                                                                    Homo sapiens
                                                                                                             /product= "Conductin" 446..814
/bound_moiety= beta-catenin
/note= "as described in Claim 21"
2561..2713
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/bound_molety= GSK-3beta
/note= "as described in Claim
1403..1609
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/note= "regulator of G-protein signalling region
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Query Match 89.3%;
Best Local Similarity 100.0%;
Matches 2523; Conservative
                                                                             This invention describes a novel human conductin protein which has anti-tumour activity. Detecting the presence or amount of conductin, at protein or nucleic acid levels, is used to diagnose tumours, while agents that (re)activate conductin are used for tumour therapy. Conductin binds to beta-catenin and induces its cytoplasmic degradatio resulting in blockade of the Wntt-Wingless signalling pathway in vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC) fragments and, in conjunction with APC, acts as a tumour suppressor.
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81 <b>4</b> 600	5 gtgatggaggaaaatgcctaccaggtgttcttgacttctgacatttacctggaatatgtg 	75 54
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694 480	5 aacaacagcyttytotoccaagcagctydagcocgccaccaagacctacatacgagatggc 	42
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51 <b>4</b> 300	5 tetttacaeteettgttgggtgaceaggatggtgcatacetetteeggacttteetggag 	45 24
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                Nucleic acids encoding mutant and wild type Axin and oligonucleotides derived from them are useful for detecting mutations in the Axin gene and for determining whether a subject is likely to develop cancer (including breast, colorectal, gastrointestinal, esophageal, carcinomas or melanomas). The wild type Axin and homologues of Axin are useful for treating subjects who are likely to develop cancer (thyroid carcinomas). The nucleic acids are also useful for diagnosing cancer and for detecting mutations in cancerous cells. Wild type Axin, its antisense
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detecting, diagnosing

and

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Nucleic acids encoding mutant and wild type Axin and coligonucleotides derived from them are useful for detecting ultations in the Axin gene and for determining whether a subject is likely to develop cancer (including breast, colorectal, The wild gastrointestinal, esophageal, carcinomas or melanomas). The wild type Axin and homologues of Axin are useful for treating subjects who are likely to develop cancer (thyroid carcinomas). The nucleic acids are also useful for diagnosing cancer and for detecting mutations in cancerous cells. Wild type Axin, its antisense molecule and identified compounds form pharmaceutical compositions in the treatment of cancer. The compositions are also useful for treating cancer by inhibiting tumorigenesis (by inducing degradation of beta-catenin). The nucleic acid encoding Axin acts through
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pred. No. 2.7e-80;
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otherapy; diagnosis; progression;
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99US-0347496.
99US-0401064.
99US-0444242.
99US-0454150.
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Query Match Best Local

Similarity

11.4%;

Mismatches

43;

0;

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Score 322.2; DB 21; pred. No. 2.1e-76;

Length 1205

Sequence 1205 BP;

316

A;

248 C;

324 G;

317

Τ;

0 other;

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Cancer calls and comparing the unrent to inhibit cancer colls against the polypeptides and then administered back to the polypeptides and antibodies cancer cells are received to another back to the patient to inhibit cancer to inhibit cancer development. CD4+ and/or CC nucleic acid of the invention, or an APC expressing such a polypeptide, or closes the proliferation of specific T-cells. The T-cells can be CC cloned and then administered back to the patient to inhibit cancer CC development. Nucleic acids encoding the polypeptides and antibodies cagainst the polypeptides may be used to determine the expression level concer cells are present. Such diagnostic methods may also be used to cancer cells are present. Such diagnostic methods may also be used to present sequence represents a cDNA encoding a human colon tumour The progression of a cancer by repeating the processes at time of the invention and therefore to determine the time intervals, and comparing the current result to previous results. The present sequence represents a cDNA encoding a human colon tumour
                                                                                                                                                                                                                                                                                                                                                                Sequences A77722-A78199 represent 478 cDNAs encoding proteins or portions of proteins which are associated with human colon tumours. The invention also specifically discloses 8 human colon tumour proteins (B11897-B11904). The nucleic acids, the polypeptides they encode, and antigen presenting cells (APCs, preferably dendritic cells) expressing such polypeptides may be used in vaccines that target tumour cells, especially colon tumour cells, thereby inhibiting the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New colon tumor polypeptides especially colon cancer, and
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                                    present sequence polypeptide.
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aagtggagcggatcgattgagccctgcggtc
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                                  ttgaggagatctgggaggatgagacggtgctcccgatgtatgaaggccggattctgggca
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CC The invention also specifically discloses 8 human colon tumours.

CC (B18897-B11904). The nucleic acids, the polypeptides they encode, and cantigen presenting cells (APCs, preferably dendritic cells) expressing colon tumour cells, thereby inhibiting the development of color cancer. T-cells specific for the polypeptide expressed by the APC are used to remove tumour cells, thereby inhibiting the development of color cancer. The sample or the isolated T-cells specific for the polypeptide expressed by the APC are colored to remove tumour cells from biological samples, especially blood or cractions thereof. The sample or the isolated T-cells specific for the polypeptide can then be used to inhibit cancer development. CO4+ and/or color T-cells from a patient may be incubated with a polypeptide or colored and then administered back to the patient to inhibit cancer colored and then administered back to the patient to inhibit cancer colored and then administered back to the patient to inhibit cancer colored and then administered back to the patient to inhibit cancer comparities and the polypeptides and antibodies against the polypeptides may be used to determine the expression level concer cells are prosesent. Such diagnostic methods may also be used to concer cells are progression of a cancer by repeating the processes at time color two professions of a cancer by repeating the processes at time color versions results. The color present sequence represents a cDNA encoding a human colon tumour color tumour color tumour cells and comparing the current result to previous results. The color present sequence represents a cDNA encoding a human colon tumour color tumour color tumour color tumour color tumour cells and comparing the current result to previous results.
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19-NOV-1999;
02-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 96-97; 229pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New colon tumor polypeptides especially colon cancer, and
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02-JUL-1999;
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                                                                                                                                                              Sequence 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequences A77722-A78199 represent 478 cDNAs encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  progression of the cancer
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Pred. No. 1.8e
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                  Recombinant production of PIGI-1 allows the study of the structure, function and role in oncogeness of the protein. PIGI-1 and nucleic acid encoding it can also be used to develop products for use in treating tumours and cancer and in the diagnosis of cancer.
                                                                                           New isolated nucleic acid encoding p53 response protein PIGI-1 used to develop prods. for the study, diagnosis and treatment tumours and cancer
                                                                                                                                       WPI; 1996-097636/10.
P-PSDB; R89895.
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                                                                         Claim 3;
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Sequence 2383

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ilarity 47.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   565 A; 621 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and genes - used in the detection and by a mutation in the CR coding region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 58.8; DB 18;
Pred. No. 1.1e-05;
0; Mismatches 272;
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Best Local Similarity
Matches 251; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel isolated antibody or antibody fragment (I) which selectively binds to a polypeptide encoded by cytokine response gene 2 (CR2) and modulates CR2 activity. The products of the invention have cytostatic, anti-allergic, immunosuppressive and antimicrobial activity. The antibodies are useful as therapeutic agents for regulating cellular proliferation and differentiation and for treating all kinds of cancers, immune diseases such as allergic, autoimmune, and rheumatologic diseases, transplant rejection, and as anti-infectives for fighting viral, bacterial, parasitic and fungal infections. This sequence encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-NOV-1991;
10-AUG-1993;
27-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                               diseases, transplant rejection, and as viral, bacterial, parasitic and fungal the human CR1 protein described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CR2; human; antibody; immunosuppressive; and cell differentiation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel antibody or antibody fragment which selectively binds polypeptide encoded by cytokine response gene 2 -
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96WO-US08992.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dy. cytokine response gene; cytostatic; anti-allergic;
antimicrobial; therapy; cell proliferation; treatment
on; cancer; immune disease; rheumatologic disease;
on; anti-infective; CR1; ss.
                                                                                                                                                                                                                                                                                                      2.1%;
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Pred. No. 1.1e-05;
0; Mismatches 272;
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This invention describes a novel isolated antibody or antibody fragment (I) which selectively binds to a polypeptide encoded by cytokine response gene 2 (CR2) and modulates CR2 activity. The products of the invention have cytostatic, anti-allergic, immunosuppressive and antimicrobial activity. The antibodies are useful as therapeutic agents for regulating cellular proliferation and differentiation and for treating all kinds of cancers, immune diseases such as allergic, autoimmune, and rheumatologic diseases, transplant rejection, and as anti-infectives for fighting viral, bacterial, parasitic and fungal infections. This sequence is presented in the Seq ID list but is not described in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CR2; human; antibody; cytokine response gene; cytostatic; anti-allergic; immunosuppressive; antimicrobial; therapy; cell proliferation; treatment cell differentiation; cancer; immune disease; rheumatologic disease;
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                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Column 113-116; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel antibody or antibody fragment which selectively binds polypeptide encoded by cytokine response gene 2 -
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94US-0330108.
96WO-US08992.
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                                     WPI; 1998-240085/21.
P-PSDB; W59294.
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                                                                                                                                                            (MILL-) MILLENNIUM PHARM INC
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No. 1.5e-05;
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                                                     CDS
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Pred. No. 1.7e-05;
0; Mismatches 168
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              19-DEC-2000
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04-OCT-1996;
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Pred. No. 0.0015;
0; Mismatches 17
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roles in immune responses, cell death, cell proliferation and stimulation of cell differentiation. M68 lacks a transmembrane domain and is a secreted factor suggesting that it functions as a natural inhibitor for its ligand. The altered expression pattern of M68 in a multitude of tissues suggests that M68 may play a role in cancer by binding to its ligand and blocking apoptotic cell death induced by such a ligand. This anti-apoptopic role of M68 suggests that modulators of M68 will be useful in treatment of apoptosis related diseases such as various forms of cancer and various bone disorders. M68 nucleic acids and proteins are therefore useful for treating conditions involving atypical apoptosis and for identifying modulators of M68. Modulators of M68 are useful for treatment of cancer and other diseases associated with abnormal levels of cancer and other diseases associated with abnormal levels of

The

protein is a member of a family of proteins which n immune responses, cell death, cell proliferation

have and

Claim 19; Page 76-78; 80pp; English osteoporosis, Alzheimer's disease

Isolated human M68 nucleic acids and proteins which are part of the tumor necrosis factor receptor (TNFR) family, useful for identifyin modulators that may be used to treat various diseases e.g. cancer,  $\frac{1}{2}$ 

identifying

apoptosis including systemic lupus erythematosus, Hashimoto's thyrolditis, Grave's disease, idiopathic myzodema, autoimmune diabetes, thrombotic thrombotycopenic purpura, multiple scelerc liver diseases, autoimmune gastritis, ulcerative colitis,

multiple sclerosis

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grave's disease; idiopathic myxodema; autoimmune diabete thrombotic thrombocytopenic purpura; multiple sclerosis;
                                                                                                                                                                                                                     P-PSDB;
                                                                                                                                                                                                                      WPI; 2000-506066/45
P-PSDB; Y97246.
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20-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                              (MERI )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     iver diseases; autoimmune gastritis; ulcerative colitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumour necrosis factor; TNF; programmed cell death; ptor; immune response; cell differentiation; ligand; disease; systemic lupus erythematosus; Hashimoto's
                                                                                                                                                                                                                                                               MERCK & CO INC
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99US-0172754.
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                          Baszczynski CJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brassica root-specific promoter sequence and vectors containing it - for expression of e.g. toxins in the roots of crops susceptible to root diseases \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 4; 54pp; English.
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                                                                                                                                                                                                                                                                                               soil; groundwater; decontamination;
                                                                                                                                                                                                                                                                                                        TapCS1; wheat; phytochelatin synthase; heavy metal;
transgenic plant; bioremediation; phytoremedation;
soil; groundwater; decontamination; detoxification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wheat phytochelatin synthase TaPCS1 cDNA.
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                                         /*tag=
                                                                                               211..1710
                                                                                                                               Location/Qualifiers
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         /EC_number=
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Pred. No. 0.000
0; Mismatches
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                  "2.3.2.15"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid is provided in antisense orientation, the transgenic plant is used to prevent removal of a heavy metal from soil. When the nucleic acid is provided in sense orientation, the transgenic the nucleic acid is provided in sense orientation, the transgenic plant is capable of removing a heavy metal from soil or groundwater, the heavy metal being e.g. cadmium, arsenate, arsenite, mercury, lead, zinc, nickel, bismuth, selenium, silver, gold or copper. PCS nucleic acids can also be used to decrease the level of heavy metal in the harvestable portion of a plant by expressing PCS in a non-harvestable portion and involves inhibiting expression of PCS in the harvestable portion of the plant. PCS polypeptides are used for in vitro or in vivo biosynthesis of phytochelatins, and in a method of transferring a gamma-glutamylcysteine unit from 1 thiol peptide to another. The methods allow cost-effective and efficient bioremediation of contaminated soils and groundwaters, as well as the plant of the plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 186; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expressed in yeast. The cDNA was obtained from a screening assay designed to identify genes that conferred tolerance to cadmium. Phytochelatins play major roles in metal detoxification in plants. Phytochelatins provides PCS nucleic acids (see A89183-97) and enzymes (see B1934-38) from Arabidopsis, wheat, yeast and nematode. The nucleic acids are used to generate transgenic plants. When the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is that of cDNA encoding TaPCS1 (see B19936), a novel wheat phytochelatin synthase (PCS) that is capable of high rates of Cd2+-activated phytochelatin biosynthesis from glutathione, and which confers strong cadmium tolerance when
                                                                                                                                                                                            1482
                                                                                                                                                                                                                                                                                                                                                                                                                1362 tggagctggaaagccgccatagtctggaggagcggctgcagcagatccgggaggatgaag 1421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Fig 18A-B; 119pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-MAY-1999;
15-JUL-1999;
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                                   1542 totocagggtoctcaagacccccggctgtcaatcccctggtgtgggtcgctacagcccac 160:
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P-PSDB; B19936.
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         392
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                                                                                                                                                               tggccctcctaccctccggcagctatgaagaggacccaccaaaccattttggacgaccacc 1541
                                                                                                                                                                                                                                                                                        aaaaggagggtctgagcaggccctgagctcacgggatggagcaccggtccagcaccccc 1481
                                                                                                                                                                                                                                                    cggcggaggggaagcggctgttcgcggaggcgctgcagggcgggaccatggagggcttct 331
                                                                                                                                                                                                                                                                                                                                                                         tggaggtggcgtcgctgtaccggcgggtgctgccqtcgccgccggcggtggagttcgcgt 271
tcaacctcatctcctacttccagacgcagtcggagccggccttctgcggcctcgcctccc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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99US-0354123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42.6; DB 22;
Pred. No. 0.23;
0; Mismatches 239;
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

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tacactccttgttgggtgaccaggatggtgcatacctcttccgga 503	2.1%; Score 58.8; DB 1; Length 47.2%; Pred. No. 2.5e-06; tive 0; Mismatches 272; Indel:	ication US/08274318 87710N: UCXbinder, Leonard albott, Randy elzinger, Bernd R. ley, Nikolai NTION: NO. 5667987el p53 Response Genes UENCES: 3 E ADDRESS: Bristol-Myers Squibb Company 05 First Avenue hington SA ABLE FORM: :: Floppy disk IIBM PC compatible YSTEM: PC-DOS/MS-DOS PatentIn Release #1.0, Version #1.25 CATION DATA: CATION DATA: INVERMATION: en, James M. N NUMBER: 32,962 OCKET NUMBER: ON0127- TION INFORMATION: en, James M. N NUMBER: 32,962 OCKET NUMBER: ON0127- TION INFORMATION: 83 base pairs eic acid S: single linear	52 2 US-09-130-114-1 96 1 US-07-884-811-15 96 1 US-07-885-971-15 96 1 US-08-77-83A-15 96 1 US-08-194-088B-15 96 2 US-08-194-088B-15 96 5 PCT-US93-04648-15 97 1 US-08-194-087-15 98 1 US-08-194-087-15 99 1 US-08-195-947-3 99 2 US-08-195-947-3 99 2 US-08-433-885-3 99 2 US-08-433-885-3 99 2 US-08-433-885-3 90 2 US-08-804-227C-1 144 2 US-08-997-362-144 154 4 US-08-997-362-144 155 1 US-08-997-362-144 156 2 US-08-9864-038A-1 157 2 US-08-864-038A-1 158 2 US-08-864-038A-1 159 2 US-09-010-928B-1 150 2 US-09-010-928B-1
cttccgga 503 	2383; 9; Gaps 2;		Sequence 1, Appli Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 144, App Sequence 144, App Sequence 144, App Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli

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TELEFAX: 20 INFORMATION FOR
              NAME: Bogden, James M.
REGISTRATION NUMBER: 32,962
REFERENCE/DOCKET NUMBER: ON01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-727-3688
TELEPHONE: 206-727-3681
                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                APPLICATION NUMBER: 08/274,318
FILING DATE: 11-JUL-1994
ATTORNEY/AGENT INFORMATION:
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                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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US-08-463-081B-1; Sequence 1, Application US/08463081B
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Patent No. 5871960 5837487
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Best Local Similarity 47.2%;
Matches 251; Conservative
                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR5
TITLE OF INVENTION: Vector and Transformed Cel
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                                                                                                NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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CITY: Los Angeles
STATE: California
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              COUNTRY:
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Pred. No. 2.5e-06;
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CURRENT APPLICATION DATA:

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                US-08-461-379A-1
                                  RESULT
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Best Local Similarity
Matches 251; Conserv
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FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Application US/08461379A
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ilarity 47.28;
Conservative
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; LOCATION:
US-08-461-379A-1
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Best Local Similarity 47.2%;
Matches 251; Conservative
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: USSN 08/330,108; 08/104,736
APPLICATION NUMBER: 6 07/796,066
FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Anzel, ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART-070
TELECOMMUNICATION INFORMATION:
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LENGTH: 2406 base pair
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744 agatccaggcagtgatggaggaaaatgcctaccaggtgttcttgacttctgacatttacc
                                                    528 AGCTGACGAGGATGAACCTGCAGACTGCCACAGCCACATGCTTTGATGCGGCTCAGGGGA 587
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
SOFTWARE: Version #1.25
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STATE: Pennsylvania
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ADDRESSEE: Ratner & Prestia
ADDRESSEE: (B) STREET:One Westlakes-Berwyn
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NO: 1:
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IBM PC compatible
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5-JUNE-1995
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: Nucleic Acids Encoding CR5 Polypeptide,
: Vector and Transformed Cell Thereof, and
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                                                                  Query Match
Best Local Similarity
Matches 251; Conserv
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INFORMATION FOR SEQ ID NO:
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TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 2406 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 20-NOV-91 ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                FEATURE:
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 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: USSN 08/330,108 FILING DATE: 27-OCT-1994 APPLICATION NUMBER: USSN 08/104,736 FILING DATE: 10-AUG-1993 APPLICATION NUMBER: USSN 07/796,066 FILING DATE: 20-NOV-91.
                                                                                                                                                                           NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Pennsylvania
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                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Viviana Amzel, Ph. D. REGISTRATION NUMBER: 30,930
                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ccgacctcaagtgcaaactctcacccaccgtggttggcttgtccagcaaaac
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                                                                      Conservative
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                                                                                      Score 58.8; DB 2; Pred. No. 2.5e-06;
                                                                      Mismatches
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                                                                        272;
                                                                                                       Length 2406;
                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
INFORMATION FOR SEQ
                                                                                                         APPLICATION NUMBER: US 08/
FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                      FILING DATE: 5-JUN-1991
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/104,736
                            TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 622-7700
                                                                                                                                                                                                                                                             SOFTWARE: Version #1.2
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Smith, Kendall A. & Beadling, Carol TITLE OF INVENTION: Nucleic Acids Encoding CRl
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               TELEFAX:
                                                                            NAME: Viviana Amzel, Ph. D. REGISTRATION NUMBER: 30,930
                                                                                                                                                                                                                                APPLICATION NUMBER: US/
FILING DATE: 5-JUN-1995
                                                                                                                                                                                                                                                                                            SOFTWARE:
                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Los Angeles
STATE: California
                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
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Version #1.25
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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RESULT 7
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                                                                                                                                                     Sequence 1, Application US/08465585C
Patent No. 6027914
GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR6 Polypeptide, Vecto
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 251;
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Best Local Similarity
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
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                                                                         COUNTRY: US
ZIP: 900071
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                                                                                                  CITY: Los Angeles
STATE: Californiaa
                                                                                                                                ADDRESSEE:
                                                                                                                                               ADDRESSEE:
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                                                                                                                                             PRETTY, SCHROEDER & POPLAWSKI
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                                                                                                                                (B) STREET:
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  Version #1.25
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US-08-652-446-1
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; NAME/KEY:
; LOCATION:
US-08-465-585C-1
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TELEPHONE: (213) 622-7700
TELEPAX: (213) 4894210
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/01
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN
FILING DATE: 27-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 20-NOV-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                      444 ggtggaccaagtctttacactccttgttgggtgaccaggatggtgcatacctcttccgga 503
768 TCACCCATCCCCGAGGTGGCTGCCCCTGTGTGGGAGGCAGGTTCTGCAAAGC
                                                                                                        924 ccgacctcaagtgcaaactctcacccaccgtggttggcttgtccagcaaaac 975
                                                                                                                                                                                                   804 tggaatatgtgaggagtgggggggaaaacacagcttacatgagtaacgggggactgggga
                                                                                                                                                                                                                                                                                                                                                   684 tacgagatggcatcaagaagcaacagatcggctcggtcatgtttgaccaggcacagaccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Viviana Amzel, Ph. D. REGISTRATION NUMBER: 30,930 REFERENCE/DOCKET NUMBER: P66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: USSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: USSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tcaggcagatgaacctgaaggataccaaaactttgcgagtggccaaagcaatctataaga
                                                                                                                                                               GGGACCTGGCTGCCCAAGCCTCAGCCGCCTCTGCCACTCTGTCCAGCTGCAGCCTGGACC
                                                                                                                                                                                                                                                                agatccaggcagtgatggaggaaaatgcctaccaggtgttcttgacttctgacatttacc
                                                                                                                                                                                                                                                                                                                        AGCTGACGAGGATGAACCTGCAGACTGCCACAGCCACATGCTTTGATGCGGCTCAGGGGA 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCA - - - AGAAGATCCGATCAGCTACCAAGCTGGCCTCCAGGGCACACCAGATCTTTGAGG
                                                                               AGCCCTCACACCTGAGTCTCCACGGCAGTGAGGAAGCCCAGCCGGGAAGAGGTTGAG
                                                                                                                                                                                                                                             AGACACGTACCCTGATGGAGAAGGACTCCTACCCACGCTTCCTGAAGTCGCCTGCTTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGTGGAGAGAGTCGTTCGACCTGCTGCTGAGCAGTAAAAATGGAGTGGCTGCCTTCCACG
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116..722
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Pred. No. 2.5e-06;
0; Mismatches 272;
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US-08-652-446-1
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PRIOR APPLICATION DATA:

APPLICATION UNMBER: 08/462,337

FILING DATE: 5-JUN-1995

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

08/462,390
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                                                                                                                                                                       NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENERAL INFORMATION:
                                                                 FEATURE:
                                                                                MOLECULE TYPE:
                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 2406 base pair
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CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICATION NUMBER: 08/461,379
FILING DATE: 5-JUN-1991
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                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
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                                                 NAME/KEY:
                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                    REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: FP66 40035
                                                                                                                                                                                                                                                 NAME: Viviana Amzel, Ph. REGISTRATION NUMBER: 30,9
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 5-JUN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/465,585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: EP APP. # 96921319.8 FILING DATE: 5-JUN-1998 APPLICATION NUMBER: PCT/US/96/09194 FILING DATE: 5-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: LOS Angeles
STATE: California
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                                 CATION:
                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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                                                                                                                          nucleic acid
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116..722
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VENTION: Nucleic Acids Encoding CR5
VENTION: Polypeptide, Vector and Transformed Cell Thereof, and
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Version #1.25
                                                                                          linear
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                                                                                                                                                                                                     (213) 622-7
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29-OCT-1996
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5-JUN-1995
                                                                                                          single
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US-08-463-081B-27
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Best Local Sim
Matches 251;
                                                        APPLICATION NUMBER: US/(FILING DATE: 5-JUN-1995 PRIOR APPLICATION DATA:
                PRIOR APPLICATION DATA:
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                              APPLICATION NUMBER: US 08/104,736 FILING DATE: 10-AUG-1993
                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                              STREET:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                            ADDRESSEE:
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Sequence 27, Application US/08463081B Patent No. 5871960 Patent No. 5871960 5837487
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                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                768 TCACCCATCCCCGAGGTGGCTGCCCCTGTGTGGGAGGCAGGTTCTGCAAAGC 819
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                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGACCTGGCCGAGCCTCAGCCGCCTCTGCCACTCTGTCCAGCTGCAGCCTGGACC
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California
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                                                                                                                                                                                                                                                                                444 South Flower
                                                                                                                                                                                                                                                                                                                                                                     Smith, Kendall A. & Beadling, Carol /ENTION: Nucleic Acids Encoding CR5 Polypeptide, /ENTION: Vector and Transformed Cell Thereof, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                           PatentIn Release #1.0,
Version #1.25
                                                                                                                                                                                                                                                                                                      PRETTY,
                                                                                                                                         Floppy disk
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Flower St. - Suite 1900
US/08/463,081B
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Pred. No. 2.5e-06;
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US 07/796,066

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RESULT 10
US-08-461-379A-27
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 606 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                       Sequence 27, Application US/08461379A Patent No. 5871961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.0%;
Best Local Similarity 51.4%;
Matches 187; Conservative
                                                                                                                                                                                                                                                ARENI INCORMATION:

GAPPLICANT: Smith, Kendall A. & Beadling, Carol
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
TITLE OF INVENTION: Vector and Transformed Cell Thereof, and
                                                                                                                                                                                                                     TITLE OF INVENTION: Nuc
TITLE OF INVENTION: Vec
TITLE OF INVENTION: Exp
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: VIVIANA AMZE1, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P60
TELECOMMUNICATION INFORMATION:
                                                                     MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                              COUNTRY: UZIP: 19482
                                                                                                                                           CITY: Valley Forge
STATE: Pennsylvania
                                                                                                                                                                                ADDRESSEE: Ratner & Prestia
ADDRESSEE: (B) STREET:One Westlakes-Berwyn
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                                                                                                                              USA
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OR SEQ ID NO: 27:
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PatentIn Release #1.0,
Version #1.25
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Pred. No. 3.4e-06;
0; Mismatches 168;
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                                                                                                                                                                                                                                   Sequence 27, Application US/08462390B Patent No. 5882894
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Best Local Similarity 51.4%;
Matches 187; Conservative
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TELEFAX: (610)470-0701
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE:
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APPLICATION NUMBER: & 07/796,066
FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
ATTORNEY/AGENT INFORMATION:
                                                                                                                  NUMBER OF SEQUENCES: 3
                                                                                                                                     APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Therec
NUMBER OF SEQUENCES: 35
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LENGTH: 606 base pairs
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PRIOR APPLICATION DATA:
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STORTION NUMBER: US/08/461,379A
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COUNTRY: UZIP: 19482
                                    CITY: Valley Forge
STATE: Pennsylvania
                                                                             ADDRESSEE: Ratner & Prestia ADDRESSEE: . (B) ST
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                                                                           (B)
                                                                             STREET:One Westlakes-Berwyn
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CURRENT APPLICATION DATA:

PatentIn Release #1.0, Version

#1

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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                                                                                                              RESULT 12
US-08-463-074B-27
Sequence 27, Application US/08463074B
Patent No. 6020155

GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR1 Fusion Protein,
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.0%;
Best Local Similarity 51.4%;
Matches 187; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 05-NOVI-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: DATELECOMMUNICATION INFORMATION: (610)407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                          AGACACGTACCCTGATGGAGAAGGACTCCTACCCACGCTTCCTGAAGTCGCCTGCTTACC
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FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/104,736
FILING DATE: 10-AUG-1993
PRIOR APPLICATION UNBER: US 07/796,066
APPLICATION UNBER: US 07/796,066
FILING DATE: 20-NOV-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (213) 489-4210 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REGISTRATION NUMBER: 30,930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: P66
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Releasoftware: Version #1.25
CURRENT APPLICATION DATA:
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ADDRESSEE:
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                               182 GGTGGAGAGAGTCGTTCGACCTGCTGCTGAGCAGTAAAAATGGAGTGGCTGCCTTCCACG
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC
OPERATING SYSTEM:
533
                                  804 tgga 807
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                                                                                          agatocaggcagtgatggaggaaaatgoctaccaggtgttcttgacttctgacatttacc 803
                                                                                                                                             AGCTGACGAGGATGAACCTGCAGACTGCCACAGCCACATGCTTTGATGCGGCTCAGGGGA
                                                                                                                                                                                                                      AGTTCATTTG-----CAGTGAGGCCCCTAAAGAGGTCAACATTGACCATGAGACCCGCG 412
                                                                                                                                                                                                                                                                                                TCA---AGAAGATCCGATCAGCTACCAAGCTGGCCTCCAGGGCACACCAGATCTTTGAGG
                                                                     AGACACGTACCCTGATGGAGAAGGACTCCTACCCACGCTTCCTGAAGTCGCCTGCTTACC
536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              606 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patentin Release #1.0,
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SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity
Matches 187; Conserv
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FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: V101ana Anzel, ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38149 (D/
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/0 FILING DATE: 5-JUNE-1995 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                          CITY: Los Angeles
STATE: California
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agatccaggcagtgatggaggaaaatgcctaccaggtgttcttgacttctgacatttacc 803
                                                                                                                                                    ggtacattgagaacaacagcgttgtctccaagcagctgaagcccgccaccaagacctaca 683
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                                                                                                                                                                                                                                                                                                                                                                                 ggtggaccaagtctttacactccttgttgggtgaccaggatggtgcatacctcttccgga 503
                                                       AGCTGACGAGGATGAACCTGCAGACTGCCACAGGCCACATGCTTTGATGCGGCTCAGGGGA 472
                                                                                                                             AGTTCATTTG-----CAGTGAGGCCCCTAAAGAGGTCAACATTGACCATGAGACCCGCG
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ilarity 51.4%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (213) 622-7700
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                                                                                                                                                                                                                                                                                                                                                                                                                         Score 57.2; DB 3;
Pred. No. 3.4e-06;
0; Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Encoding CR6 Polypeptide, Vecto ell Thereof, and Expression Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                           168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 606;
                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                     TELEFAX: (213) 489-42
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Rel
SOFTWARE: Version #1.2
CURRENT APPLICATION DATA:
SEQUENCE CHARACTERISTICS:
                                                                       REFERENCE/DOCKET NUMBER: FP
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APPLICATION NUMBER: US 08/330,108
FILING DATE: 27-OCT-1994
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP App. # 96921319.8
FILING DATE: 5-JAN-1998
                                                                                                                                               FILING DATE: 29-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 5-JUN 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,390
FILING DATE: 5-JUN-1995
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FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                       APPLICATION NUMBER: 08//
FILING DATE: 5-JUN-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/4
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
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                                                                                                        NAME: Viviana Amzel, Ph. D. REGISTRATION NUMBER: 30,930
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 5-JUN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 5-JUN-
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                                                                                                                                                                                    APPLICATION NUMBER:
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                                      (213)
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                                                          (213)
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(B) STREET:
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5-JUN-1995
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                                      489-4210
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: Nucleic Acids Encoding CR5
: Polypeptide, Vector and Transformed Cell Thereof, and
                                                          622-7700
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; STRANDEDNESS: sin; TOPOLOGY: linear; MOLECULE TYPE: cDNA US-08-652-446-27

single

Length 606;

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RESULT 15
US-08-870-815-3
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Best Local Similarity
Matches 187; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                             ATTORNEY/AGENT INFORMATION:
NAME: Laura A. COTUZZI
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-074
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATEN: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Levinson, Douglas A.

APPLICANT: Gimeno, Carlos J.

TITLE OF INVENTION: RATH GENES AND POLYPEPTIDES AND METHODS

TITLE OF INVENTION: FOR THE TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                                                                                                       APPLICATION NUMBER: US/08/870,815
FILING DATE: 06-JUN-1997
CLASSIFICATION: 435
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                            TELEPHONE:
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STATE: New Yor
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1155 Avenue of the Americas
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(212) 896-8864/9741
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                                                           AGACACGTACCCTGATGGAGAAGGACTCCTACCCACGCTTCCTGAAGTCGCCTGCTTACC
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Search completed: June Job time: 19729 sec 7, 2001, 00:26:26

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Copyright (c) 1993 - 2000 Compugen Ltd.
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44: em\_esthum10:\*
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gb\_est52:\*
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Result
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140 BE872155
102 A7818109
140 BE882875
122 AW962356
17 A1220032
7 AA446378
149 BF521997
169 BF812711
168 BF757617
103 A1912345
231 CNS03YW0
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BE872155 601446262
AIB18109 wk27c05.x
BE882875 601509279
AW962356 EST374429
AI220032 qq78h02.x
AA446378 zw58b07.r
BF521397 UI-R Y0-a
BF812711 RC3-CI019
BF757617 MR2-CT059
AI1912475 tz24c04.x
AL266841 Tetraodon
AL17875 Tetraodon
AL17875 Tetraodon
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AI41942 tg40d11.x
AI41942 tg40d11.x
AI41943 tg43h03.x
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AA937585 of71h02.s
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BE872155
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1 (bases 1 to 798)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                   http://lmage.llnl.gov
Plate: LLAM9569 row: k column:
                                                                                                                                                                                                    Email: Robert_Strausberg@nih.gov Tissue Procurement: ATCC
                                                                                                                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                               BE872155.1 GI:10320931
                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                              CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
  218
                                                                                                                quality sequence stop: 544.
Location/Qualifiers
                                                                                                                                                                                                                       (301) 496-1550
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/lissue_type="adenocarcinoma"
/lab_host="DH108 (phage-resistant)"
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/Site_2: Sall; Cloned unidirectionally. Primer: Oligo dratege insert size 1.8 kb. Library constructed by Litechnologies."

Technologies. "
                                                                                     /organism="Homo sapiens"
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AA884421 am16b12.s
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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Location/Qualifiers
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National Cancer Institute / National Institute of Neurological
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

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/clone="IMAGE:2413544"
/clone_1ib="NCI_CGAP_Brn25"
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/lab_host="DH10B"
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plate: LLAM9726 row: n column:
High quality sequence stop: 679.
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CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium
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Contact: Robert Strausberg, Ph.D.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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/tisue_type="leiomyosarcoma"
/tlab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
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/clone="IMAGE:3910867"
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                                                                                                                                                             Assessment of gene expression patterns in a model of colon metastasis using a 19,200 element CDNA microarray Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
                                                                                                                                                                                                                                                                     1 (bases 1 to 621)
Hegde,P., Q1,R., Abernathy,K., Dharap,S.,
,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Y
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EST374429 MAGE resequences,
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Plate: 174
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                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
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/clone_"Vector: pBluescriptSKm"
/note="Vector: pBluescriptSKm"
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REFERENCE
AUTHORS
TITLE
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VERSION
KEYWORDS
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AI220032/c
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Matches 535; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGCAGGCTAGCTGAGGTGTCGAAGCCCCCAAAGCAGCGGTGCTGTGTGGCCAGTCAGCAG
           Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 752 Std Error: 0.00
                                                                                                                                                                                                                                                                                                            A1220032 543 bp mRNA septiens cDNA clone gg78h02_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841331 3′ similar to TR:042400 042400 AXIN. ;, i
                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae;
A (bases 1 to 543)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Pro
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Seq primer:
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DEFINITION
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                                                                                                                                                                                                                             attttggacgaccacctctccagggtcctcaagacccccggctgtcaatcccctggtgtg 1585
                                                                                                                                                                                                                                                                                                                                                     atocgggaggatgaagaaaaggagggtctgagcaggccctgagctcacgggatggagca 1465
                                                                                                                                                                                                                                                                                                                                                                                               CTGGAAAAGCTGAAGCTGGAGTTGGAGAGCCGCCACAGCCTGGAGGAGCGCCTGCAGCAG
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                                                                                                                                                                                                                                                                                         ccggtccagcacccctggcctcctaccctccggcagctatgaagaggacccacaaacc 1525
                                                                                                                                                   GGCCGCTATAGCCCCCGCTCCCGCTCCCCGGACCACCACCACCACCACCATTCGCAGTAC
                                                                                                                                                                                                               ATACTGGACGATCACCTGTCCAGGGTCCTCAAGACCCCTGGCTGCCAGTCTCCGGGCGTA
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                                                                                                                                                                                                                                                                                                                                     ATCCGAGAGGATGAAGAGAGAGAGGGCTCCGAGCTCACACTCAATTCGCGGGAGGGGGGCG 184
AA446378 548 bp mRNA zw58b07.rl Soares_total_fetus_Nb2HF8_9w
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by E Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"Organ: pooled; Vector: pT/T3D-Pac (pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="IMAGE:1841331"
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82.7%;
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Pred. No. 5.4e-90;
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Homo sapiens cDNA clone
                 EST
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Fax: 314 286 1810
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AA446378.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMAGE:774229 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               141
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/clone="IMAGE:774229"
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2297 gaggaagcctgccgcaggctggcagaggtgtcgaagccccagaagccagcagcggtgctgcgtg 2356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCAGTCAGCAGAGGGACAGGAATCATTCGGCCCACTGTTCAGACGGGAGCCCACACCCTTC 132
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                                                                                                                                                                                       CGGAGGATGCTGAAGGCTCAGAGCTTGACCCTGGGCCACTTTAAAGAGCAGCTCAGCAAA
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1 (bases 1 to 548)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.

WashU_Merck_EST_project 1997.
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28m13 rev2 ET from Amersham
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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/dev_stage="8-9 weeks"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: msoares@blue.weeg.ulowa.edu cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) This clone is also available through the I.M.A.G.E. Consortium at LLNL (info@image.linl.gov). IMAGE ID- 1791410 Seg primer: M13 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaila; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       451 Eckstein Medical Research Building Iowa
Tel: 319 335 8250
Fax: 319 335 9565
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University of Iowa
451 Eckstein Medical Research Building Iow
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                                                                                                                                                                                                                                                                                                             /lab_host="DHIOB (Life Technologies)"
/note="Vector: pT/T3D-Pac (Pharmacia) with a modified
/note="Vector: pT/T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-Y0
library is a subtracted library derived from an
individually tagged normalized whole-eye (minus the lens)
library. The driver for the subtraction consisted of a
pool of all previous libraries (UI-R-AO, UI-R-AI, UI-R-EO,
UI-R-EI, UI-R-CO, and UI-R-C1). The tag is a string of
UI-R-EI, UI-R-CO, and UI-R-C1) is the and the
oligo-dT track which allows identification of the library
of origin of a clone within the mixture. The subtracted
              wingle-Stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-Y0 library. This procedure has been previously described (Bonaldo, Lennon and Scarce Commence)
                                                                                                                                        library (UI-R-Y0) was constructed as follows: PCR amplified cDNA inserts from previous library clones from which 3' ESTs had been derived were used as a driver in hybridization with the normalized whole-eye library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the co
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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Email: asimpson@ludwlg.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwlg.org.br/scripts/gethtml2.pl?tl=RC3st2=RC3-CI0195-
221100-021-a10st3=2000-11-22st4*1)
Seq primer: puc 18 forward
                                                                                                                                                                                                                                                           Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
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Fax: +55-11-2707001
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                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                           caccagccaccagcgccaaccgacagcgagttatccagcgacgcactgaccgacgattcca
                                                                                                                                                       caaaactcttcgggccaccgcgagtgtgagatccacggaaaacagctgaaaacggattcag
                                                                                   CACCAGCCACCAGCGCCAACGAAAGTGAGATATCCAGTGATGCGCTGAGGGATGATTCCA
                                                                                                                                         GTCCTTCAAGAGGAGCGATCCTGTTAATCCTTTATCACATAGGTTCTGGCTATGTCTTTG
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/clone_lib="CT0596"
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/db_xref≖"taxon:9606"
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84.1%;
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Pred. No. 1.7e-82;
0; Mismatches 80;
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426

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366

1029

969 186 909

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Fax: +55-11-2/0/004
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human
This sequence was derived from the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (http://www.ludwig.org.br/scripts/gethtml2.pl?t1-MR2&t2-MR2-CT0596-091100-001-f12&t3=2000-11-09&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
/note-"Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from .ORESTES PCR (U.S. Letters Patent application No. 196; 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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accttgccaaaacggaatgcaaagggcaccgaaccgggtcttgcactgtcggccagggat 1996
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 2487 Std Error: 0.00
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D
Tel: (301) 496-1550
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Mammalia; Eutheria;
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quality sequence stop: 414.
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.85 kb. Life Technologies catalog #
11539-012"
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adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="IMAGE:2289510"
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Pred. No. 5.4e-77;
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Tetraodon nigroviridis genome survey sequence PUC-Ori end of clo
069C20 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                        Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of scale clone-end sequencing project of the Tetraodon nigrovil genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha; Holacanthopterygii; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Tetraodon.
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Direct Submission
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Tetraodon nigroviridis DNA
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Roest-Crollius, H., Jaillon, O.,
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Roest-Crollius, H., Ja
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a 294 c
                                                                                                                                                                                                                      /organism="Tetraodon nigroviridis'
/db_xref="taxon:99883"
/clone="069C20"
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                                                                                                                                                                                   /note="Genoscope sequence ID : C0BG069BB10SP1-end
                                                                                                                                                                                                                                                                                         Location/Qualifiers
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64.9%;
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Quetier,F., Sauri
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9	REFERENCE AUTHORS			SOURCE ORGANISM	KEYWORDS	ACCESSION	DEFINITION	LOCUS	RESULT 12	,	0 7 0		2 0	916	717	750	0 40	5 9	636	537	Qy 576	477	Qy 516	Db 417	Qy 456	357	Qу 396	Db 297	Оу 353	Db 237	Qу 293	179	Qy 233	Db 119
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	Oy 753	Db 339	Оу 693	Db 399	Qу 633	Db 459	Qy 573	Db 519	Qy 513	Db 579	Оу 453	Db 639	Qу 393	Db 699	Qу . 338	Db 759	Оу 282	Db 819	Qy 222	Best Loc Matches	Query Ma	BASE COUNT			100	FEATURES		COMMENT	TITLE	REFERENCE	TOTTOMAT		AUTHORS	JOURNAL

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                                                                                                      GCGTCAAGAGGCAGCAGATCGACTCGGCCATGTTCGACCAGGCGCAGCTGGAGGTTCAGA
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Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
Unpublished
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Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
Scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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/note="Genoscope sequence ID : C0AG218AH09LP1-end :
/note="Genoscope sequence ID : C0AG218AH09LP1-end :
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/db_xref="taxon:99883"
/clone="218017"
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cgtggttggcttgtccagcaaaactcttcgggccaccgcgagtgtgagatccaccggaaac 1011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               agtgcaaactctcacccaccgtggttggcttgtccagcaaaactcttcggg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGCTAAATCCTTGGGKGCTGTCGTGGGGCTGTCGGCTAAAAGCCTGNAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
Washu-Merck EST Project 1997
Unpublished (1997)
Contact: Wilson RK
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AA489748
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aa43d02.rl Soares_NhHMPu_S1 Homo saplens cDNA clone IMAGE:823683
5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
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                                                           h 11.6%;
Similarity 88.7%;
54; Conservative
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                                                                                                                                                                                   Ø
                                                                                                                                                                             were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of IM.A.G.B. clones 260232-265223, 340488-34479, and 484488-489479."
                                                                                                                                                                                                                                                                                                               /note-*Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and so circles
                                                                                                                                                                                                                                                                                                                                                                                                                                             pregnant uterus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Pooled human melanocyte, fetal heart,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Soares_NhHMPu_S1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:823683"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                    'lab_host-"DH10B"
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                                                           Score 327; DB Pred. No. 3e-7 0; Mismatches
                                                                              ; DB 8;
3e-73;
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                                                                                                   Length 399;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the TMAGE ConsortLum (info@1mage.llnl.gov) for further information.
TMAGE ConsortLum (info@1mage.llnl.gov) for further information.
Seg primer: -40UP from Gibco
Seg primer: -40UP from Gibco
High quality sequence stop: 471.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria;
1 (bases 1 to 487)
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National Cancer Institute, Cancer Genome Ana
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    71
/note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
                                                                                                                                                                                                                                                                                           /clone_lib="Soares_NhHMPu_S1"
/tissue_type="Pooled human melanocyte,
pregnant uterus"
                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:1879513"
                                                                                                                                                                                                                                                                      /lab_host="DH10B"
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ORIGIN

Query Match
Best Local Similarity
Matches 403; Conser

Conservative

0;

11.5%;

Score 325.6; Pred. No. 7.2 Mismatches

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Length

487;

7; Gaps

2;

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JOURNAL COMMENT
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                                                          This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further i Insert Length: 740 Std Error: 0.00 Seq primer: -40UP from Gibco
                                                                                                                         Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                           Mammalia; Eutheria; Primates; Catarrhin1; Hor
1 (bases 1 to 460)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
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AI419942.1
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tg40dll.xl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:2111253 3' similar to TR:042400 042400 AXIN. ;, r
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                           quality sequence stop: 421.
Location/Qualifiers
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="DH10B"
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/clone_lib="Soares_NFL_T_GBC_S1"
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82.6%;
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Pred. No. 2.9e-72;
0; Mismatches 78;
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Search completed: June Job time: 15523 sec 6 2001,

Page 13

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Perfect score:
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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9b_pat2: *
9b_ph: *
9b_pl1: *
9b_pl2: *
9b_pl3: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIE

ç 10 11	8765	0 4 3 2 1	Result No.
308.2 227.2 163.4	365.8 337 308.2 308.2	369 369 69	Score
	99.1 91.3 83.5		% Query Match Length DB
184263 3485 3156	3016 3216 2538 3072	369 2825 2825 2825 191041	ength
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BIRCHMEIER WALTER (DE); BEHRENS JUERGEN (DE)
Location/Qualifiers
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Birchmeier, W. and Behrens, J.
CONDUCTINE PROTEIN AND A RELATED AGENT FOR DIAGNOSING
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BIRCHMEIER WALTER (DE); BEHRENS JUE
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Birchmeier, W. and Behrens, J.
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Functional interaction of an axin homolog, conductin, with beta-catenin, APC, and GSK3beta Science 280 (5363), 596-599 (1998)
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Behrens, J., Jerchow, B.-A., Wurtele, M.,
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PPLTPPNTLAQLEEACRRLAEVSKPQKQRCCVASQQRDRNHSAAGQAGASPFANPSLA
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REMHRSVKANGQVSLDHFPRTHRLPKEMTPVEPAAFAAELISRLEKLKLELESHRISLE
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/translation="MSSAVLVTLTPDDFSSFREDAPRPVPGEEGETPPCQPSVGKVQ
/translation="MSSAVLVTLTPDFSSFREDAPRPVPGEEGETPPCQPSVGKVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2825;
                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
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AC024114/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 cgagatggcatcaagaagcaacagatcggctcggtcatgtttgaccaggcacagaccgag 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TACATTGAGAACAACAGCGTTGTCTCCAAGCAGCTGAAGCCCGCCACCAAGACCTACATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tacattgagaacaacagcgttgtctccaagcagctgaagcccgccaccaagacctacata 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hosak, H., Hou, X., Huber, J., Jackson, L., Jia, Y., Kelly, J., Kelly, S., Kovar, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Martin, R., Massey, E., McLeod, M.P., Mei, G., Moore, S., Morgan, M., Morris, S., Neal, D., Nelson, A., Nguyen, R., Nguyen, N., Oguh, M., Parish, B., Neal, D., Nelson, A., Nguyen, R., Nguyen, N., Oguh, M., Parish, B., Perez, L., Retter, D., Say, J., Shen, H., Vasquez, L., Watlington, S., Williamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, A., Muzny, D.M., Rives, M., Scherer, S., Sodergren, E., Weinstock, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Metzker, M.L., Lewis, L.R., Hume, J., Edwards, C., Harris, C., Dederich, D., Thomas, S., Okwuonu, G., Carlock, C., Garner, T., Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brow Buhay, C., Bunac, C., Burkett, C., Chacko, J., Chen, G., Chen, Z., Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S., Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fernandez,C., Ferraguto,D., Forcum-Tansey,J., Gill,R.,
Gorrell,J.H., Gunaratne,P., Haller,G., Hernandez,J., Hogues,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC024114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Worley, K. and Gibbs, R.
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                      Center project name: MACA
Center clone name: RP23-278J12
Center clone name: RP23-278J12
Center clone name: RP23-278J12
Sequencing vector: M13; L08821
Chemistry: Dye-primer Bodiby: 95% of reads
Chemistry: Dye-reterminator Big Dye: 5% of reads
Assembly program: Phrap: version 0.990329
Consensus quality: 1780 bases at least Q40
Consensus quality: 179030 bases at least Q30
Consensus quality: 179030 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 191041)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 191041)
                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                            Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.
                                                                                                                                                                                                                                                                                                                                  ------ Project Information
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insert size: 180377; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A HTG 06-NOV-200 Clone RP23-278J12, WORKING DRAFT
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 30 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: Estimated insert size may differ from sequence length
        185024
187055
187155
188273
188373
188373
189635
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167355
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                                                                                                 182421
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86706
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Location/Qualifiers
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gap of
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                                                gap of unknown contig of 1118
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1g of 2031
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g of 7199 bp in langth
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g of 2842
f unknown
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of 6612
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of 5780
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unknown
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of 4682
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of 13875 bp in
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Bukaryota; Metazoa; Chordata; Craniata; Vertek
Bukaryota; Metazoa; Chordata; Craniata; Mi

1 (bases 1 to 3016)

2 hang. T., Fagotto, F., Hsu, W., Zeng, L., Gilbert
Jenkins, N.A., Warburton, D. and Costantini, F.

Properties of mouse Axin2 and human AXIN2: che
expression pattern, interaction with Axin and
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AF205889.1
                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus Axin2 (Axin2) mRNA, complete cds
                                                                                                                         Submitted (16-NOV-1999) Genetics & Development, University, 701 W168th St. HHSC 1416, New York,
                                                                                                                                                     Zhang, T. and Costantini, F. Direct Submission
                                                                                                                                                                                               Unpublished
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/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="11"
/clone="RP23-278J12"
a 43523 c 42989 g 51816 t
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/gene="Axin2"
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                                               /db_xref="taxon:10090"
/chromosome="11"
                                                                           organism="Mus musculus"
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367; Conser
                                  Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; F
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                       AF017757 3216 bp mRNA Rattus norvegicus GSK-3beta interacting
1 (bases 1 to 3216)
Yamamoto, H., Kishida, S., Uochi, T.,
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/codon_start=1
/product="Axin2"
/protein_id="AAF22800.1"
/db_xref="GI:6653586"
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REMHRSVKANGQVSLPHFPRTHRLPKEMTPVEPAAFAALISRLKLKLELESHSLE
ERLQQIREDEEKEGSEQALSSBOGADFVQHFALLPSGSYEEDPGTILDDHLSRVLTF
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OFCGSRGGTLPKRNAKGTEFGLIALSARDSGMSSAAGAPOLFGEEDRSODVWOWMLES
ERGSKSKFHSAQSIRKSYVLESARAAPGERVSKHHLLGASGHSRSVARAHPFTODPAM
PPLTPBNTLAQLEFACRALAFYSKPOKORCCVASQORDRNHSSAAGQACASFFANDSLA
PEDHKEPKKLASYHALQASELVVTYFFGCEEIFYRRMLKAQSLTLGHFKEQLSKKGNY
RYYFKKASDEFACGAVFEEIWDDETVLHWYEGRILGKVERID*

858 C 837 g 555 t
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stkmpvssnarrnedolgepegraspdspltmttkslhsllgddgatlfrtftleke
KCVDTLDFWFACNGFROMNLKDTKTLRVAKAITKRYIENUSVSSQLKFATKTYIRDG
IKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDIYLEYVRSGEENTAYMSNGGIGSL
KVLCGYLPTLNEEEEMTCADLKCKLSPTVVGLSSKTLRATASVRSTETAENGFRSFKR
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Pred. No. 3.6e-93;
0; Mismatches 2
 Ikeda, S.,
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                                                  Euteleostomi;
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Axil, a member of the Axin family, interacts with both glycogen synthase kinase 3beta and beta-catenin and inhibits axis formation of xenopus embryos
Mol. Cell. Biol. 18 (5), 2867-2875 (1998)
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Direct Submission
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namoto,H., Ikeda,S., Murai,H., Kishida,S. and
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                                                                                                                                                                                                                                                                                                                                                                  Conservative
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STKPMPVSSNARRNEDGLGEPBGRASPDSPLTWTKSLHSLLGDDGAXLFRTFLERE
KCVDTLDFWFACNGFROMNLKDTKTLRVAKAITKYLENVSVSKQLKPATKTYLRDG
KKVDDTLDFWFACNGFROMNLKDTKTLRVAKAITKYLENVSVSKQLKPATKTYLRDG
KKVDCTSVHEDQAQTEIQAVWEENAKVOFLTSDYLEVYRSGGENTAVMSNGGLGSL
KVLCGYLPTLNEEEEWTCADLKCKLSPTVVGLSSKTLRATASVRSTETAENGFRSFKR
SEPVNPYHVGSGYVFAPATSANDSELSSDALTDDSMSWTDSSVDGIPPYRMGSKKQLQ
REMHRSVKANGQVSLPHFPRTHRLPKEMTPVEPAFAPAELISRLEKLKLELESRHSLE
ERLQOITAEDEEKEGSEQALSSRDGAPVQHPLALLPSGSYEEDPQTILDDHLSRVLKTP
GCQSPGGRYSPRSRSPDHHHHHQOCHALLPTGGKLPEAACPLLGGKSFLTKCTTK
HVHHHYIHHHAVPKTKEEIEAEATQPVRCCLFGGTDYYCYSKCKSHSKPDEPLPGEQF
GCGSRGGTLPKRNTKGTEPGLALPAREGGMSSAACAPQLPGEEGDRSQDVWQWMLESER
QSKSKPHSTQSIRKSYPLESARAPPGERVSRHHLLGASGHPRSAARAPPTQDPAMPP
LTPPNTLAQLEEACRRLAEVSKPOKORCCVASQQRDRNHPATGQAGPTSFSNPSLASE
LTPPNTLAQLEEACRRLAEVSKPOKORCCVASQQRDRNHPATGGAGPTSFSNPSLASE
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YFKKASDEFACGAYFEEIWDDETVLPMYEGRILGKVERID*
1 914 c 872 9 570 t
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/db_xref="GI:3080759"
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/db_xref="taxon:10116"
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ATTCAGGCGGTGATGGAGGAAAATGCCTATCAGGTGTTCTTGACTTCTGACATATACCTC atccaggcagtgatggaggaaaatgcctaccaggtgttcttgacttctgacatttacctg

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DPVNPYHIGSGYVFAFAJTSANDSEISSDALTDDSMSMTDSSVGI PPYRYGSKKQLQR
EMHRSVKANGRVSLPHFFRTHLLPKEKMIPVEPBATFAAELISRLEKLKLEESRHSLEE
RLQQIREDEEREGSELTLNSREGAPTQHPLSLLPSGSYEEDPQTILDDHLSRVLKTPG
CQSPGVGRYSPRSRSPDHHHHHHSQYHSLLPPGGKLPPAAASPGACPLLGGKGFVTKQ
TTKHYHHHY LHHHAVPKIEELEAEATQRVHGCPGGGSEYCY SKCKSHSKAPETMPS
EQPGAQSTKKAYPLESARSPGERASATORVHGCPGGGSEYCY SKCKSHSKAPETMPS
EQPGAQSTKKAYPLESARSSPGERASRHLMGGNSGHPRTTPRAHLFTQDPAMPSLTP
BYTLAHLEEACRRLAEVSKPPKQRCCVASQQRDRNHSATVQTGATPFSNPSLAPEDHK
EPKKLAGVHALQASELTVTYFFCGEELIPYRMLKAQSLTLGHFKEQLSKKGNYRYYFK
KASDEFACGAVFEELMEDETVLPMYEGRILGKVERID"
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/protein_id="AAF22799.1"
/protein_id="AAF22799.1"
/protein_id="AAF22799.1"
/db_xref="G1:663584"
/translation="MS$AMLVTCLPDPSSSFREDAPRPPVPGEEGETPPCHHGGOGPG-/translation="MS$AMLVTCLPDPSSSFREDAPRPPVPGEEGETPPCHHGGOGPG-/translation="MS$AMLVTCLPDPSSSFREDAPRPVPGEEGETPPCHHGGOGPG-/translation="MS$AMLVTCLPDPSSSFREDAPRPVPGEEGETPPCHHGGOGPG-/translation="MS$AMLVTCLPDPSSSFREDAPRPVPGEEGETPPCHHGGOGPG-/translation="MS$AMLVTCLPDPSSSFREDAPRPVPGEEGETPPCHHGGOGPG-/translation="MS$AMLVTCLPDPSSSFREDAPRPVPGEEGETPPCHHGGOGPG-/translation="MS$AMLVTCLPDPSSSFREDAPRPVPGEEGETPPCHHGGOGPG-/translation="MS$AMLVTCLPDPSSSFREDAPRPVPGEEGETPPCHHGGOGPG-/translation="MS$AMLVTCLPDPSSSFREDAPRPVPGEEGETPPCHHGGOGPG-/translation="MS$AMLVTCLPDPSSSFREDAPRPVPGEEGETPPCHHGGOGPG-/translation="MS$AMLVTCLPDPSSSFREDAPRPVPGEEGETPPCHHGGOGPG-/translation="MS$AMLVTCLPDPSSSFREDAPRPVPGEEGETPPCHHGGOGPG-/translation="MS$AMLVTCLPDPSSSFREDAPRPVPGEEGETPPCHHGGOGPG-/translation="MS$AMLVTCLPDPSSSFREDAPRPVPGEEGETPPCHHGGOGPG-/translation="MS$AMLVTCLPDPSSSFREDAPRPVPGEEGETPPCHHGGOGPG-/translation="MS$AMLVTCLPPSSSFREDAPRPVPGEEGETPPCHHGGOGPG-/translation="MS$AMLVTCLPPSSSFREDAPRPVPGEEGETPPCHHGGOGPG-/translation="MS$AMLVTCLPPSSSFREDAPRPVPGEEGETPPCHHGGOGPG-/translation="MS$AMLVTCLPPSSSFREDAPRPVPGEEGETPPCHHGGOGPG-/translation="MS$AMLVTCLPPSSSFREDAPRPVPGEEGETPPCHHGGOGPG-/translation="MS$AMLVTCLPPSSSFREDAPRPVPGEEGETPPCHHGGOGPG-/translation="MS$AMLVTCLPPSSSFREDAPRPVPGEEGETPPCHHGGOGPG-/translation="MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"-""MS$AMLVTCLP"-"MS$AMLVTCLP"-"MS$AMLVTCLP"
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/db_xref="taxon:9606"
/chromosome="17"
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/note="similar to ESTs 823683 and 446378"
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AF078165.1 GI:4454790
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99168905
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Direct Submission
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RENDOJREDEREGSELT LUSREGAPTOH PLSLLPSGS YEEDPOI I LDDHLSRVLKTP
GCQS PGVGRYSPRSRSPDHHHHHSQYHSLLPPGGKLPPAAASPGACCHLJGGKGFVK
QOTKHYHHHY LHHHAVKTKEEL EABATQRVHGFCPGGSEYYCYSKCKSHSKAPETMP
SEQFGGSRGSTLPKRNGKGTEPGLALPAREGGAPGAALQLPEEGDRSQDVWQWML
                      GNYRYYFKKASDEFACGAVFĒEIWEDETVLPMYEGRILGKVERID"
1 838 c 883 g 582 t
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KVVCGYLPTLNEEEEWTCADFKCKLSPTVVGLSSKTLRATASVRSTETVDSGYRSFKR
SDPVNPYHIGSGYVFAPATSANDSEISSDALTDDSMSWIDSSVDGIPPYRVGSKKOLQ
                                                                PAMPPLTPPNTLAGLEEACRRLAEVSKPPKQRCCVASQQRDRNHSATVQTGATPFSNP
SLAPEDHKEPKKLAGVHALQASELVVTYFFCGEEIPYRRMLKAQSLTLGHFKEQLSKK
                                                                                                        ESERQSKPKPHSAQSTKKAYPLESARSSPGERASRHHLWGGNSGHPRTTPRAHLFTQD
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yTkpmsyssntrrnedglgepegraspdspltrwTkslhslldqdqbaxlfrtflere
kCydtldfwfaCngfrqmnlkdTkTlryakaTykRyIennsIyskQkkpaftkTyIrQ
                                                                                                                                                                                                                                                                                                                                                                /product="conductin"
/protein_id="AAD20976.1"
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Query Match Best Local Similarity

83.5%; 89.7%;

Score 308.2; DB 88; Pred. No. 7.7e-77;

Length 3072;

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Worley,K.C.

Direct Submission

Submitted (07-OCT-1998) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Oct 1, 1998 this sequence version replaced gi:3482897.
                                                                                                                                                            Submitted (01-OCT-1998) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA (bases 1 to 184263)
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Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality does not meet this standard, it will be indicated in the annotation.

The repeat regions shown were identified using RepeatMasker by Adrian Smit.

Sequence similarities were identified using Powerblast by Jinghui  $\mathtt{Z}\mathsf{hang}$  .

Exon/Intron boundaries of identified genes were chosen if there were canonical splice junctions that maintained sequence continuity across the splice junctions.

Location/Qualifiers

repeat\_region source repeat\_region /rpt\_famil 14538. .14 4032. /rpt\_family-"MLT1f"
complement(13861..14169)
/rpt\_family-"AluSx" /rpt\_family="(CA)n" 8392. .8694 /rpt\_family="AluSx" 7129. .7410 complement(17311.
/rpt\_family="L2" /rpt\_t 15211. /rpt\_1 11922 /rpt\_family="AluSx"
complement(11332. . /rpt\_family="GC\_rich"
5406. .5436 /rpt\_family="MIR" 17679. .17977 /rpt\_family="Alux" 15682. .15827 complement(12591. /organism="Homo sapiens" /db\_xref="taxon:9606" /clone="GSHB-531117" /rpt\_family-"AluSg" /chromosome="xp22-16-17" /rpt\_family="Alusx" /rpt\_family="(CCCCG)n" rpt\_family="GC\_rich" rpt\_famil rpt\_family="GC\_rich" t\_fami \_famil \_famil \_family="AluJ" famil family-"AluJ" \_famil tamil \_family-"(GAAA)n" .4073 (ly-"Alusg" 2218 y="L1PA9" y="AluSq" .y="AluSq" y-" (TAAA)n" y-"MIR" y="AluSp" y="AluSq" .12905)

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complement (25147 . .2529)
/rpt_family="AluJo"
complement (25699 . .25985)
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complement(30433. .30589)
/rpt_family="MLT1AA"
complement(30640
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complement(26521: .26812)
/rpt_family="x"
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/rpt_family="LTR16C"
complement(33298..33423)
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/rpt_family="(CAAA)n"
complement(40374. .40687)
/rpt_family="AluSx"
41491. .41619
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complement(35781..35902)
/rpt_family="FLAM_C"
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/rpt_family="AluSx"
complement(29910. .30126)
/rpt_family="MLT1A2"
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complement/10070
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/rpt_family="L2"
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/rpt_family="AluJo"
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complement(2)(/^
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2 (bases 1 to 3485)
2 (bases 1 to 3485)
Birect Submission
Submitted (09-SEP-1999) to the DDBJ/EMBL/GenBank databases. Toshio
Hirano, Biomedical research center, Osaka Univ. Med. scool,
Department of Molecular Oncology; 2-2, Yamadaoka, Suita, Osaka
                                                                                             Shimizu,T., Yamanaka,Y., Ryu,S.L., Hashimoto,H., Yabe,T., Hirata,T., Bae,Y.K., Hibi,M. and Hirano,T. Cooperative roles of Bozozok,/Dharma and Nodal-related proteins the formation of the dorsal organizer in zebrafish the formation of the dorsal organizer in zebrafish Mech. Dev. 91 (1-2), 293-303 (2000)
                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi Cypriniformes; Cyprinidae; Rasborinae; Danio.
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GEEIPYRRMMKTHSLTLGHFKEQLRKKGNYRYFFKRASDEFECGAVFEEVWDDCTVLP
MYEGKILGKVDRMD"

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SPGLLRHSPRSRSPEQRPLPRGGLSTRSQSSSMNGYVPAKTFISRQSTKHIHHHYIHH
HAGPKSKEQIEVEATQRVQCLCHGTSECCTAPYIRSRSLGRDQCASPAEVALGHSSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RDNIKROQIDSAMFDQAQMEIQTAMEENAYQMFLTSDIYLEYVRTGCENPSHVNPNGL
GGLKLYCGYLFTLNEEEEWSCNDFKARALATVGLLSAKTLRSPPDLRAYEALEKGYRSY
RRSDDGNPNRFTSGYSFAPATSANDSEVSSDALTDDSMSMTDSSVDAIPPYKLGSKKQ
LQREMQRNMRNNGQVSLPPFPRTRRPPKEMTPVEPAAFAAQLIARLERLKREQETMSS
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297. .2735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKRLCKSGEEVNMEGLENSLLQLPADSTDRSQNVWQWILESDRQTKHKPHSTQNVKKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="BAA92440.1"
/db_xref="GI:7229080"
/translation="MNRTLTDPMVSSFREDDPRPPVPGEEGETTCHHPSKLAMMRPKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Danio rerio"
/db_xref="taxon:7955"
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  229 aagacctacatacgagatggcatcaagaagcaacagatcggctcggtcatgtttgaccag
                                                                                                                                                                                                                                                61
                                                                                                                                               aggcagatgaacctg-----aaggataccaaaactttgcgagtggccaaagcaatc 171
                                                                                                                                                                                                                               ttcctggagagggagaaatgtgtggatacgctggacttctggttttgcttgtaatgggttc 120
                                                                                                                                                                                                                                                                                      TGGGCCGAGTCGCTGCACTCCTTGCTGGACGATCAAGACGGTATCAATCTCTTCAGGACT 569
                                                                                                                                                                                                                                                                                                            tggaccaagtctttacactccttgttgggtgaccaggatggtgcatacctcttccggact 60
                                          TACAAAAAGTACATTCTCGACAACAACGGCATTGTGTCCCGGCAGATCAAACCAGCCACA
                                                                             tataagaggtacatt---gagaacaacagcgttgtctccaagcagctgaagcccgccacc 228
                                                                                                                        AGGAAGCTGGAGCCGTGTGTGTCCAATGAGGAAAAAAGACTCAAACTGGCAAAAGCCATT
                                                                                                                                                                                                           TTCCTGAAACAGGAGGACTGTGCGGATCTGCTGGACTTCTGGTTTGCCTGCAGCGGCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus
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1 (bases 1 to 3156)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chicken
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KPATKSFIKOCYMKLQIDPDMEDQAQTEIQCMIEDNTYELFIKSDIYLEYTRTGGESP
KYSDESGSGTGKGLEGYLPTLNEDEEWKCDQDTEPEASRDSAPSSRLTQKLLLETA
TQRATISTRYSEGREERHGSWREDYNRYYVNTGYAMAPATSANDSEQSMSSDADTMS
LTDSSIDGIPPYRLRKQHRREMQESAKANGRVPLPHIPRTYRMPKDIHVEPEKFAAEL
INRLEEVQKEREAEEKLEERLKRVRAEEEGEDADISGGESVISKMPSAQDFHHFAPR
YSEMGCAGMQMRDAHEENPESILDEHVQFVMKTPGCOSPGPGHRSKPRSPESGHIGK
LSGTLGTIPPGGKKHTYKSGMKLDAANLYHHKHYYHHIHHSMMKPKEQIEAEATQRV
QNSFAMNVDSHNYATKSRNYSENLGMAPVPMOSLGYSGKASLLSKRNIKKTDSGKSDG
ANYEMPGSPEDVERNQKILQWIIESISRHKKTHGSGVKKQLSHDMVRPLSIER
PVAVHPWVSAQLRMVVQDSHPFIQDFYMPLDFABNPLTQLEEARRRLEEEEKRAGKLP
LKQRLKPOKRPGSGASQPCENIVVAYYFCGEPIPYRTLVKGRVVTLGQFKELLTKKGN
YRYKKVSDEFDCGVVFEEVNEDDTILPIFEEKIIGKVEKID*
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YSSKSDAVRNETSTATPRRSDLDLGYEPEGSASPTPPYLKWAESLHSLLDDQDGINLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutation due
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/db_xref="GI:2252818"
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/db_xref="taxon:9031"
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Pred. No. 9e-36;
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JOURNAL REFERENCE AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vasicek,T.J., Tilghman,S.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3411)
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                       REPVNPYYVNAGYALAÞATSANDSEQQSLSSDADTLSLTDSSVDGIPPYRIRKQHRRE
MQESAQVNGRVPLPHIPRTYRVPKEVRVEPQKFAEELIHRLEAVQRTREAEEKLEERL
KRVRMEEEGEDGDPSSGPPGPCHKLPPAPAWHHFPPRLCWTWACAGLRDAHEENPESI
                                                                                                      /Protein_id="AAC51624.1"
//db_xref="G1:2253820"
//db_xref="G1:225382
                                                                                                                                                                                                                                                                                                                                                                                             /note="contains RGS domain
may inhibit embryonic axis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mutation due
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adults"
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/map="16p13.3"
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/db_xref="taxon:9606"
LDEHVQRVLRTTGRQSPGPGHRSPDSGHVAKMPVALGGAASGHGKHVPKSGAKLDAAG
                                                                                                                                                                                                                                                                                                                                      /product="axin"
                                                                                                                                                                                                                                                                                                                                                                      /codon_start=2
                                                                                                                                                                                                                                                                                                                                                                                                                           /function="may inhibit embryonic axis formation"
/note="contains RGS domain and Daughterless similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="AXIN"
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640 Memorial Drive, Cambridge, MA
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BASE COUNT ORIGIN REFERENCE AUTHORS COMMENT VERSION KEYWORDS RESULT 13 HS415C1/c SOURCE ACCESSION DEFINITION Query Match Best Local S Matches 258 TITLE JOURNAL 425 485 121 365 665 605 545 172 725 349 289 229 61 1 tggaccaagtotttacactcottgttgggtgaccaggatggtgcatacctcttccggact 60 AGGAAGCTGGAGCCCTGTGACTCGAACGAGGAGAAGAGGCTGAAGCTGGCGAGAGCCATC ttoctggagagggagaaatgtgtggatacgctggacttctggtttgcttgtaatgggttc 120 TGGGCTGAGTCACTGCATTCCCTGCTGGATGACCAAGATGGGATAAGCCTGTTCAGGACT 424 aagacctacatacgagatggcatcaagaagcaacagatcggctcggtcatgtttgaccag tataagaggtaca---ttgagaacaacagcgttgtctccaagcagctgaagcccgccacc TTCCTGAAGCAGGAGGCTGTGCCGACTTGCTGGACTTCTGGTTTGCCTGCACTGGCTTC GATATTTATTTGGAATAT 742 gacatttacctggaatat 366 gcacagaccgagatccaggcagtgatggaggaaaatgcctaccaggtgttcttgacttct aggcagatg---l Similarity 258; Conserv Clonerequest@sanger.ac.uk
On Apr 8, 1998 this sequence version replaced gi:2578104.
IMPORTANT: This sequence is the entire insert of clone 415C1. The
true left end of clone 415C1 is at 1 in this sequence. The true
right end of clone C333B10 is at 8634.
The true left end of clone C367G8 is at 23683.
The true left end of clone C367G8 is at 23683.
Higgs D.R.; Flint J. unpublished. MRC Molecular Haematology Unit,
Institute of Molecular Medicine, Oxford.

415C1 came from the Los Alamos flow sorted human Chromosome 16 Submitted (23-OCT-1997) Chromosome 16 Project Group (http://www.sanger.ac.uk/HGP/Chr16/) Sanger Centre, Wel Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. enquires: humquery@sanger.ac.uk Clone requests: Eutheria; Primates; Cata; 1 (bases 1 to 23786) Smye,R. and Lightning,J. Direct Submission Human DNA sequence from cosmid 415C1 from a contig the short arm of chromosome 16, spanning 2Mb of 16p EST and CpG islands. Homo sapiens Z98272.1 GI:3036780 16p13.3; CpG. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo human. 752 Conservative b SYRYYFKKVSDEFDCGVVFEEVREDEAVLPVFEEKIIGKVEKVD" RHRRTGHGSSGTRKPQDHENSRELSLEHPWAGPQLRTSVQPSHLFIQDPTMPPHPAPN PLTQLEEARRRLEEEEKRASRAPSKQRYVQEVMRRGRACVRPACAPVLHVVPAVSDME LSETETRSQRKVGGGSAQPCDSIVVAYYFCGEPIPYRTLVRGRAVTLGQFKELLTKKG LHHHRHVHHHVHHSTARPKEQVEAEATRRAQSSFAWGLEPHSHGARSRGYSESVGAAP NASDGLAHSGKVGVACKRNAKKAESGKSASTEVPGASEDAEKNQKIMQWIIEGEKEIS 1010 c ---acctgaaggataccaaaactttgcgagtggccaaagcaatc 171 43.7%; 1066 g Score 161.2; | Pred. No. 3.8e 0; Mismatches 0 582 t 415C1 from a contig from the tip of spanning 2Mb of 16p13.3. Contains 2; DB 8 108; 88; 1 others Indels Length 3411; 23-NOV-1999 Wellcome 12; E-mail Gaps 484 724 348 664 288 604 228 544 Trust 2

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BASE COUNT
ORIGIN
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Query Match 43.7%;
Best Local Similarity 68.3%;
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/note="Alux repeat: n
incomplete repeat"
a 7039 c 6768 g
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/note="match: mouse 5'
6320. .6615
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23258. .23548
/note-"AluY repeat: matches 298.
23549. .23786
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/note="AluSg repeat: matches 1.
14042. .14348
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/note="AluJb repeat: matches 301. .21 of consensus.incomplete repeat"
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/map="16p13.3"
/clone="LA16-415C1"
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/db_xref="taxon:9606"
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Location/Qualifiers
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16370. .16505
/note="AluSq repeat: matches 1.
incomplete repeat"
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15009. .15277
/note="AluJb repeat: matches 1.
lncomplete repeat"
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'Moote="AluJb repeat: matches 10.
Ancomplete repeat"
9773. 11262
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te="AluSx_repeat:
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   Score 161.2; DB 91;
Pred. No. 4.7e-35;
0; Mismatches 108;
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                                                                                                                                                                                                                                                                                                     Submitted (04-NOV-1996) Sanger Centre, Hinxton, Cambridgeshire, CB10 1RQ, UK. E-mail enquires: humpub@sanger.ac.uk IMPORRANT: This sequence is the entire insert of clone 333B10. The true left end of clone 333B10 is at 1 in this sequence. The true right end of clone 419Cl is at 10356.

The true right end of clone 333B10 is at 35054.

333B10 is from a 280kb clone contig extending from the telomere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     z81450.1
16p13.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human
                                                                                                                                                                                                             Institute of Molecular Medicine, Oxford.
333B10 came from the Los Alamos, flow sorted human Chromosome
libraries constructed by Norman Doggett (unpublished).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 35054)
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                                                                                                                                                                                                                                                                            Daniels R, Flint J, Higgs D.R. unpublished. MRC Molecular Haematology
                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              310 35054 bp DNA PRI 23-NOV-1999
DNA sequence from cosmid 333B10 from a contig from the tip of nort arm of chromosome 16, spanning 2Mb of 16p13.3 contains
    74. .292
/note="AluSx repeat:
incomplete repeat"
                                               /note="AluJb repeat:
incomplete repeat"
                                                                                          /clone="LA16-333B10"
/clone_lib="LA16"
                                                                                                                       /chromosome="16"
/map="16p13.3"
                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:1666062
                    matches
                                                                matches
                                                                234.
                     82.
                    .300
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                     consensus;
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                           3151. .3242
/note="2 copies of 46
}418. .3558
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3050. .3155
/note="2 copies of 53
                                                                                    note="match: 3' EST AA007531 clone 429378; match: 9202. .>19484; Paired with EST AA007530 matching
                                                                                                                                                          note="MER44A repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="MER44A repeat: matches 313. .178 of consensus"
 note="Alux repeat: matches 1.
7136. .17272
                                                                                                                    'note="AluJo repeat: matches 294. 5755. .>16037
                                                                                                                                                                                                                                                                                                                                                          note="AluSp repeat: matches 2. 3215. .13515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="3 copies of 58 mer 98 % conserved" 240. .7360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="AluJb repeat: matches 193.
ncomplete repeat"
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ote="AluY repeat: matches 1.
complete repeat"
                                                                                                                                                                                                                     665. .13834
ote="Alusx repeat: matches 302.
complete repeat"
835. .14153
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te="Alux repeat: matches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e="AluSg repeat: matches 294. .1 of consensus"
                                                                                                                                                                                                                                                                                                                            e="Alux repeat: matches 1.
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. .6036
                                                                                                                                                                                                                                                                                              e="TAGCT consensus
2. .13568
                                                                                                                                                                                                                                                                                                                                                                                                    e="AluJb repéat: matches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a="AluSq repeat: matches 1. .302 of consensus"
. .10635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .889
                                                                                                                                                                                                                                                                                 ="7bp from single read"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ="20 copies of 2 mer 85 % conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "2 copies of 51 mer 100 % conserved" .5917
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                                                          .16246
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               .301 of consensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .294 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluJo repeat: matches 13.
                                                                                                                    'note="AluY repeat:
                                                                                                                                                                                                                                                                                                                                                         note-"pTR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ncomplete repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ce="match:
 43.7%;
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                                                           8620 g
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complement(<17999. .20054)
/note="match: 5 'EST AA007530 clone 429378; Paired EST AA007531 matching this clone; contains L1 repeated."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="pTR5 repeat: matches 743. .1641 of consensus" 25932. .26608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24246. .24281
/note="12_copies of 3
                                                                                                             /note="AluJo repeat: matches 2.
33038. .33342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="AluSp repeat: matches
17566. .17634
/note="AluJb repeat: matches
incomplete repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="AluSx repeat: matches 132. .296 of consensus;
incomplete repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Alux repeat: matches 1. .301 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="A,C rich region"
                                          'note="AluJb repeat: matches 301.
                                                                                                                                                                                                                             note="AluSp repeat: matches 303. .1 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                           'note="AluSx repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="FLAM_C repeat: matches 1. .133 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03226. .23280
Onote="MaluSp/q repeat: matches 169. .121 of consensus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="AluSg repeat: matches 2.
1089. .21390
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13. .21738
te="13.copies of 2 mer 92 % conserved"
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20. .23259
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                                                                                                                                                                                                                                                                                             e="AluY repeat: matches 1. .297 of consensus"
6. .28587
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                                                                                        matches 1. .301 of consensus"
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Goodwin, L., Bryant, J., Tesmer, J., Meincke, L., Longmire, J., White, S., Ueng, S., Tatum, O., Campbell, C., Fawcett, J., Maltbie, M., Misra, M. and Deaven, L. TITLE Direct Submission JOURNAL Submitted (30-JUN-1998) Center for Human Genome Studies, DOE Joint Genome Institute, Los Alamos National Laboratory, MS M888, Los Alamos, NM 87545, USA Location/Qualifiers source /organism="Homo sapiens" /db_xref="taxon:9606" /clone="RT290" /chromosome="16"	AUTHORS Ricke, D.O. AUTHORS Comparison Analysis (SCAN) System  JOURNAL Unpublished  REFERENCE 2 (bases 1 to 39170)  AUTHORS Ricke, D.O. AUTHORS Ricke, D.O. Bruce, D., Mundt, M., Doggett, N., Munk, C., Saunders, E.,  ROSINSON, D., Jones, M., Buckingham, J., Chasteen, L., Thompson, S.,  Control of the contr	Manmalia; Eutheria; Primates; Catarrhini; Hominidae 1 (bases 1 to 3970) Ricke, D.O., Bruce, D., Mundt, M., Doggett, N., Munk, C., Robinson, D., Jones, M., Buckingham, J., Chasteen, L., Goodwin, L., Bryant, J., Tesmer, J., Meincke, L., Longm White, S., Ueng, S., Tatum, O., Campbell, C., Fawcett, J. Misra, M., and Deaven, L.	RESULT 15 AC005202/c AC005202/c AC005202/c AC005202 AC005202 AC005202 VERSION AC005202 VERSION AC005202 VERSION AC005202 AC005202 VERSION AC005202 AC005202 AC005202 AC005202 VERSION AC005202.1 GI:3273384 ACVERSION AC	Qy 289 gcacagaccgagatccaggcagtgatggaggaaaatgcctaccaggtgttcttgacttct 348	121 aggasgtaacctgaaggataccaaacttgcgagtggccaaagcaatc   1   1   1   1   1   1   1   1   1	Best Local Similarity 68.3%; Pred. No. 4.9e-35; Matches 258; Conservative 0; Mismatches 108; Indels 12; Ga  1 tygaccasgtctttacactccttgttgggtgaccaggatggtgcatacctcttccggact
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X23370

X23370 standard; cDNA; 2523

ВP

17-JUN-1999 (first entry)

X23370;

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Tumor-suppressing protein conductin diagnosis of tumors
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                           WPI; 1999-214706/18
P-PSDB; W93570.
                                                     Behrens J, Birchmeier
                                                                                         02-SEP-1997;
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                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                               Human conductin cDNA.
                                                                       (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
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                                                misc_signal
                                                                                       CDS
                                                                                                                                                                Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour; therapy; cytoplasmic degradation; blockade; Wnt signalling pathway; Wingless signalling pathway; Adenomatous Polyposis Coli; APC;
                                                                                                                            Homo sapiens
                                                                                                                                                                                                                      Human conductin DNA.
                                                                                                                                                                                                                                              17-JUN-1999
                                                                                                                                                                                                                                                                                                   X23369 standard; cDNA;
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446..814
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Pred. No. 1.1e-110;
Mismatches 0;
        of G-protein
in Claim 19"
                     signalling
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumor-suppressing protein conductin diagnosis of tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-214706/18
P-PSDB; W93569.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2825 BP;
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                      atccaggcagtgatggaggaaaatgcctaccaggtgttcttgacttctgacatttacctg
                                                                                                                     cgagatggcatcaagaagcaacagatcggctcggtcatgtttgaccaggcacagaccgag
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atccaggcagtgatggaggaaaatgcctaccaggtgttcttgacttctgacatttacctg
                                                                                                                                                                                     tacattgagaacaacagcgttgtctccaagcagctgaagcccgccaccaagacctacata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conjunction with APC, acts as a tumour
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described in Claim
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Pred. No. 1.1e-110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                    Nucleic acids encoding mutant and wild type Axin and colloquous derived from them are useful for detecting mutations in the Axin gene and for determining whether a subject is likely to develop cancer (including breast, colorectal, castrointestinal, esophageal, carcinomas or melanomas). The wild type Axin and homologues of Axin are useful for treating subjects who are likely to develop cancer (thyroid carcinomas). The nucleic acids are also useful for diagnosing cancer and for detecting mutations in cancerous cells. Wild type Axin, its antisense conjugations are also useful for diagnositions are also useful for cancer. The compositions are also useful for compounds form pharmaceutical compositions of treating cancer by inhibiting tumorigenesis (by inducing degradation of beta-catenin). The nucleic acid encoding Axin acts through cancer regulation of the Wnt pathway in the Nieuwkoop Center.
                                                         Matches
                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Constantini F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                       Newly isolated nucleic acid encoding "axis inhibition" protein (Axin) - useful for detecting, diagnosing and treating cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYCO ) UNIV COLUMBIA NEW YORK
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diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
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                                                                                                                               Sequence 3411
                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Figure 10A-10B; 95pp; English.
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tgggctgagtcactgcattccctgctggatgaccaagatgggataagcctgttcaggact 424
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                                                       h 43.7%;
Similarity 68.3%;
58; Conservative
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                                                                                                                               BP; 752 A; 1010 C; 1066 G;
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                                                      Score 161.2; DB 2
pred. No. 1.3e-42;
0; Mismatches 108
                                                                                                                               582 T; 1 other;
                                                                                    DB 20;
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Nucleic acids encoding mutant and wild type Axin and oligonucleotides derived from them are useful for detecting mutations in the Axin gene and for determining whether a sullikely to develop cancer (including breast, colorectal, gastrointestinal, esophageal, carcinomas or melanomas). The type Axin and homologues of Axin are useful for treating sul
                                                                                                                                                                                                                                                                                                                       CDS
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                                                                                                                                                                                                                                                                                                                                                                                    Axin; cancer; breast cancer; colorectal cancer; gastrointestinal cancer; esophageal cancer; carcinoma; diagnosis; treatment; therapy; thyroid carcinoma; tumor
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                                                                             Claim
                                                                                                 Newly isolated nucleic acid encoding "axis inhibition" (Axin) - useful for detecting, diagnosing and treating
                                                                                                                                   P-PSDB;
                                                                                                                                                                  Constantini F,
                                                                                                                                                                                                             10-JUL-1997;
                                                                                                                                                                                                                                  09-JUL-1998;
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                                                                                                                                                                                       (UYCO ) UNIV COLUMBIA NEW YORK
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                                                                            Figure 9A-9B;
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tumorigenesis;
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Best Local :
               10-AUG-1993;
27-OCT-1994;
05-JUN-1996;
                                                                                                                                                                    CR2; human; antibody; cytokine response gene; cytostatic; anti-allergic; immunosuppressive; antimicrobial; therapy; cell proliferation; treatment; cell differentiation; cancer; immune disease; rheumatologic disease; transplant rejection; anti-infective; ss.
                                                   20-NOV-1991;
                                                                          05-JUN-1996;
                                                                                                  02-MAY-2000
                                                                                                                         US6057427-A
                                                                                                                                                 Unidentified
                                                                                                                                                                                                                                Cytokine response gene-related cDNA sequence (Seq
                                                                                                                                                                                                                                                           18-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                      1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         who are likely to develop cancer (thyroid carcinomas). The nucleic acids are also useful for diagnosing cancer and for detecting mutations in cancerous cells. Wild type Axin, its antisense molecule and identified compounds form pharmaceutical compositions in the treatment of cancer. The compositions are also useful for treating cancer by inhibiting tumorigenesis (by inducing degradation of beta-catenin). The nucleic acid encoding Axin acts through negative regulation of the Wnt pathway in the Nieuwkoop Center.
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             91US-0796066.
93US-0104736.
94US-0330108.
96WO-US08992.
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Pred. No. 4.6e
0; Mismatches
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ches 116;
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Best Local
          RATH.1.; RGS gene family; regulator of G-protein signalling; human; regulation; activation; modulation; signal transduction; T Cell; T helper cell; treatment, autoimmune disorders; arthritis; infection graft rejection; asthma; allergy; neoplasm; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel isolated antibody or antibody fragment (I) which selectively binds to a polypeptide encoded by cytokine response gene 2 (CR2) and modulates CR2 activity. The products of the invention have cytostatic, anti-allergic, immunosuppressive and antimicrobial activity. The antibodies are useful as therapeutic agents for regulating cellular proliferation and differentiation and for treating all kinds of cancers, immune diseases such as allergic, autoimmune, and rheumatologic diseases, transplant rejection, and as anti-infectives for fighting viral, bacterial, parasitic and fungal infections. This sequence is
                                                                                   Human
                                                                                                              11-SEP-1998
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51.1%;
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Pred. No. 2.9e
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2.9e-08;
nes 168;
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                          arthritis; infection;
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Best Local :
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P-PSDB; W59294.
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04-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New activated T helper cell specific gene, RATH - used for developing products for treating e.g. autoimmune disorders, arthritis, graft rejection, asthma, allergy, infections or neoplasms
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96US-0726228.
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'Pred. No. 3.2e-08;
0; Mismatches 168;
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                                                                                                                                                                                                                                                                                                                                                         Recombinant production of PIGI-1 allows the study of the structure, function and role in oncogenesis of the protein. PIGI-1 and nucleic acid encoding it can also be used to develop products for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T11418;
                                                                                                                                                                                                                                                                                                                       Sequence 2383 BP;
                                                                                                                                                                                                                                                                                                                                             use in treating tumours and cancer and in the diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Figure 6; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid encoding p53 response used to develop prods. for the study, diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Buckbinder L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09601907-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Response protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  p53 response
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BRIM ) BRISTOL-MYERS SQUIBB CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-JUL-1994;
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                                                                                                                                                                 276
                                                                                                                                                                              61 ttcctggagagggagaaatgtgtggatacgctggacttctggttttgcttgtaatgggttc 120
                                                                                                                                                                                                                                                                          Match 15.0%;
Local Similarity 51.1%;
                                                                                                                                                                                                                           1 tggaccaagtctttacactccttgttgggtgaccaggatggtgcatacctcttccggact 60
atccaggcagtgatggaggaaaatgcctaccaggtgttcttgacttctgacatttacctg
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                                                                                                                                aggcagatgaacctgaaggataccaaaactttgcgagtggccaaagcaatctataagagg 180
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                                                                                                                                                                                                           tggagagagtcgttcgacctgctgctgagcagtaaaaatggagtggctgccttccacgct 335
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                        ctgacgaggatgaacctgcagactgccacagccacatgctttgatgcggctcaggggaag
                                       cgagatggcatcaagaagcaacagatcggctcggtcatgtttgaccaggcacagaccgag
                                                                     ttcatttg----cagtgaggcccctaaagaggtcaacattgaccatgagacccgcgag
                                                                                   tacattgagaacaacagcgttgtctccaagcagctgaagcccgccaccaagacctacata
                                                                                                                                                                                                                                                               185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R89895
                                                                                                                                                                                                                                                                                                                                                                                                                                and cancer
                                                                                                                   -agaagatccgatcagctaccaagctggcctccagggcacaccagatctttgaggag
                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94US-0274318
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                                                                                                                                                                                                                                                                                                                      561 A; 603 C; 657 G; 562 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     þ
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                                                                                                                                                                                                                                                            Score 55.2; DB 17; Pred. No. 5.7e-08; 0; Mismatches 168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Talbott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein PIGI-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumour; p53;
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                                                                                                                                                                                                                                                                                    Length 2383;
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Best Local
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05-JUN-1995;
05-JUN-1995;
05-JUN-1995;
05-JUN-1995;
05-JUN-1995;
                                                                                                       8 Clones (T43376-83) contg. interleukin-2 (IL-2)-induced genes were isolated from a human IL2 receptor-positive T blast cell cDNA library following IL-2 stimulation. 6 Of these ligand-induced genes (CRI, 2, 3, 5, 6, 8) are novel. CRI expression is rapidly and transiently induced by IL-2, and mRNA expression is suppressed by elevated intracellular cAMP. It encodes an intracellular protein (W08133) that shows homology to GOS8 and BL-34. CR genes and polypeptides (W08133-40) can be used as diagnostic or therapeutic agents; CR gene sequences can be used to detect and treat allelic
                                                                                Sequence 2406 BP; 565 A; 621 C;
                                                                                                                                                                                                  Disclosure; Page 11-12; 81pp; English.
                                                                                                                                                                                                                   Cytokine response proteins and genes - used in the detection and therapy of diseases caused by a mutation in the CR coding region
                                                                                                                                                                                                                                                                          Beadling C,
                                                                                                                                                                                                                                                                                                                                                                           05-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytokine response gene; CR1; interleukin-2; IL-2; ligand-stimulated gene expression; diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                             12-DEC-1996
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    299
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                                               Local Similarity
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            tggaccaagtctttacactccttgttgggtgaccaggatggtgcatacctcttccggact 60
tggagagagtcgttcgacctgctgctgagcagtaaaaatggagtggctgccttccacgct 358
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                                                                                                                                                                                                                                                 W08133
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                                      Conservative
                                                                                                                                                                                                                                                                           Smith KA;
                                                                                                                                                                                                                                                                                                            95US-0465585.
95US-0461379.
95US-0462337.
95US-0462390.
95US-0463074.
95US-0463081.
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                                              15.0%;
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Pred.
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                                     Mismatches 168;
                                                                                 656 G;
                                             55.2; DB 18;
No. 5.7e-08;
                                                                                 564 T; 0 other;
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This invention describes a novel isolated antibody or antibody fragment (I) which selectively binds to a polypeptide encoded by cytokine response
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20-NOV-1991;
10-AUG-1993;
27-OCT-1994;
                                                                                                  WPI; 2000-338623/29.
P-PSDB; Y87952.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CR2; human; antibody; cytokine response gene; cytostatic; anti-allergic; immunosuppressive; antimicrobial; therapy; cell proliferation; treatment cell differentiation; cancer; immune disease; rheumatologic disease; transplant rejection; anti-infective; CR1; ss.
                                      Novel antibody or antibody fragment which selectively binds polypeptide encoded by cytokine response gene 2\,
                                                                                                                                                         Beadling
                                                                                                                                                                                                                                         05-JUN-1996
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Example IV; Column 75-78; 66pp; English.
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93US-0104736.
94US-0330108.
96WO-US08992.
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Matches 185;
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Best Local
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                                                                                                                                                                                                regulation; activation; modulation; signal transduction; T Cell; T helper cell; treatment; autoimmune disorders; arthritis; infection; graft rejection; asthma; allergy; neoplasm; ss.
                                                                                                                                                                                                                                                                                                                                     V34779;
               06-OCT-1997;
                                          09-APR-1998.
                                                                                                                                                                        Mus sp.
                                                                                                                                                                                                                                             RATH1.1; RGS gene family; regulator of G-protein signalling; murine;
                                                                                                                                                                                                                                                                            Mouse RATH1.1 DNA.
                                                                                                                                                                                                                                                                                                      11-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                V34779 standard;
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             97WO-US18259
                                                                                                                            Location/Qualifiers
                                                                                                 /product-
                                                                                                              /+tag-
                                                                                                                                                                                                                                                                                                                                                                DNA;
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51.1%;
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Pred. No. 5.7e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 21;
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RESULT 11
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Best Local Similarity 50.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence encodes a novel member of the mouse regulator of G-protein signalling (RGS) gene family, RATH1.1. The encoded protein participates in the regulation, control and/or modulation of G-protein mediated signal transduction, involved in T cell activation, including T-helper (TH) cell and TH cell subpopulation activation. The protein can be used to develop products for treating autoimmune disorders, arthritis, graft rejection, asthma, allergy, infections or neoplasms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New activated T helper cell specific gene, RATH - used for developing products for treating e.g. autoimmune disorders, arthritis, graft rejection, asthma, allergy, infections or neoplasms \frac{1}{2}
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04-OCT-1996;
                  Human; regulator; G-protein signalling; HRGS; cancer;
hypertension; cardiovascular shock; arrhythmias; asthm
                                                               Human regulator of G-protein signalling encoding cDNA.
                                                                                               14-SEP-1998
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                                                                                                                                                             V38084 standard; cDNA;
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                                                                                             (first entry)
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96US-0726228.
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Pred. No. 2.1e-06;
0; Mismatches 171;
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                                   inflammation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Regulator of G-protein signalling - treating e.g. cancer, inflammation, shock, arrhythmias or asthma
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                          gaat 364
                                                        atccatgccctgatggaaaaggattctctgcctcgctttgtgcgctctgagttttatcag
                                                                       atccaggcagtgatggaggaaaatgcctaccaggtgttcttgacttctgacatttacctg
                                                                                                                atgaagaacctggtggaac----cttccctgagcagctttgacatggcccagaaaaga
                                                                                                                               cgagatggcatcaagaagcaacagatcggctcggtcatgtttgaccaggcacagaccgag
                                                                                                                                                                                      tacattgagaacaacagcgttgtctccaagcagctgaagcccgccaccaagacctacata
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gagt 604
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                                                                                                                                                                                                                                                                                                                                               tggcgtgattccctggacaaactcctgcagaacaactatggacttgccagtttcaaaagt
                                                                                                                                                                                                                                                                                                                                                                                                        175;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221 A; 174 C;
                                                                                                                                                                                                                                                                                                                                                                                                                     48.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Score 38; DB 19
Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169 G;
                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                        180;
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                                                                                                                                                                                                                                                              The RGS (regulators of G-protein signaling) protein genes, clones h16395 and m1975, were identified in human and murine spleen cDNA libraries, respectively. Both proteins have unique N- and C-terminal sequences. The C-terminal location of the RGS domain is consistent with RGSs known to act as GTPase activating proteins (GAPs) for G-alpha proteins. G-alpha-1 linked receptors support rapid adhesion and directed migration of leukocytes and other cell types. The novel RGS proteins may be used to modulate cell adhesion and chemotaxis, e.g. for aiding wound repair. The RGS proteins, related cDNAs and anti-RGS antibodies are useful for modulation, diagnosis and treatment of immune and respiratory disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RGS; regulators of G-protein signaling; GTPase activating protein; GAP; G-alpha protein; cell adhesion; chemotaxis; vulnerary; immunosuppressor; anti-rheumatic; anti-arthritic; anti-diabetic; anti-inflamatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel regulator of G-protein signaling nucleic acids and polypeptides, useful as diagnostic and investigative tools and to treat G-protein signaling disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 102-104; 105pp; English
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P-PSDB; Y97154.
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               121
                                                          Local Similarity
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                                          tttcttaaaactgaattcagtgaggagaacattgaattttgggtcgcctgtgaagacttc
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                                                                                                                                                                 Conservative
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                                                                                                                                                                              10.3%;
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0; Mismatches
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           protein, RGS5. The specification also describes an activator of G protein signalling (AGS) protein. The AGS CDNA sequence was isolated from a human liver cDNA library. The AGS protein exhibits homology to ras-related G proteins, and contains alterations in conserved amino acids consistent with a deficiency in GTP hydrolysis activity. AGS stimulates G protein activity, G protein-coupled signal transduction and the pheromone response pathway in a receptor-independent manner. The AGS protein also shows G-gamma selectivity, as measured by growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Activator of G protein signalling; AGS; ras-related G protein; GTP hydrolysis; G protein activity; pheromone response pathway G protein-coupled signal transduction; G-gamma seelectivity; cellular signal transduction; regulator of G protein signallin
                                                                                                                                                                                                                                                                                                                           08-MAY-1998;
07-OCT-1998;
                                                                                                                                                       Claim
                                                                                                                                                                             A new activator of G protein signalling used to treat disorders characterized by an aberrant {\sf AGS} protein activity -
                                                                                                                                                                                                                                                                     Cismowski M,
                                                                                                                                                                                                                                                                                                                                                                   07-MAY-1999;
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                                                                                                                          The present sequence encodes a regulator of G protein signalling (AGS)
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98US-0103355.
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expressing various mammalian
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G-gamma
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Best Local
12-SEP-1997;
05-SEP-1997;
05-SEP-1997;
05-SEP-1997;
12-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissue-specific expression, as measured by Northern blot analysis. The AGS protein can be used to screen for compounds that modulate cellular signal transduction. The protein is used to treat disorders characterized by an aberrant AGS protein activity or AGS nucleic activity.
                                                                                                                                                                                  inflammatory disorder; skin disorder; tumour; atherosclerosis; restenosis; autoimmune disorder; Alzheimer's disease; peripheral neuropathy; trauma; spinal cord injury; allergy; hematopoietic disorder; skeletal disorder; neurological disord arthritic disorder; asthma; immunodeficiency disease; AIDS;
                                                                                                                                                                                                                                                                                                17-JUN-1999
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                                                                        03-SEP-1998;
                                                                                                 11-MAR-1999
                                                                                                                        WO9911293-A1
                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                              Human secreted protein; cancer; immune disorder; infection;
                                                                                                                                                                                                                                                                       DNA encoding a human secreted protein
                                                                                                                                                                        transplant rejection; ss.
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97US-0058974.
97US-0057626.
97US-0057663.
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RESULT 15
C41294
ID C41294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          x51701-55 encode human secreted proteins. The polynucleotides and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Pathological conditions can also be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each polynucleotide, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer; immune disorders, inflammatory disorders, skin disorders, tunours, atherosclerosis, restenosis, autoimmune disorders, Alzheimer's disease, peripheral neuropathies, trauma, spinal cord injuries, altergy, hematopoietic disorders, asthma, immunodeficiency diseases, AIDS and transplant rejection. The polypeptides are also useful for identifying their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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P-PSDB; Y12958.
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12-SEP-1997;
   C41294 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1923 BP; 604 A;
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Ruben SM,
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23-APR-1999
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16-JUN-1999
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09-MAR-1999
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99US-0136392.
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                                        INFORMATION FOR SEQ ID NO:
                                                                           APPLICATION NUMBER: USSN 08/330,108; 08/104,736
APPLICATION NUMBER: 6.07/796,066
FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART-070
TELEPHONE: (610,470-0700
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/461,379A FILING DATE: 5-JUNE-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1,0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Valley Forge
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
      ENGTH:
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606 base pairs
                                                             (610)470-0701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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0; Mismatches 168;
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US-08-462-390B-27
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Best Local Similarity
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APPLICANT: Smith, K. A., & Beadling, C.

TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and

TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
                                                                                  APPLICATION NUMBER: US/08
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN
FILING DATE: 27-OCT-1994
APPLICATION UMBER: USSN
FILING DATE: 10-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph.
REGISTRATION NUMBER: 30,9
                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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ZIP: 19482
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                                                 APPLICATION NUMBER: US:
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                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                   STATE: Pennsylvania
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TOPOLOGY: 111
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                                                                    07/796,066
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Pred. No. 8.4e-09;
0; Mismatches 168;
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US-08-463-074B-27; Sequence 27, Application US/08463074B
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 606 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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Best Local Similarity
Matches 185; Conserv
              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
SOFTWARE: Patentin #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,074B
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                              BENERAL INFORMATION:
                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                              APPLICANT: Smith, Kendall A. & Beadling, Carol TITLE OF INVENTION: Nucleic Acids Encoding CR1 NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (610)407-0700
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                                                                                                                                                                                                                                                     CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                    ZIP: 90071
                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                              ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
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                                                         US/08/463,074B
US 08/104,736
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Pred. No. 8.4e-09;
D; Mismatches 168;
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; Patent No. 6027914
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Best Local Similarity 51.1
Matches 185; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 606 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling, C.
                                                                                                                                                                                TITLE OF INVENTION: Nucleic Acids Encoding CR6 Pol
TITLE OF INVENTION: Transformed Cell Thereof, and
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
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FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38143 (DART-020)
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PRIOR APPLICATION DATA:
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                                                             ZIP:
                                                                                                    CITY: Los Angeles
STATE: California
                                                                              COUNTRY:
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51.1%;
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Pred. No. 8.4e-09;
0; Mismatches 168;
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                                  GENERAL INFORMATION:
APPLICANT: Smith, Ke
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                 Sequence 27, Application US/08652446 Patent No. 6057427
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Best Local Similarity
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TELEPHONE: (213) 622-7700
TELEPAX: (213) 4894210
INFORMATION FOR SEQ ID NO: 27:
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FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-1991
ATTORNEY/AGENT INFORMATION:
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LENGTH: 606 base pairs
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CORRESPONDENCE ADDRESS:
                    NUMBER OF SEQUENCES:
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TYPE: nucleic acid
STRANDEDNESS: single
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REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38149 (DART-050)
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                                                                                            Smith, Kendall A. & Beadling, Carol
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51.1%;
                                  Nucleic Acids Encoding Polypeptide, Vector and Expression Thereof
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Pred. No. 8.4e-09;
                                                           and Transformed Cell Thereof,
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; TOPOLOGY: linear; MOLECULE TYPE: CDNA US-08-652-446-27
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Best Local
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APPLICATION NUMBER: 08/465,585
FILING DATE: 5-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,081
APPLICATION NUMBER: 08/463,081
FILING DATE: 5-UN-1995
PRIOR APPLICATION DATA:
OR/461,379
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                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/739,5
FILING DATE: 29-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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FILING DATE: 5-JUN-1
PRIOR APPLICATION DATA:
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PRIOR APPLICATION UNIMBER: US 08/330,108
                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: FP66 40035 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/461,379
FILING DATE: 5-JUN-1991
PRIOR APPLICATION DATA:
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184
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FILING DATE: 5-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/652,446
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STATE: California
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                                                                              1 tggaccaagtctttacactccttgttgggtgaccaggatggtgcatacctcttccggact
                                                                                                                                                                                                                                                                                    LENGTH:
                                                              TGGAGAGAGTCGTTCGACCTGCTGCTGAGCAGTAAAAATGGAGTGGCTGCCTTCCACGCT
                                                                                                                            185;
                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                     nucleic acid
                                                                                                                                                                                                                                                                                    606 base pairs
                                                                                                                                                                                                                                                                                                                   (213) 489-4210
OR SEQ ID NO: 2
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                                                                                                                            Conservative
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Version #1.25
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                                                                                                                                                                                                                                                                                                                                                    (213)
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5-JUN-1995
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                                                                                                                                          Score 55.2; DB 3; Pred. No. 8.4e-09;
                                                                                                                              Mismatches
                                                                                                                                                            DB 3;
                                                                                                                              168;
                                                                                                                                                          Length 606;
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NAME/KEY: Coding Sequence;
LOCATION: 39...644;
PTHER INFORMATION:
US-08-870-815-3
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              Query Match 15.0%;
Best Local Similarity 51.1%;
 Matches 185;
                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Laura A. COLUZZI
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-074
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 896-8864/9741
TELEX: 66141 PENNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Levinson, Douglas A.
APPLICANT: Gimeno, Carlos J.
APPLICANT: Gimeno, Carlos J.
TITLE OF INVENTION: FATH GENES AND POLYPEPTIDES AND METHODS
TITLE OF INVENTION: FOR THE TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/870,815
                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 746 base pairs
                                                                                                                                       FEATURE:
                                                                                                                                                  MOLECULE TYPE: DNA
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CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                               STRANDEDNESS: single
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1155 Avenue of the Americas
Conservative
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              Score 55.2; DB 3; Pred. No. 9.3e-09;
 Mismatches
                            Length 746;
Gaps
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; NAME/KEY: CDS
; LOCATION: (39)..(644)
US-08-949-004-3
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                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Levinson, Douglas A.
APPLICANT: Gimeno, Carlos J.
TITLE OF INVENTION: RATH GENES AND POLYPEPTIDES AND METHODS FOR
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
FILE REFERENCE: 7853-109
CURRENT APPLICATION NUMBER: US/08/949,004
CURRENT FILING DATE: 1997-10-10
EARLIER APPLICATION NUMBER: 08/870,815
EARLIER APPLICATION NUMBER: 08/870,815
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1996-10-04
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                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                            15.0%;
                                                                                                                                                                                                                                                                                                              Score 55.2; DB 4;
Pred. No. 9.3e-09;
0; Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                  Length 746;
                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                 Query Match 15.0%;
Best Local Similarity 51.1%;
Matches 185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/274,318
FILING DATE: 11-JUL-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: BOGDEN, James M.
REGISTRATION NUMBER: 32,962
REFERENCE/DOCKET NUMBER: 000127-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-727-3688
                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 206-727-3601
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ITM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: No. 5667987el p53 Response Genes NUMBER OF SEQUENCES: 3
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                                                                       276 TGGAGAGAGTCGTTCGACCTGCTGAGCAGTAAAAATGGAGTGGCTGCCTTCCACGCT 335
 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Seattle
STATE: Washington
                                      61
                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                     ENGTH:
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                                                                                             tggaccaagtctttacactccttgttgggtgaccaggatggtgcatacctcttccggact 60
   INFORMATION:
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                                                                                                                                                                                                                                                                                                                                   2383 base pairs
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                                                                                                                                               Score 55.2; DB 1;
Pred. No. 1.6e-08;
0; Mismatches 168;
                                                                                                                                                                                      Length 2383;
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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-754-108-1
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                                         Matches
                                                           Query Match
Best Local
                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/274,318
FILING DATE: 11-JUL-1994
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 2383 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 11-JUL-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Rel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                           Similarity
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                                                           Score 55.2; DB 2;
Pred. No. 1.6e-08;
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                                            Mismatches
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Patent No. 5871960
Patent No. 5871960 5837487
                                                                                     COMPOTER: IBM PC COMPATIBLE
COMPOTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,081B
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/104,736
FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,066
FILING DATE: 20-NOV-91
APPLICATION NUMBER: US 07/796,066
FILING DATE: 20-NOV-91
APPLICATION NUMBER: US 07/796,066
FILING DATE: 30-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: V1v1ana Amzel, Ph. D.
REGISTRATION NUMBER: 90.930
REFERENCE/DOCKET NUMBER: P66 38150 (UTELEPHONE: (213) 622-7700
TELEPHONE: (213) 622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
TITLE OF INVENTION: Vector and Transformed Cell Thereof, and Expression
                                                                        TELEFAX: (213) 489-4210 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                   SEQUENCE CHARACTERISTICS:
LENGTH: 2406 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
STREET: 444 South Flower St. - Suite 1900
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
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TYPE: nucleic acid
STRANDEDNESS: single
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RESULT 12
US-08-461-379A-1
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Best Local Similarity 51.7
Matches 185; Conservative
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TITLE OF INVENTION: Vec
TITLE OF INVENTION: Exp
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
APPLICATION NUMBER: USSN 08/330,108; 08/104,736
APPLICATION NUMBER: 607/796,066
FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                              APPLICATION NUMBER: US/OFILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                               CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                       CITY: Valley Forge
STATE: Pennsylvania
COUNTRY: USA
                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, SOFTWARE: Version #1.25
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Pred. No. 1.
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2406 base pairs
TYPE: nucleic acid
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GENERAL INFORMATION:
Smith, K.
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             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTED:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                    APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
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                                                                                                                              ZIP: 19482
                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                     ADDRESSEE:
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APPLICATION NUMBER:
                                                                                                                                                                                                                       ADDRESSEE: Ratner & Prestia
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116..722
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51.1%;
 US/08/462,390B
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                                                                                                                                                                                                         STREET:One Westlakes-Berwyn
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Pred. No. 1.6e-08;
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US-08-462-390B-1
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                                                RESULT 14
US-08-463-074B-1
               Sequence 1, Application US/08463074B Patent No. 6020155
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Matches
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Best Local Similarity
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 20-NOV-91 ATTORNEY/AGENT INFORMATION: NAME: Viviana Amzel, Ph.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN
FILING DATE: 27-OCT-1994
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(770 TD NO: 1:
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51.1%;
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Pred. No. 1.6e-08;
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NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:

ADDRESSEE:

PRETTY,
Angeles

TITLE OF INVENTION:

Smith, Kendall A. & Beadling, Carol VENTION: Nucleic Acids Encoding CR1 EQUENCES: 35

Fusion

SCHROEDER & POPLAWSKI

(B) STREET

444 South Flower St.

Suite

APPLICANT:

STATE: California

90071

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RESULT 15
US-08-465-585C-1
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Best Local Similarity 51.1%;
Matches 185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (213) 489-4210 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/ACENT INFORMATION:
NAME: VIVIANA AMZE1, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38143 (DART-020)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, SOFTWARE: Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08 FILING DATE: 10-AUG-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/463,074B
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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                                                                              650 GA 651
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (213) 4894210
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FR PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN
FILING DATE: 27-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38149 (DART-050)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR6 Polypeptide, Vecto
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                              241 cgagatggcatcaagaagcaacagatcggctcggtcatgtttgaccaggcacagaccgag 300
530 CTGACGAGGATGAACCTGCAGACTGCCACAGCCACATGCTTTGATGCGGCTCAGGGGAAG
                                                                                                                                                                  419 A---AGAAGATCCGATCAGCTACCAAGCTGGCCTCCAGGGCACACCAGATCTTTGAGGAG
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LOCATION:
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STATE: Californiaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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. (B) STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER: USSN 08/104,736
10-AUG-1993
IUMBER: USSN 07/796,066
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Pred. No. 1.6e-08;
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		Search completed: June 7, 2001, 00:26:30 Job time: 19733 sec	2001,	7,	June ec	Search completed: J Job time: 19733 sec	rch cor time:	Sea. Job
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649	590 ACACGTACCCTGATGGAGAAGGACTCCTACCCCACGCTTCCTGAAGTCGCCTGCTTACCGG 649	ACTCCTAC	AGAAGG	TGG	CCTGA	ACACGTAG	590	фd
360	301 atccaggcagtgatggaggaaaatgcctaccaggtgttcttgacttctgacatttacctg 360	atgectaco	aggaaa 	tgg   t	cagtga	atccagg	301	Qy

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seq length:
June 6, 2001, 23:00:39 ; Search time 3054.04 Seconds (without alignments)
1055.527 Million cell updates/sec
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369
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gb_est3:
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em\_estpl2:
em\_estpl3:
em\_estpl5:
em\_estpl6:
em\_estpl6:
em\_estpl6:
em\_estpl10:

em\_estro7:\*
em\_estro8:\*
em\_estro9:\*

em\_estro6:\*

em\_esthum28:\*
em\_estin1:\*
em\_estin2:\*
em\_estin3:\*
em\_estin4:\*
em\_estin5:\*

em\_estom1:\* em\_estom2:\* em\_esthum18:
em\_esthum29:
em\_esthum21:
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em\_esthum10:\*
em\_esthum11:\*
em\_esthum13:\*
em\_esthum13:\*
em\_esthum14:\*
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100: 101: 103: 105: 106: 107: 1107: 1109: 1111: 1111: 1111: 1111: 1111: 1111: 1111: 1111: 1111: 1111: 1111: 1111:

em\_estro10: em\_estro11: em\_estro13: em\_estro14: em\_estro16: em\_estro16: em\_estro16: em\_estro19: em\_estro29: em\_estro29: em\_estro20: gb\_est26: gb\_est29: gb\_est29: gb\_est29: gb\_est21: gb\_est23: gb\_est23: gb\_est41: gb\_est41: gb\_est43: gb\_est44: gb\_est44: gb\_est44: gb\_est45: gb\_est47:

gb\_est54:\*
gb\_est55:\*

gb\_est57

gb\_est60:

gb\_est63:\*

gb\_est48:\*
gb\_est49:\*
gb\_est50:\*
gb\_est51:\*

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Result
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                    247.4
237.4
218.2
207.2
207.2
207.2
162
161.2
147.4
147.4
143.6
1126.8
1126.8
1120.2
114.8
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231 CNSO3YWO
230 CNSO1YDU
231 CNSO3GZO
140 BE872155
230 CNSO33J4
141 BE8944510
140 BE8944108
150 BF582324
3 AA198606
147 BF406997
169 BF802488
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105 AL645145
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AL266841 Tetraodon
AL172875 Tetraodon
AL172875 Tetraodon
AL243621 Tetraodon
BE872155 601446262
AL26621 Tetraodon
BE894571 601433182
BE854108 ux27903.y
BF582324 602101153
AA198606 mu15604.r
BF406997 UI-R-BJ2-BF80248B CM0-C1009
AL526136 AL526136
AL045145 DKFZp4340
AL044479 DKFZp434C
BF559312 UI-R-E1-f
AL339465 Tetraodon
AV138493 AV138493
BF892872 QVI-MT013
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gb\_est99:\*
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gb\_est89: gb\_est90: gb\_est82:\*
gb\_est84:\*
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gb\_est102:\*
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gb\_est105: gb\_est106: gb\_est67:\* gb\_est68:\*

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9b\_est70:\*
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em\_gss\_hum1:\*
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em\_gss\_inv3:\*

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                                    Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a lar scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                            2 (bases 1 to 1068)
Roest-Crollius,H., Jaillon,O., Dasilva,C.,
Bernot,A., Fizames,C., Wincker,P., Brotties
Saurin,W. and Weissenbach,J.
Human gene number estimate provided by geno
                                                                                                                                                                                                                                                                                     Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleost
Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;
Holacanthopterygii; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Tetraodon.
1 (bases 1 to 1068)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNS03YW0 1068 bp DNA GSS 18-MAY-2000
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
069C20 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                      Charaterization and repeat analysis of the compact freshwater pufferfish Tetraodon nigroviridis
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Eukaryota; Metazoa; Chordata;
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                                                                                                  Direct Submission
                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                               Bouneau, L., Billault, A., Weissenbach, J.
                                                                                                                                                Tetraodon nigroviridis
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/organism="Tetraodon nigroviridis"
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Brottier,P., Quetier,F.,
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AI769888 wj30a08.x
BF304996 601888511
BE795291 601592385
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AW195671 xm29b11.x
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293;
                                                 Unpublished
2 (bases 1 to 830)
2 (bases 1 to 830)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Boune
Roest-Crollius, H., Jaillon, O., Dasilva, C., Boune
                                                                                                                                                                                                                                                   GSS; genome survey sequence Tetraodon nigroviridis. Tetraodon nigroviridis
                       Human gene number estimate provided Tetraodon nigroviridis DNA sequence
                                                Bernot, A., Fizames, C., Winch Saurin, W. and Weissenbach, J.
                                                                                                            Charaterization and refreshwater pufferfish
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                                                                                                                                       Weissenbach,J.
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Roest-Crollius, H., Jaillon, O.,
                                                                                                                                                                                                              Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;
                                                                                                                                                                                                                                                                                          AL172875.1
                                                                                                                                                                                                                                                                                                                   sequence.
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                                                                                                                                                                                      Holacanthopterygii; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontida
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/clone_lib="G"
/note="Genoscope sequence ID : C0BG069BB10SP1-end
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                                                                          Bouneau, L., Fisher, C.,
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                                                                                             Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;
Holacanthopterygii; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                   sequence.
AL243621
AL243621.1 GI:7964633
GSS; genome survey sequence.
Tetraodon nigroviridis.
                                                                                                                                                                                                                                                                                           Tetraodon
025B16 of
                                            1 (bases 1 to 902)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fi.
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A.
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               Charaterization and repeat analysis of the
                                    Weissenbach,J.
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/db_xref="taxon:99883"
/clone="218017"
/clone_lib="G"
/note="Genoscope sequence ID : COAV
/note="Genoscope sequence ID : COAV
pufferfish
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Tetraodon nigroviridis
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Pred. No. 7.6e-60;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 798) NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collec Unpublished (1999)
                                                                                                                                                                    BE872155 798 bp
601446262F1 NIH_MGC_65
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                                                                                      Homo sapiens
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Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
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/db_xref="taxon:99883"
/clone="025B16"
/clone_1ib="G"
/clone_1ib="G"
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GSS; genome survey sequence.

Tetraodon nigroviridis

Tetraodon nigroviridis

Tetraodon nigroviridis

Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostet; Euteleosteti; Neoteleosteti;
Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;
Holacanthopterygii; Acanthopterygii; Percomorpha;
Holacanthopterygii; Tetraodontoidei; Tetraodontidae; Tetraodon.

1 (basea 1 to 975)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
                                                                                                                                                                                                                                                                  CNS033J4 975 bp DNA
Tetraodon nigroviridis genome survey sequence PUC-Ori
209G17 of library G from Tetraodon nigroviridis, genom
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Syrage insert size 1.8 kb. Library constructed by Life
"mechnologies."
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This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
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/db_xref="taxon:99883"
/clone="209G17"
/clone_lib="G"
/clone_fenoscope sequence ID : COP
PUC-Ori"
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ORGANISM

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258;
             ux27g03.y1 Soares_NWMAX_maxillary_process Mus musculus cDNA IMAGE:3511540 5' similar to TR:070239 070239 RAXIN. ;, mRNA
                                                  BE854108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC/DTPDTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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/clone_lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/lab_host="DH10M (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo of Average insert size 2 kb. Library constructed by Life Technologies."

171 c 188 g 130 t
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/db_xref="taxon:9606"
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68.3%;
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                      gacatttacctggaata
                                                                  gcacagaccgagatccaggcagtgatggaggaaaatgcctaccaggtgttcttgacttct
                                                                                                                                  aagacctacatacgagatggcatcaagaagcaacagatcggctcggtcatgtttgaccag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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Unpublished (1997)
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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Mammalia; Eutheria;
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157 c 142 g 156 t 1 others
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/clone="IMAGE:3511540"
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Pred. No. 3.7e-33;
0; Mismatches 116; 1
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http://image.llnl.gov
Plate: LLAM9814 row: 1 column: 14
High quality sequence start: 5
High quality sequence stop: 688.
Location/Qualifiers
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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1 (bases 1 to 956)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BF582324 956 bp mRNA EST 12-DEC-2000 602101153F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4224469 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF582324
BF582324.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dbxref* taxon:10090"
/dbxref* taxon:10090"
/dlone="IMAGE:4224469"
/clone=11b-"NCI_CGAP_CO24"
/clone=1b-"NCI_CGAP_CO24"
/lab_host="DH10B (T1 phage resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT.
Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 234 C 288 g 176 t
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/strain="FVB/N"
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Pred. No. 4.3e-33;
0; Mismatches 116; Indels 12; Gaps
                                                                        385
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533

1 tggaccaagtotttacaotcottgttgggtgaccaggatggtgcatacctcttccggact 60

TGGGCTGAGTCACTGCATTCCTTACTGGATGACCAAGATGGGATCAGCCTGTTCAGGACT 474

Matches

246;

Conservative

Indels

Gaps

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KEYWORDS
SOURCE
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VERSION
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AA198606/c
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JOURNAL
                Query Match
Best Local Similarity
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mu15d04.rl Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:639463 5' similar to SW:BL34_HUMAN Q07918 B-CELL ACTIVATION PROTEIN BL34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA198606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 496.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA198606.1 GI:1794333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Possible reversed clone: similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            house mouse
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                                                                                                      118
                                                                                      /sex-"male"
                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Soares_thymus_2NbMT"
                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="IMAGE:639463"
                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                  38.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               539 bp
Score 143.6; DB 3;
Pred. No. 4.9e-32;
0; Mismatches 119;
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                                Length 539;
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REFERENCE
AUTHORS
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KEYWORDS
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BF406997/c
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agacctacatacgagatggcatcaagaagcaacagatcggctcggtcatgtttgaccagg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome R
97044477
                                                                                                                                                                                                                                                                                                                             Research Genetics (www.resgen.
Seq primer: M13 Forward
POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                Email: msoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of seque
is likely internal to the message. cDNA Library Preparation: M.E
Soares Lab Clone distribution: colones will be available through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University of Iowa
451 Eckstein Medical Research Building Iowa
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Soares, MB Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BF406997.1
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bonaldo, M.F., Lennon, G. and Soares, Normalization and subtraction: two
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Bonaldo, M.F., Lenno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-BJZ-bpq-b-01-0-UI"
/clone=lib="UI-R-BJZ"
/clone_lib="UI-R-BJZ"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/note="vector: pf773D-pac (Pharmacia) with a modified
/note="vector: pf773D-pac (Pharmacia) with a modified
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                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                organism="Rattus norvegicus"
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae;
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MEDLINE
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Seq_primer: puc 18 forward
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1 (bases 1 to 406)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
                                                                                                                                                                                                                                                                                                                                                                                  Simpson, A.J
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CMO-CI0096-311000-652-h03
                                                                                                                                                                                                                Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                              Contact: Simpson A.J.G.
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                                                                                                                            Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
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1 (bases 1 to 935)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope
                                                                                                                Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France
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               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODC015YE11"
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1 (bases 1 to 491)
Wambutt, R., Heubner, D., Mewes, H.W., Gassenhuber, J. and Wiemann, S. EST (Wambutt, et al.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                    ALO45.145 491 bp mRNA
DKFZp4340084_r1 434 (synonym: htes3)
DKFZp4340084 5', mRNA sequence.
ALO45.145
consortium of the German Genome Project.

No sl sequence available.

This clone (DKFZp4340084) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 140

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                Clone from S. Wiemann, Molecular Genome Analysis, German Can
Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de
sequenced by ACOWA (Berlin/Germany) within the cDNA sequenc
                                                                                                                                                                                                                   Contact: Wambutt R
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/lab_host="DH10B"
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1 (bases 1 to 364)
Wambutt,R., Heubner,D., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
EST (Wambutt, et al.)
Unpublished (1999)
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DKFZp434C044_r1 434 (synonym: htes3) Homo
DKFZp434C044 5', mRNA sequence.
                                                                                                                                                                                                                                                     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.
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/db_xref="taxon:9606"
/clone="DKFZp4340084"
/clone_lib="434 (synonym: h
/tissue_type="testis"
/dev_stage="adult"
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                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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/note-"Vector: pSport1;
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/clone="DKFZp434C044"
/clone_lib="434 (synonym:
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                                                                                                                                               Email: msoares@blue.weeg.uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.
This clone is also available through the I.M.A.G.E. Consortium
LLNL (info@image.lln1.gov). IMAGE ID= 1779287
Seq primer: M13 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BF559312 217 bp mRNA
UI-R-E1-fa-e-06-0-UI.rl UI-R-E1 Rattus
UI-R-E1-fa-e-06-0-UI 5', mRNA sequence
                                                                                                                                                                                                                                                                           Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                       Genome Res. 6 (9), 97044477
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Bonaldo, M.F., Lenno
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/note="Vector: 99 g 74 t 1 others
1 92 c
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                                            /strain="Sprague-Dawley
/db_xref="taxon:10116"
                                                                                                                           Location/Qualifiers
                                                                                      ∕organism="Rattus norvegicus"
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(Life Technologies)"

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Query Match
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97 GTG 95
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Search completed: June 6, 2001, 23:00:43 Job time: 15527 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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56.4	82.8	128.4	131.6	131.6	133.4	147.6	162	162	162	162	Score
		79.3									Query Match
3411	3485	2538	3072	2104	191041	3216	3016	2825	2825	162	Query Match Length DB
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A98523
                                                                                                  Patent: WO 9911780-A 8 11-MAR-1999;
BIRCHMEIER WALTER (DE); BEHRENS JUE
Location/Qualifiers
                                                                                                                        Birchmeier, W. and Behrens, J. CONDUCTINE PROTEIN AND A RELATED AGENT FOR DIAGNOSING AND TREATING
                                                                                                                    TUMOR ILLNESSES
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AC040933 Homo sapi
AF097313 Xenopus l
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V01238 Rat gene fo
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Behrens, J., Jerchow, B.-A. and Birchmeier, W.
Direct Submission
Submitted (22-JUN-1998) Cellular Biology, Max Delbrueck Center
Molecular Medicine, Robert-Roessle 10, Berlin 13122, Germany
Location/Qualifiers
1. .2825
                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 2825)
Behrens, J., Jerchow, B.-A., Wurtele, M., Grimm, J., Asbrand, C., Wirtz, R., Kuhl, M., Wedlich, D. and Birchmeier, W. Functional interaction of an axin homolog, conductin, with beta-catenin, APC, and GSK3beta Science 280 (5363), 596-599 (1998)
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BIRCHMEIER WALTER (DE); BEHRENS JUERGEN (DE)
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                                                                                                                              Direct Submission
Submitted (16-NOV-1999) Genetics & Development, Columbia
University, 701 W168th St. HHSC 1416, New York, NY 10032,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                             Zhang, T., Fagotto, F., Hsu, W., Zeng, L., Gilbert, D., Copeland, N.G., Jenkins, N.A., Warburton, D. and Costantini, F. Properties of mouse Axin2 and human AXIN2: chromosomal location, expression pattern, interaction with Axin and effects on embryoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus Axin2 (Axin2) mRNA, complete cds. AF205889
                                                                                                                                                                                                                                                                                                        Unpublished
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GCQSPGVGRYSPRSRSDHHHQHHHQCHTLLSTGGKLPPVAKELLGGKSPLTKQT
TKHVHHYIHHAVPRYKEELEABATQRVRLLCPGGTDYYCYSRCKSHPKARPEDLPGE
QFCGSRGGTLPKRNAKGTEPGLALSARDGGMSSAAGGPQLPGEEGDRSQDVWQWMLES
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KVLCCYLPTLMEEEEMYCADLKCKLSPTVGLLSKTLRATASVESTETAENGFRSFKR
SDPVNPYHVGSGYVFAA PATSANDSELGSDALTDDSMSMTDSVDGVPPYRMGSKKQL
REMHRSVKANGQVSLPHFPRTHRLPKEMTPVEPAAFAAELISRLEKLKLELESRHSLE
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PPLTPPNTLAQLEEACRRLAEVSKPQKQRCCVASQQRDRNHSAAGQAGASPFANPSLA
PEDHKEPKKLASVHALQASELVVTYFFCGEEIPYRRMLKAQSLTLGHFKEQLSKKGNY
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STKPMPVSSNARRNEDGLGEPEGRASPDSPLTRWTKSLHSLLGDQDGAYLFRTFLERE
KCYUTLDFWFACNGFRQMNLKDTKTLRYAKAIYKRYIENNSVVSKQLKPATKTYIRDG
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/db_xref="taxon:10090"
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                                                                            Yamamoto,H., Ikeda,Ś., Murai,H., Kishida,S. and Kikuchi,A.
Direčt Submission
Submitted (08-AUG-1997) Biochemistry, Hiroshima University,
of Medicine, 1-2-3 Kasumi, Minami-ku, Hiroshima, Hiroshima
                                                                                                                                                                                                                                                synthase kinase 3beta and beta-catenin and of Xenopus embryos Mol. Cell. Biol. 18 (5), 2867-2875 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF017757 3216 bp mRNA ROD 24-APR-1998 Rattus norvegicus GSK-3beta interacting protein Axil mRNA, complete
                                                                                                                                                                                                                                                                                                                                     Axil, a member of the Axin family, interacts with both glycogen
                                                                                                                                                                                                                                                                                                                                                                Yamamoto, H., K
and Kikuchi, A.
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                                                    Japan
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Mammalia; Eutheria; Rodentia;
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55. .2577
Location/Qualifiers
1, .3216
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/db_xref="GI:6653586"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:3080758
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Pred. No. 6.2e-32;
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Sciurognathi; Muridae;
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                                                                  Metzker,M.L., Lewis,J.R., Hume,J., Edwards,C., Harris,C.,

Dederich,D., Thomas,S., Okwuonu,G., Carlock,C., Garner,T.,

Addison,S., Pace,A., Williams,G., Bonnin,D., Brooks,A., Brown,J.,

Buhay,C., Bunac,C., Burkett,C., Chacko,J., Chen,G., Chen,Z.,

Cox,C., Davis,C., Delgado,O., Ding,Y., Dugan-Rocha,S.,

Fernandez,C., Ferraguto,D., Forcum-Tansey,J., Gill,R.,

Gorrell,J.H., Gunaratne,P., Haller,G., Hernandez,J., Hogues,M.,

Hosak,H., Hou,X., Huber,J., Jackson,L., Jia,Y., Kelly,J., Kelly,S.,

Kovar,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Martin,R.,

Massey,E., McLeod,M.P., Mei,G., Moore,S., Morgan,M., Morris,S.,

Neal,D., Nelson,A., Nguyen,R., Nguyen,N., Oguh,M., Parish,B.,

Perez,L., Reiter,D., Say,J., Shen,H., Vasquez,L., Watlington,S.,

Williamson,A., Wrensford,G., Zhou,X., Bouck,J., Hodgson,A.,

Milliamson,A., Wrensford,G., Zhou,X., Bouck,J., Hodgson,A.,
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                                                   Williamson, A., Wrensford, Muzny, D.M., Rives, M., Sch
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 191041)
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REMHRSVKANGQVSLPHFPRTHRLPKEMTPVEPAAFAAELISRLEKLKLELESHSLE
ERLQQIREDEEKEGSEQALSSRDGAPVQHPLALLPGSGYEEDPQTILDGHLSRVLKTF
GCQSPGVGRYSPRSRSPDHHHHHQQCHALLPTGGKLPPEAACPLLGGKSFLTKQTTK
HVHHHYIHHHAVPKTKEEIEAEATQRVBCLCPGGTDYYCYSKCKSHSKPPEPLLGEQF
CGSRGGTLPKRNTKGTEPGLALPAREGGMSSAAGAPQLPGEEGDRSQDVWQWMLESER
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DHKEPKRLASVHALQASELIVTYFFCGEEIPYRRMLKAQSLTLGHFKEQLSKKGNYRY
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IKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDIYLEYVRSGGENTAYMSNGGLGSL
KVLCGYLPTLNEEEEWTCADLKCKLSPTVVGLSSKTLRATASVRSTETAENGFRSFKR
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/protein_id="Aac40089.1"
/db_xref="G1:3080759"
/translation="MSSAVLVTLLPDPSSSFREDAPRPPVPGEEGETPPCQPSVGKVQ
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/db_xref="taxon:10116"
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94.48;
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Pred. No. 3.1e-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 191041)
Worley, K.C:
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 30 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          be preserved
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Chemistry: Dye-terminator Big Dye: 5% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 158769 bases at least Q40
Consensus quality: 172780 bases at least Q30
Consensus quality: 172780 bases at least Q30
Estimated insert size: 180377; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; sum-of-contigs estimation
                             150789
150889
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Contact: hgsc-help@bcm.tmc.edu
Contact: ngsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Center project name: MACA
Center clone name: RP23-278J12
Center clone name: Statistics
                                                                                                                                   126090
131870
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120272
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Homo sapiens cDNA: FLJ22065 fis,
AF078165 Homo sapiene conduction
Unpublished (2000)
2 (bases 1 to 2104)
3 (bases 1 to 2104)
Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T., Shibahara, T., Tanaka, T. and Nakamura, Y.
                                                  Kawabata,A. Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S. NEDO human cDNA sequencing project
                                                                                                                                                                 AK025718.1 GI:10438327
oligo capping; fis (full insert sequence).
Homo sapiens hepatoma cell_line:HepG2 cDNA
                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                          clone: HEP10566.
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43523 c 42989 g !
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/db_xref="taxon:10090"
/chromosome="11"
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                                                Mai,M., Qian,C., Smith,D.I. and Liu,W.
Direct Submission
Submitted (15-JUL-1998) Lab Medicine and Pathology, Mayo clinic,
200 First Street SW, Rochester, MN 55905, USA
Location/Qualifiers
                                                                                                                                                                                                                       Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3072)

1 (bases 1 to 3072)

Mai,M., Qian,C., Yokomizo,A., Smith,D.I. and Liu,W.

Cloning of the human homolog of conductin (AXIN2), a gene mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
                                                                                                                                                                      Genomics 55 (3),
99168905
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nilarity 88.3%;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/cell_type="hepatoma"
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Pred. No. 4.4e-24;
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                                                                                  Submitted (16-NOV-1999) Genetics & Development, University, 701 W168th St. HHSC 1416, New York,
                                                                                                                                 Zhang, T. and Cost.
Direct Submission
                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                          axis formation
                                                                                                                                                                                                                                             expression pattern, interaction with Axin and effects on embryonic
                                                                                                                                                                                                                                                               Jenkins, N.A., Warburton, D. and Costantini, F. Properties of mouse Axin2 and human AXIN2: chromosomal location,
                                                                                                                                                                                                                                                                                        Jenkins, N.A.,
                                                                                                                                                                                                                                                                                                        Zhang,T., Fagotto,F., Hsu,W., Zeng,L., Gilbert,D., Copeland,N.G.,
                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REMHRSVKANGQVSLDHFPRTHRLPKEMTPVEPATFAAELISRLEKLKLESSRHSLE
REMLOGUSLDHFPRTHRLPKEMTPVEPATFAAELISRLEKLKLESSRHSLE
RELOQIREDEREGSELTLNREGAPTQHPLSLLPSGSYEEDPQTILDDHLSRVLKTE
GCQSPGVGRYSPRSRSPDHHHHHHSQYHSLLPFGGKLPPAASSECPLLGGKGFVKR
QTYKHYHHYLHHHAVYKKEEIEABATQRWPCFCPGGSEYYCYSKCKSHSKAPETMK
QTKHYHHHYLHHHAVKKEEIBABATQRWPCFCPGGSEYCYSKCKSHSKAPETM
SEQFGGSRGSTLPKRNGKGTEPGLALPAREGGAPGAGALQLPREEGDRSQDYWQWM
/organism="Homo sapiens"
/db_xref="taxon:9606"
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KCVDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKRYIENNSIVSKQLKPATKTYIRDG
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                                                                  ocation/Qualifiers
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/protein_id="AAD20976.1"
/db_xref="GI:4454791"
/translation="MSSAMLVTCLPDPSSSFREDAPRPPVPGEEGETPPCQPGVGKGQ
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Hirano, Biomedical research center, Osaka Univ. Med. scool, bepartment of Molecular Oncology; 2-2, Yamadaoka, Suita, Osaka 565-0871, Japan (E-mail:hirano@molonc.med.osaka-u.ac.jp, URL:http://www.med.osaka-u.ac.jp/pub/molonc/www/index.html, Tel:81-6-879-3880, Fax:81-6-879-3889)
                                                                                                                                                                                                                                  Shimizu,T., Yamanaka,Y., Ryu,S.L., Hashimoto,H., Yabe,T., Hirata,T., Bae,Y.K., Hibi,M. and Hirano,T. Cooperative roles of Bozook/Dharma and Nodal-related proteins the formation of the dorsal organizer in zebrafish Mech. Dev. 91 (1-2), 293-303 (2000)
                                                                                                                                                Hirano,T., Hibi,M. and Shimizu,T. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Rasborinae; Danio.
                                                                                                                    Submitted (09-SEP-1999) to the DDBJ/EMBL/GenBank databases. Toshio
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CQSPGVGRYSPRSRSPDHHHHHHSQYHSLLPPGGKLPPAAASPGACPLLGGKGFVTKQ
TTKHVHHHYIHHHAVPKTKEEIEAEATQRVHCFCPGGSEYYCYSKCKSHSKAPETMPS
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DPVNPYHIGSGYVFAPATSANDSEISSDALTDDSMSMTDSSVDGIPPYRVGSKKQLQR
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/db_xref="GI:6653584"
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/note="similar to ESTs 823683 and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aatggccaagtgtctctacctcattttccgagaacccaccgcctgcccaaggagatgacg 63
                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens axin (
AF009674
                                Two dominant mutations in the mouse Fused gene are the result transposon insertions genetics (1997) In press genetics (1997) In press 2 (bases 1 to 3411)
2 eng,L., Fagotto,F., Zhang,T., Hsu,W., Vasicek,T.J., Perry,W.,J. 3rd, Lee,J.J., Tilghman,S.W., Gumbiner,B.M. and Costantini,F. The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling pathway that regulates embryonic axis formation (2011 90 (1), 181-192 (1997)
                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo. 1 (bases 1 to 3411)
                                                                                                                                                                                                                                              vasicek, T.J., zeng, \tilde{L}., Guan, X.-J., zhang, T., Costantini, F. and Tilghman, S.M.
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(bases 1 to 3411)
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MYEGKILGKVDRMD"
1 839 c 864 g 796 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="axin2"
/protein_id="saya440.1"
/protein_id="saya440.1"
/db_xref="Gi:7229080"
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/translation="murtLTDDMVSSFREDDPRPPVPGEEGETTCHHPSKLAMMRPKD
/translation="murtLTDDMVSSFREDDPRPPVPGEEGETTCHHPSKLAMMRPKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKRLCKSGEEVNMEGLENSLLQLPADSTDRSQNVWQWILESDRQTKHKPHSTQNVKKS
HSLEPTRTHTWGGGGSSGHLRAHQPAHPFVQDPAMPPLPPPNTLAQLEEARRRLEEVS
KPSKQRHSTSSLQRDKSHPVPVQNGSSAFPMDERKDPKKMSGCHSSLGSETVVTYFFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LQREMORNMENNGOVSLPPEPBTRRPPKEMTPVEPAAFAAQLIARLERLKREQETMSS
LQREMORNMENNGOVSLPPEPBTRRPPKEMTPVEPAAFAAQLIARLERLKRECETMSS
LEERLOOIGEEEERDESEMSSSSASHSLPLLPPGTCEEDPQAILDEHLSRVLKTPGCQ
SPGLLRHSPRARRSPEORPLPRGGLSTBSOSSSMIGYVPAKTFISROSTRHIHHYIHH
HAGPKSKEQIEVEATORVQCLCHGTSECCTAPYIRSRSLGRDQCASPAEVALGHSSTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EREKCYDTLDEWFACNGFRQMDLKDTKTHRVAKAIYKRYIENNSIVAKQLKPATKTFI
RDNIKRQQIIDSAMFDQAQMEIQTAMEERAYQMFIJSDIYLEYYETGCERPSHVRPNGL
GGLKLVCGYLPTLNEEEEMSCNDFKAKALATVYGLSAKTLRSPPLRAVEALEKCYSKY
RRSDPGNPNRFTSGYSFAPATSANDSEVSSDALTDDSMSMTDSSVDAIPPYKLGSKKQ
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                                                                                                                                                                                                                                                                                                                                              acgcctgtggaacctgctgccttcgccgccgagctcatctccaggctggagaaactgaaa 120
                                                                                                                                                                                                                                                                                                                                                                                                                                gccaatggccaagtgtctctacctcattttccgagaacccaccgcctgcccaaggagatg 60
                                                                                                                                                                                                                                             CGCACGCGGGAGGCCGAGGAGGAGCTGGAGGAGCGGCTGAAG 1354
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                                                                                                                                                                                                                                                                                                                                                                                                           GTCAATGGGCGGGTGCCCCTACCTCACATTCCCCGCACGTACCGGGTGCCGAAGGAGGT- 1254
                                                                           Xenopus laevis a
AF140243
AF140243.1 GI:6
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                     Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                     African clawed frog
                                                                                                                                          AF140243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="GPGSRHHRARDRLIHFGAVSTDVLGCSAHCSLTQSPKMNIQEOG
FPLDLGASTTEDAPRPPVPGEBGELVSTDPRASYSFCGKGVGIKGETSTATPRRSD
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FRKLEPCDSNEEKRLKLARAIYRKYILDNNGIVSROTKBATKSFIKGCIMKQLIDPAM
FDQAQTEIQATMEENTYPSFLKSDIYLEYTRTGSESPKVCSDQSSGSGTGKGISGYLP
TLNEDEEMKCDQDMDEDDGRDAAPGRLPQKLLLETAAPRSSSRRYSEGREFRYGSW
REPVNPYYVNAGYALAPATSANDSEQQSLSSDADTLSLTDSSVDGIPPYRIKKQHRRE
MQESAQVNGRVPLPHIPTYTKYPXEVNYEPQKFAEELHRLEAVQRTREAEEKLEERL
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LDEHYQRVLRTTGROSSGPBGPCHKLPPAPAWHHFPPRLCWTWACAGLRDAHEENPESI
LDHHHRVHHYHHSTARPKEOVEAEATRRAQSSFAWGLEPHSHGAKSGCYSESVGAAP
NASDGLAHSGKVGVACKRNAKKAESGKSASTEVPGASEDAEKNOXIMOWIIEGEKEIS
RHRRTGHGSSGTRKPQPHENSRPLSLEHPWAGPQLRTSVQPSHLFIQDDTMPPHRAPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLTQLEEARRRLEEEEKRASRAPSKQRYVQEVWRRGRAVCAPVLIVVPAVSDIE LSETETRSQRKVGGGSAQPCDSIVVAYYFCGEPIPYRTLVRGRAVTLGQFKELLTKKG SYRYYFKKVSDEFDCGVVFEEVREDEAVLPVFEEKIIGKVEKVD"
1 1010 c 1066 g 582 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function="may inhibit embryonic axis formation" /note="contains RGS domain and Daughterless similarity; may inhibit embryonic axis formation"
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mutation due
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/map="16p13.3"
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/db_xref="taxon:9606"
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/db_xref="GI:2252820"
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Danio rerio Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi Cypriniformes; Cyprinidae; Rasborinae; Danio.
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RLYEDKRYPKLHKSRCVQSTTLKEKGKTAESVPSSGFSTLKLSEEQKTAKKPSSECPG
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Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Department of Molecular Oncology; 2-2, Yamadaoka, Suita,
565-0871, Japan (E-mail:hirano@molonc.med.osaka-u.ac.jp,
                                                 chicken.
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Tel:81-6-879-3880, Fax:81-6-879-3889)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 51.8; DB 8;
Pred. No. 0.0014;
0; Mismatches 57;
                                                                                                                                         complete
                                                                                                                                            cds.
                                                                                                                                                                 VRT
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Wellcome Trust

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                                                                                                                                                                                                                                                                                                                                                                                             1341 GCAAATGGACGTGTGCCACTACCTCACATTCCTCGTACATATCGAATGCCAAAGGATAT - 1399
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                                                                                                                                                                                                                     1458 AAGGAACGTGAAGCAGAGGAGGAAATTGGAGGAGCGCCT 1495
                                                                                                                                                                                                                                                              121
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                                                                                                                                                                                                                                                                                                                                                                                                                                    1 gccaatggccaagtgtctctacctcattttccgagaacccaccgcctgcccaaggagatg 60
                                                                                                                                                                                                                                            ctggagctggaaagccgccatagtctggaggagcggct 158
                                                                                                                                                                                                                                                                                                                                acgcctgtggaacctgcttcgccttcgccgccgagctcatctccaggctggagaaactgaaa 120
                                                                                                                                                                                                                                                                                                         --CCACGTTGAACCAGAAAAGTTTGCTGCAGAACTGATCAATCGTTTGGAAGAAGTACAG 1457
  Human DNA sequence from cosmid 419C1 from the short arm of chromosome 16, spanning 29754 299754.1 GI:303577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zeng,L., Fagotto,F., Zhang,T., Hsu,W., Vasicek,T.J., Perry,W. 3rd, Lee,J.J., Tilghman,S.M., Gumbiner,B.M. and Costantini,F. The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling pathway that regulates embryonic axis formation Cell 90 (1), 181-192 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (13-JUN-1997) Genetics and University, 701 W. 168th Street, New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zeng, L., Zhang, r. Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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LKQRLKPQKRPGSGASQPCENIVVAYYFCGEPTPYRTLVKGRVVTLGQFKELLTKKGN
YRYYFKKVSDEFDCGVVFEEVREDDTILPIFEEKIIGKVEKID*
825 c 858 g 598 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QNSFAWNVDSHNYATKSRNYSENLGMAPVPMDSLGYSGKASLLSKRNIKKTDSGKSDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTDSSIDGIPPYRLRKOHRREMOESAKANGRVPLPHIPRTYRMPKDIHVEPEKFAAELINRLEEVOKKREAEEKELEERLKRVRAEEEGEDADISGPSVISHKMPSAOPEHHFAPRKSKEMEGCAGMOMRDAHEEMPESILDEHVORVWKTPGCOSPPGRHSPKPRSPESGHLEK VSEMGCAGMOMRDAHEEMPESILDEHVORVWKTPGCOSPPGRHSPKPRSPESGHEKK VSEMGCAGMOMRDAHEMPESILDEHVORVWKTPGCOSPGRAENFKPKDIEAEATORV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KPATKSFIKDCVMKLQIDPDMFDQAQTEIQCMIEDNTYPLFLKSDIYLEYTRTGGESP
KIYSDPSSGSGTGKGLPGYLPTLNEDEEWKCDQDTEPEASRDSAPSSRLTQKLLLETA
TQRATSTRRYSEGREFRHGSWREPVNPYYVNTGYAMAPATSANDSEQQSMSSDADTMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutation due to an iap insertion in the 258...2783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>ANYEMPGSPEDVERNQKILQWIIEGEKEISRHKKTNHGSSGVKKQLSHDMVRPLSIER</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RTFLKQEDCADLLDFWFACSGFRKLEPCVSNEEKRLKLAKAIYKKYILDNNGIVSRQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAC60245.1"
/db_xref="GI:2252818"
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/db_xref-"taxon:9031"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'function="may inhibit embryonic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 42.8; DB Pred. No. 0.29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                           PRI 23-NOV-1999 419C1 from a contig from the tip spanning 2Mb of 16p13.3.
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York, NY 10032, USA
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The true left end of Clone 419Cl is at 1 in this sequence. The true right end of clone 314C4 is at 104.

The true left end of clone 333Bl0 is at 21926.

The true left end of clone 333Bl0 is at 21926.

The true left end of clone contig on 16p.

The true left at 400kb clone contig on 16p.

Higgs D.R., Flint J. unpublished. MRC Molecular Haematology Unit, Institute of Molecular Medicine, Oxford.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (27-OCT-1997) Chromosome 16 Project Group (http://www.sanger.ac.uk/HGP/Chr16/) Sanger Centre, Wellcome Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 22029)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              libraries constructed by Norman Doggett (unpublished).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clonerequest@sanger.ac.uk
On Apr 8, 1998 this sequence version replaced gi:2465054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smye, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              enquires: humquery@sanger.ac.uk Clone requests:
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incomplete repeat"
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/db_xref="taxon:9606"
/note="AluJo repeat:
incomplete repeat"
                                           7656.
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incomplete repeat"
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incomplete repeat"
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incomplete repeat"
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/clone_lib="LA16"
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incomplete repeat"
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                                                             Alux repeat: matches 15. .301 of consensus"
                                                                                                                                                                                                                   AluY repeat: matches 298.
                      matches
                                                                                                                            matches 247.
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                        .124 of consensus;
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of consensus" of consensus;

of

consensus;

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BASE COUNT
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Best Local Similarity 60.
Matches 84; Conservative
10598 TCCCTCGCAGCGCACGTACCGGGGTGCCGAAGGAGGT----CCGCGTGGAGCCTCAGAAGTT 10542
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                                                                                                                                                                                                                                                                                                                                                           5145 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="MERIB repeat: matches 333. .139 of consensus"
14879. .14912
/note="17 copies of 2 mer 82 % conserved"
15202. .15422
/note="Alux repeat: matches 7. .227 of consensus;
incomplete repeat"
16542. .16847
/note="Alux repeat: matches 301. .1 of consensus"
17178. .17476
/note="Alux repeat: matches 301. .1 of consensus"
17637. .17936
/note="Alux repeat: matches 301. .1 of consensus"
17637. .17936
                                                                                                                                                                                                                                                                                                                                                 incomplete repeat" 6217 c 5887 g 4780 t
                                                                                                                                                                                                                                                                                                                                                                          21999. .22028
/note="AluSx/g repeat: matches 82. .111 of consensus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Alusq repeat: matches 297. .1 of consensus"
9967. .10175
/note="match: 5' EST AA085320"
10450. .>16291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9042. .9307
/note="AluJb repeat: matches 267. .1 of consensus; incomplete repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                   'note="AluY repeat: matches 1. .301 of consensus"
1999. .22028
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="4 copies of 44 mer 88 % conserved"
21693. .21994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hote-"AluJo repeat: matches 2. .302 of consensus" 0549. .20724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="AluJo repeat: matches 2. .124 of consensus;
nocomplete repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="AluY repeat: matches 301..1 of consensus" 2003..12110
note="AluSg repeat: matches 123..1 of consensus; mcomplete repeat" 2124.
                                                                                                                                                                                                                                                       24.6%;
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14. .19163
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2. .12743
                                                                                                                                                                                                                                    Score 39.8; DB 91; Length 22029; Pred. No. 1.2; O; Mismatches 52; Indels 3;
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Minimum DB
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Maximum Match 100%
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length: 2000000000
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Murine axin gene.
Mouse brain CNG-2
Human In ion chann
Human In ion chann
Human In ion chann
Human METHI relate
AC004449 CDNA clon
Rat Olfactory Ih i
                                                                                                                                                                                                        Description
                                                                                                                                                    Human conductin cD
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Human porphobilino	X87633	20	1035		28.8	45
Human porphobilino	X87632	20	1035		28.8	44
Human porphobilino	X87630	20	1035		28.8	43
Human porphobilino	X87638	20	1035		. 28.8	42
Human porphobilino	X87637	20	1034		28.8	41
₽	X40107	20	751		28.8	40
lung	C79115	21	550		28.8	39
Human lung tumour	Z07225	20	550		28.8	38
Membrane-bound pro	Z64954	21	3531		29.2	37
Human PRO290 nucle	C58368	21	3531		29.2	36
Human heart tissue	Z09496	20	4751	18.3	29.6	35
Bovine retina Ih i	Z09488	20	1820		29.6	34
CNG-	X84445	20	1790		29.6	ω ω
Mouse brain CNG-3	X84446	20	1507		.29.6	32
	X25488	20	1307		29.6	31
Human secreted pro	F33247	22	1246		29.6	30
Human porphobilino	X87634	20	1034		29.6	29
Human secreted pro	C00205	21	372		29.6	28
Eucalyptus grandis	C56489	21	537		29.8	27
9	A42312	21	533		30.2	26
_	Z58958	21	1914		30.4	25
_	258953	21	1553		30.4	24
hGDF-1 and hUOG-1	Q20690	13	2510		30.8	23
Mouse GDF-1 encodi	239482	21	1247		30.8	22
Human GDF-1 (fx) p	V19538	19	1247	19.0	30.8	21
Human GDF-1 cDNA.	V32588	19	1247		30.8	20
cDNA sequence enco	T97883	18	1247		30.8	19
÷	V10351	18	1247	•	30.8	18
Human GDF-1(fx) mo	Q67402	15	1247		30.8	17
-	Q45120	15	1247	19.0	30.8	16
GDF-	Q67315	15	1247		30.8	15
Human morphogenic	Q58055	15	1247	٠	30.8	14
ရှ	88	14	1247	19.0	30.8	13
Human GDF-1 coding	Q41354	14	1247	19.0	30.8	12

## ALIGNMENTS

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Tumor-suppressing protein conductin diagnosis of tumors Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour; therapy; cytoplasmic degradation; blockade; Wnt signalling pathway; Mingless signalling pathway; Adenomatous Polyposis Coli; APC; tumour suppressor; ss. X23370; WPI; 1999-214706/18. P-PSDB; W93570. 02-SEP-1997; 01-SEP-1998; Human conductin cDNA 17-JUN-1999 X23370 standard; cDNA; Behrens J, Birchmeier W; 11-MAR-1999 WO9911780-A2 Homo sapiens (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX ш (first entry) 97DE-1038205 98WO-DE02621 2523 ВP . used for treatment and

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel human conductin protein which has anti-tumour activity. Detecting the presence or amount of conductin, at protein or nucleic acid levels, is used to diagnose tumours, while agents that (re)activate conductin are used for tumour therapy. Conductin binds to beta-catenin and induces its cytoplasmic degradation, resulting in blockade of the Wnt/Wingless signalling pathway in vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC) fragments and, in conjunction with APC, acts as a tumour suppressor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1147
                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                      Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour; therapy; cytoplasmic degradation; blockade; Wnt signalling pathway; Wingless signalling pathway; Adenomatous Polyposis Coli; APC;
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                                                                                                                                                                                        protein_bind
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                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                          tumour suppressor; ss
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                                                                                       /bound_moiety= beta-catenin
/note= "as described in Claim
2561..2713
                                                                                                                                                                                                                                         /product= "Conductin" 446..814
                                                                                                                                                                                          1241..1402
                                                                                                                                        1403..1609
                                                                                                                                                    /bound_moiety= GSK-3beta
/note= "as described in
                                                                                                                                                                                                    /note= "regulator
described
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA;
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                                                     "Dishevelied homology region Claim 22"
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                                                    Claim
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Pred. No. 1.2e-38;
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Matches 162
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                                                                                                                                                                                                                                                                                                                                       1361
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 09-JUL-1998;
                                             WO9902179-A1
                                                                                                                                                   beta-catenin; ss.
                                                                                                                                                                         gastrointestinal cancer;
                                                                                                                                                                                  Axin; cancer; breast cancer; colorectal cancer;
                                                                                                                                                                                                          Human axin gene.
                                                                                                                                                                                                                                 14-JUN-1999
                                                                                                                                                                                                                                                        X09012;
                                                                                                                                                                                                                                                                              X09012 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2825 BP; 703 A; 815 C; 813 G; 494 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumor-suppressing protein conductin
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                                                                                                                                                              diagnosis; treatment;
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 98WO-US14414.
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                                                                                          2..2704
                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                              er; esophageal cancer; carcinoma; melanoma;
therapy; thyroid carcinoma; tumorigenesis;
                                                                                                                                                                                                                                                                              3411
                                                                     Axin
                                                                                                                                                                                                                                                                               ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 162; DB 20;
Pred. No. 1.2e-38;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human conductin protein which
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                who are likely to develop cancer (thyroid carcinomas). The nucleic acids are also useful for diagnosing cancer and for detecting mutations in cancerous cells. Wild type Axin, its antisense molecule and identified compounds form pharmaceutical compositions in the treatment of cancer. The compositions are also useful for treating cancer by inhibiting tumorigenesis (by inducing degradation of beta-catenin). The nucleic acid encoding Axin acts through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     likely to develop cancer (including breast, colorectal, gastrointestinal, esophageal, carcinomas or melanomas). The wild type Axin and homologues of Axin are useful for treating subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding mutant and wild type Axin and oligonucleotides derived from them are useful for detecting mutations in the Axin gene and for determining whether a subject is
                                                                                                                                             Axin; cancer; breast cancer; colorectal cancer; gastrointestinal cancer; esophageal cancer; carcing diagnosis; treatment; therapy; thyroid carcinoma;
WO9902179-A1
                                                                                                                                  beta-catenin;
                                                                                                                                                                                                           Murine axin gene
                                                                                                                                                                                                                                         14-JUN-1999
                                                                                                                                                                                                                                                                        x09013;
                                                                                                                                                                                                                                                                                                   X09013 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                      1255 --ccgcgtggagcctcagaagttcgcggaggagctcatccaccgcctggaggctgtgcag 1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3411 BP; 752 A; 1010 C; 1066 G; 582 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    negative regulation of the Wnt pathway in the Nieuwkoop Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Figure 10A-10B; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Newly isolated nucleic acid encoding "axis inhibition" (Axin) - useful for detecting, diagnosing and treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYCO ) UNIV COLUMBIA NEW YORK.
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                                                                                                                                                                                                                                                                                                                                                                                                            121
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                                                                                                    musculus
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                                                                                                                                                                                                                                       (first entry)
                                                                                                                                  88.
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                                                                                                                                                                                                                                                                                                   DNA;
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                                                                                                                                                                                                                                                                                                   3761 BP
                            Axin
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Pred. No. 1.6e-07
D; Mismatches 5
                                                                                                                                               carcinoma; melanoma;
inoma; tumorigenesis;
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Best Local S
Matches 92
                                             BCNG; brain cyclic nucleotide gated ion channel; epilepsy; hyperalge Alzheimer's Disease; Parkinson's Disease; long QT syndrome; dyslexia sick sinus syndrome; age-related memory loss; cystic fibrosis; sudden death syndrome; pacemaker rhythm dysfunction; sensory disorde auditory disorder; respiratory disorder; attention deficit disorder; learning disability; drug addiction; therapy; mBCNG-2; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                          1533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3761 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Figure 9A-9B; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Newly isolated nucleic acid encoding "axis inhibition" protein (Axin) - useful for detecting, diagnosing and treating cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Constantini F,
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                                                                                                                                                                 Mouse brain
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                                                                                                                                                                                                                                    X84444;
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              дs
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                                                                                                                                                                                                                                                                                                                                                   cgcactcgagaggctgaagaaaagttggaggaacggctgaag 1631
                                                                                                                                                                                                                                                                                                                                                                                                                        ---cgggtagagccacagaaatttgctgaagagcttattcaccgtctagaggctgtccag 1589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gtcaatgggcgggtacctctacctcacattcctcgcacttaccgaatgccaaaggagatc 1532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                CNG-2 coding sequence.
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                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38.8;
Pred. No. 0
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. 026;
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                                                                                                                                                                                                                                                                                                                                                                                          162
                                                                                                                                epilepsy; hyperalgesia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 3761;
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                                                                                                                  dyslexia;
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KW Ih i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC (BCNG) of the invention, designated mBCNG-2. BCNG and BCNG-related CC proteins are useful in screening for compounds that modulate, interact or CC affect expression. Compounds, e.g. antagonists and agonists, identified CC in the methods are useful for modulating BCNG or BCNG-related protein CC activity. Modulation is increased or decreased ion permissivity or ion CC flow rate. Modulators of BCNG, can be used to treat a neurological, renal, CC pulmonary, hepatic or cardiovascular condition. Such conditions include epilepsy, Alzheimer's Disease, Parkinson's Disease, long OT syndrome, CC epilepsy, Alzheimer's Disease, Parkinson's Disease, long OT syndrome, CC death syndrome or pacemaker rhythm dysfunction. BCNG or BCNG-related protein can also be used to treat sensory disorders, e.g. blindness, loss of vision, loss of smell, numbness and lack of ability to taste. Also central nervous system areas that control respiration or defects in the drugs dyslexia, attention deficit disorder or learning disabilities, CC drug addiction and regulation of cell secretions. The proteins are useful targets for screening for drugs that are effective in the control of pain
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Best Local
Ih ion channel; human; sea urchin; fruit fly; rat; bovine; analgesi cardioactive; pacemaker; cardiac;muscle; ion channel modulator; treatment; diagnosis; ion channel-related disease; cardiac disease; circulatory disorder; sinus ganglion regulation; sleep disorder; cortico-thalamic neuron; pain; detection; mutation; ss.
                                                                                                                                                                                                                                                                                                         1177
                                                                                                                Human Ih
                                                                                                                                                   02-NOV-1999
                                                                                                                                                                                                                      Z09482 standard;
                                                                                                                                                                                                                                                                                                                                                                              1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1584 BP; 351 A; 456 C; 437 G; 340 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleotide-gated ion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                An isolated nucleic acid encoding a brain or heart cyclic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-418922/35
P-PSDB; YZ2193.
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23-DEC-1997;
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                                                                                                                                                                                                                                                                                                                            ctccaggctggagaaactgaaactggagct 128
                                                                                                                                                                                                                                                                                                                                                                                                    ccaccgcctgcccaaggagatgacgcctgtggaacctgctgccttcgccgccgagctcat 98
                                                                                                                                                                                                                                                                                                         CTCCAGGCTGGAAGACCTCAAATTTGAGCT 1148
                                                                                                                                                                                                                                                                                                                                                                         CCACCCCATGCTGGATGAAGTACATCTTCTTCCCGATGGTCCCCTCTCGGATGATGTAAT 1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
54; Conser
                                                                                                              ion channel DNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 192-193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encodes the brain cyclic nucleotide-gated ion channel invention, designated mBCNG-2. BCNG and BCNG-related
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97US-0997685.
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                                                                                                                                                                                                                    DNA;
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Pred. No. 1
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Mismatches
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Best Local
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                                                                     cardioactive; pacemaker; cardiac muscle; ion channel modulator; treatment; diagnosis; ion channel-related disease; cardiac disectriculatory disorder; sinus ganglion regulation; sleep disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acid and its encoding protein is used to identify substances (A) that modulate activity of ion channels; to treat and/or diagnose ion channel-related diseases, particularly cardiac or circulatory disorders and to prevent and/or treat cardiac/circulatory disorders (especially faulty regulation of the sinus ganglion), sleep disorders (particularly abnormal function of cortico-thalamic neurons) and/or pain. Fragments of the Ih ion channel nucleic acid are used to detect mutations e.g. for differential diagnosis. This sequence encodes a human Ih channel fragment isolated from human thalamus tissue.
                            Homo sapiens
                                                           cortico-thalamic neuron; pain;
                                                                                                                       In ion channel; human; sea urchin; fruit fly; rat; bovine; analgesic;
                                                                                                                                                         Human
                                                                                                                                                                                                                                                   Z09492 standard; DNA; 2029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1342 BP; 252 A; 451 C; 390 G; 240 T; 9 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel Ih ion channel, isolated from human, sea urchin, bovine, rat, and fruitfly. The ion channels of the invention have analyesic and cardioactive activity. The Ih ion channel participates in the pacemaker function in cardiac muscle. The Ih ion channel nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid encoding an Ih ion channel, used to identify specific modulators, and for treatment, prevention and diagnosis of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baumann
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                                                                                                                                                                                                                                                                                                                                                                                          792 CCACGCCGTGCTGGATGAAGTACATCTTCTTCCCGATGGTGCCTTCGCGGATGATGTAGT 733
                                                                                                                                                                                                                                                                                                                               732 CACCCGGCTGGAAGACCTCGAACTTGAGCTTG 701
                                                                                                                                                                                                                                                                                                                                                 99 ctccaggctggagaaactgaaactggagctgg 130
                                                                                                                                                                                                                                                                                                                                                                                                           39 ccaccgcctgcccaaggagatgacgcctgtggaacctgctgccttcgccgccgagctcat 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1999-527472/44.
                                                                                                                                                      heart tissue Ih ion channel DNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boenigk W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98DE-1006581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gauss R,
                                                                                                                                                                                                                                                    ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 31.2; D. Pred. No. 3.5; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                           detection; mutation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaupp B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        į,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DΒ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         38;
                                                                        e; cardiac disease;
sleep disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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RESULT C10491/C ID 209491/C ID 2094 XX Z 2094 XX Z 2094 Huma XX Ih I KW Card KW Card KW Ctreak KW Cort XX COT XX P COT XX P COT XX P COT XX P COT XX P COT XX P COT XX P COT XX CT XX COT XX CT 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      have analgesic and cardioactive activity. The Ih ion channel participates in the pacemaker function in cardiac muscle. The Ih ion channel nucleic acid and its encoding protein is used to identify substances (A) that modulate activity of ion channels; to treat and/or diagnose ion channel-related diseases, particularly cardiac or circulatory disorders and to prevent and/or treat cardiac/circulatory disorders (especially faulty regulation of the sinus ganglion), sleep disorders (particularly abnormal function of cortico-thalamic neurons) and/or pain. Fragments of the Ih ion channel nucleic acid are used to detect mutations e.g. for
                                                                                                                                                                                                                      Ih ion channel; human; sea urchin; fruit fly; rat; bovine; analgesic cardioactive; pacemaker; cardiac muscle; ion channel modulator; treatment; diagnosis; ion channel-related disease; cardiac disease; circulatory disorder; sinus ganglion regulation; sleep disorder; cortico-thalamic neuron; pain; detection; mutation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes a novel Ih ion channel, isolated from human, sea urchin, bovine, rat, and fruitfly. The ion channels of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      differential diagnosis. This sequence encodes a human Ih channel fragment isolated from heart tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 68-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid encoding an specific modulators, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baumann A,
Seifert R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-FEB-1998;
  12-FEB-1999;
                                                                                                                 WO9942574-A1
                                                                                                                                                                                                                                                                                                                                                                                                      Human Ih ion
                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            209491 standard; DNA; 2886 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (KERJ ) FORSCHUNGSZENTRUM JUELICH GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-AUG-1999
                                                        26-AUG-1999.
                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 CCCCAGGCTGGAAGACCTCAAAACGCAGCTTG 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ctccaggctggagaaactgaaactggagctgg 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ccaccgcctgcccaaggagatgacgcctgtggaacctgctgccttcgccgccgagctcat 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cardiac disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCACGCCATGCTGGATGAAGTACATCTTCTTGCCAATGGTGCCTTCCCGGATGATGTAGT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2029 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                   channel DNA fragment #2.
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  99WO-EP00942.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                338 A; 774 C; 509 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19.3%;
58.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gauss R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 31.2;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treatment, prevention and diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kaupp B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                356 T; 52 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scholten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38;
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                                                                                                                                                                                                                                                                                                                                             analgesic;
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PR 28-A
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acid and its encoding protein is used to identify substances (A) that modulate activity of ion channels; to treat and/or diagnose ion channel related diseases, particularly cardiac or circulatory disorders and to prevent and/or treat cardiac/circulatory disorders (especially faulty regulation of the sinus ganglion), sleep disorders (particularly abnormal function of cortico-thalamic neurons) and/or pain. Fragments of the Ih ion channel nucleic acid are used to detect mutations e.g. for differential diagnosis. This sequence encodes a human Ih channel fragment isolated from human thalamus tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baumann A,
Seifert R;
                                                                                                                                                                          Human; METH1; METH2; anti-anglogenic; metalloprotease thrombospondin; cancer; diagnosis; hyperproliferative disorder; autoimmune disease; anglogenesis inhibitor; abnormal wound healing; inflammation; rheumatoid arthritis; psoriasis; endometrial bleeding disorder; diabetic retinopathy; macula degeneration; haemangioma; detection; arterial-venous malformation; immune deficiency; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 67-68; 82pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-527472/44
                                                                                                                                                                                                                                                                                         Human METH1 related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel Ih ion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KERJ ) FORSCHUNGSZENTRUM JUELICH
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23-JAN-1998;
28-AUG-1998;
                                                22-JAN-1999;
                                                                                                              WO9937660-A1
                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                       10-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                     232028 standard; DNA; 38186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2886 BP; 605 A; 774 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sea urchin, bovine, rat, and fruitfly. The ion channels of the invention have analgesic and cardioactive activity. The Ih ion channel participates in the pacemaker function in cardiac muscle. The Ih ion channel nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        specific modulators, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ccaccgcctgcccaaggagatgacgcctgtggaacctgcttcctccgccgccgagctcat 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cardiac disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACCCGGCTGGAAGACCTCGAACTTGAGCTTG 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCACGCCGTGCTGGATGAAGTACATCTTCTTCCCGATGGTGCCTTCGCGGATGATGTAGT 1250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boenigk W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                       (first entry)
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98US-0072298.
98US-0098539.
                                                99WO-US01313.
                                                                                                                                                                                                                                                                                         EST AC004449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gauss R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g an
for
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                                                                                                                                                                                                                                                                                                                                                                                       ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 31.2;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               940 G; 558 T; 9 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         n channel, isolated from human,
The ion channels of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₽,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38;
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C90085/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     metalloprotease thrombospondin (METH) proteins METH1 and METH2

CC respectively. METH1 and METH2 have been found to be potent inhibitors of

Cangiogenesis both in vitro and in vivo. They can be used for treating

CC angiogenesis both in vitro and in vivo. They can be used for treating

CC cancer and other disorders related to angiogenesis including abnormal

CC wound healing, inflammation, rheumatoid arthritis, psoriasis,

CC macula degeneration, haemangiomas, and arterial-venous malformations.

CC They may be useful in treating deficiencies or disorders of the immune

CC system, by activating or inhibiting the proliferation, differentiation,

CC or mobilisation (chemotaxis) of immune cells. The etiology of these

CC immune deficiencies or disorders may be genetic, somatic, such as

CC cancer or some autoimmune disorders, acquired (e.g. by chemotherapy or

CC toxins), or infectious. They can also be used to treat inflammatory

CC conditions, both chronic and acute conditions. The products can also be

CC used for detection and diagnosis. Z32002 to Z32080, and Y49503 to Y49511

CC represent sequences given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                      METH; metalloprotease; thrombospondin; angiogenesis inhibition; cancer therapy; benign tumour; ocular angiogenic disease; rheumatoid arthritis; psoriasis; wound healing; endometriosis; vasculogenesis; granulation; hypertrophic scar; nonunion fracture; scleroderma, trachoma; vascular adhesion; myocardial angiogenesis; coronary collateral; cerebral collateral; arteriovenous malformation; ischaemic limb angiogenesis; Oster-Webber syndrome; wound granulation; plaque neovascularisation; telanglectasia; haemophiliac joint; EST; angiofibroma; fibromuscular dysplasia; expressed sequence tag; angiofibroma; fibromuscular dysplasia; expressed sequence tag;
                Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                     C90085 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                          Crohn's disease;
                                                                                                                                                                                                                                                                              AC004449 cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2432 CACCCGGCTGGAAGACCTCGAACTTGAGCTTG 2401
                                                                                                                                                                                                                                                                                                                      19-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 363-387; 457pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 38186 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    232000 and 232001 encode, and Y49501 and Y49502 represent,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated metalloprotease thrombospondin polypeptides, useful for treating hyperproliferative disorders, cancers or autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Iruela-Arispe L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IRUE/) IRUELA-ARISPE
(HAST/) HASTINGS G A.
(RUBE/) RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ctccaggctggagaaactgaaactggagctgg 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCACGCCGTGCTGGATGAAGTACATCTTCTTCCCGATGGTGCCTTCGCGGATGATGTAGT 2433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ccaccgcctgcccaaggagatgacgcctgtggaacctgctgccttcgccgccgagctcat 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1999-590684/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.3%;
ilarity 58.7%;
Conservative
                                                          atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                     DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hastings GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7571 A; 11503 C; 12193 G; 6919
                                                                                                                                                                                                                                                                                                                                                                                                   38186
                                                                                                                                                                                                                                                                                                                                                                                                     дB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 31.2; DB Pred. No. 7.7; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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                                                          expressed sequence control; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 38186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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RESULT 1
209494/c
ID 2094
XX 2094
AC 2094
XX 02-N
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Best Local
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22-DEC-1999;
22-FEB-2000;
                                                                                                                                                                                     2492
                                                                                                                                                                                                                                                                                                                                         ischaemic limb angiogenesis, Osler-Webber syndrome, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, fibromuscular dysplasia, wound granulation, Crohn's disease or atherosclerosis. METH can also be used in birth control. METH can also used in diagnostic methods for the prognosis of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                               arthritis, psoriasis, delayed wound healing, endometriosis, vasculogenesis, granulations, hypertrophic scars, nonunion fractures, scleroderma, trachoma, vascular adhesions, myocardial angiogenesis, coronary collaterals, cerebral collaterals, arteriovenous malformations,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        metalloprotease and TH for thrombospondin; see B50002 and B50003). present sequence is an expressed sequence tag (EST) for METH. METH used for inhibiting analogenesis in an individual, and for treating cancer, benign tumours, an ocular angiogenic disease, rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to human METH1 and METH2, metalloprotease and TH for thrombospondin; see B50002 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 7; Pages 663-687; 768pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     METH1 and METH2 polynucleotides and encoded polypeptides, used to inhibit angiogensis in the treatment of disorders such as cancer, rheumatoid arthritis and psoriasis
                              Z09494;
                                                        209494 standard;
                                                                                                                             2432 CACCCGGCTGGAAGACCTCGAACTTGAGCTTG 2401
                                                                                                                                                                                                                                                                                                                 Sequence 38186 BP; 7571 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-025136/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Iruela-Arispe
Fornwald JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAY-1999;
20-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAST/)
                                                                                                                                                         99
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                                                                                                                                               ctccaggctggagaaactgaaactggagctgg 130
| || || || || || || || || ||
                                                                                                                                                                                     CCACGCCGTGCTGGATGAAGTACATCTTCTTCCCGATGGTGCCTTCGCGGATGATGTAGT
                                                                                                                                                                                                     ccaccgcctgcccaaggagatgacgcctgtggaacctgctgccttcgccgccgagctcat 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RUBEN S M.
JONAK Z L.
TRULLI S H.
FORNWALD J A.
                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMITHKLINE BEECHAM CORP.
BETH ISRAEL DEACONESS MI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TERRETT J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HASTINGS G A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IRUELA-ARISPE L.
                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0183792.
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Terrett JA;
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99US-0373658.
99US-0171503.
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99US-0144882.
                                                         DNA;
                                                                                                                                                                                                                                                       19.3%;
58.7%;
                                                           794
                                                           ВP
                                                                                                                                                                                                                                                                                                                 11502 C; 12194 G;
                                                                                                                                                                                                                                            Score 31.2; DB Pred. No. 7.7; 0; Mismatches
                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MS
                                                                                                                                                                                                                                                                         DB
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                                                                                                                                                                                                                                             38;
                                                                                                                                                                                                                                                                                                                   6919 T; 0 other;
                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                        Length 38186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trulli SH;
                                                                                                                                                                                                                                                                                                                                                            METH can also be
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                                                                                                                                                                                                                                            Gaps
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02-NOV-1999

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RESULT 12
Q41354
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AC Q41354
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DT 15-JUL
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Human
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Best Local S
Matches 53
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Selfert R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acid and its encoding protein is used to identify substances (A) that modulate activity of ion channels; to treat and/or diagnose ion channel-related diseases, particularly cardiac or circulatory disorders and to prevent and/or treat cardiac/circulatory disorders (especially faulty regulation of the sinus ganglion), sleep disorders (particularly abnormal function of cortico-thalamic neurons) and/or pain. Fragments of the I ion channel nucleic acid are used to detect mutations e.g. for the I ion channel nucleic acid are used to detect mutations e.g. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel Ih ion channel, isolated from human, sea urchin, bovine, rat, and fruitfly. The ion channels of the invention have analyesic and cardioactive activity. The Ih ion channel participates in the pacemaker function in cardiac muscle. The Ih ion channel nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     In ion channel; human; sea urchin; fruit fly; rat; bovine; analgesic cardioactive; pacemaker; cardiac muscle; ion channel modulator; treatment; diagnosis; ion channel-related disease; cardiac disease; circulatory disorder; sinus ganglion regulation; sleep disorder;
                                                                                                Q41354;
                                                                                                                              Q41354 standard; cDNA; 1247 BP
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 794 BP; 179 A; 230 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   differential diagnosis. This sequence encodes a rat Ih channel fragment isolated from olfactory tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 71; 82pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e.g. cardiac disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-527472/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-AUG-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cortico-thalamic neuron; pain; detection; mutation; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat olfactory Ih ion channel DNA fragment #4
   Human brain; Growth/Differentiation factor;
                               Human GDF-1 coding sequence
                                                                 15-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              specific modulators, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-FEB-1999;
                                                                                                                                                                                                           558
                                                                                                                                                                                                                                                                          819
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                                                                                                                                                                                                                                                                                                                                        Local Similarity
les 53; Conserv
                                                                                                                                                                                                                             CCACCCCGTGCTGGATGAAGTACATCTTCTTCCCGATGGTCCCCTCTCGGATGATGTAGT
                                                                                                                                                                                                                                                                                           ccaccgcctgcccaaggagatgacgcctgtggaacctgctgccttcgccgccgagctcat 98
                                                                                                                                                                                                           CTCCAGGCTGGAAGACCTCAAATTTGAGCT
                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boenigk W,
                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                      19.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               German.
                                                                                                                                                                                                                                                                                                                                      ; Score 30.8; D; Pred. No. 4.1; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ih ion channel, used to identify treatment, prevention and diagno:
                                                                                                                                                                                                                                                                                                                                                                                                                     224 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kaupp B,
                                                                                                                                                                                                                                                                                                                                                                                                                     161 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                        DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scholten
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    analgesic
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RESULT
Q38862
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AC Q3
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Morphogen-induced modulation of inflammatory response resulting tissue damage, e.g. in autoimmune diseases, asthma, ischemia reperfusion injury, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         morphogenic protein; developmental cascade; morphogen; inflammation; anti-inflammatory;
 Morphogen GDF-1 coding sequence.
                      13-JUL-1993
                                            Q38862
                                                                 Q38862 standard;
                                                                                                                                                                                                                                                                                                                                                                                                            Claim 26; Page 138-140; 165pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-AUG-1991;
30-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-MAR-1993
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                                                                                                                                                                                                                                                                                                             Sequence 1247 BP; 127 A; 497 C;
                                                                                                                                                                                                                                                                                                                                          damage in e.g. inflammatory disease, autoimmune disease, arthritis, psoriasis, dermatitis, diabetes and emphysema. Proteins having at least 70% homology with GDF-1 amino acid sequences can also be used "GDF-1(fx)" (see R33407) refers to protein sequences encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cohen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-AUG-1991;
                                                                                                                                                                                                                                                                                                                                  human GDF-1 gene and defining the seven cysteine skeleton
                                                                                                                                                                                                                                                                                                                                                                                       GDF-1 is a preferred morphogen for use in treating tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1993-100652/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-AUG-1992;
                                                                                                                       831
                                                                                                                                                                                                            711
                                                                                                                                                                771
                                                                                                                                         151 gagcggctgc 160
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                                                                                                                                                                                                                      31 ccgagaacccaccgcctgcccaaggagatgacgcctgtggaacctgctgccttcgccgcc 90
                                                                                       13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RHL,
                                                                                                                                                                                   gagotoatotocaggotggagaaactgaaactggagotggaaagoogccatagtotggag 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens.
                                                                                                                     cggccgcggc 840
                                                                                                                                                               ctggccgaggcctcgctgctgctggtgaccctcgacccgcgcctgtgccaccccctggcc
                                                                                                                                                                                                           68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kuberasampath T,
Rueger DC, Smar
                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Growth Factor;
                      (first entry)
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91US-0752861
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726..1199
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/note= "contains
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                                                                  DNA;
                                                                                                                                                                                                                                                                19.0%;
52.3%;
                                                                  1247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              th T, Oppermann Smart JE;
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                                                                                                                                                                                                                                                       0;
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Pred.
                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                             448 G; 175 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conserved 7
                                                                                                                                                                                                                                                                 30.8; DI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cysteine skeleton
                                                                                                                                                                                                                                                        62;
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                                                                                                                                                                                                                                                                            Length 1247;
                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              diabetes,
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RESULT
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Matches 68
                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence encodes the morphogen growth/differentiation factor 1 (GDF-1) isolated from human brain. This morphogen is inactive when reduced but is active as an oxidised homodimer and when oxidised in combination with other morphogens. These morphogens are capable of stimulating proliferation of progenitor cell, stimulating the differentiation of progenitor cells, stimulating the proliferation of
                           Q58055;
                                                                                                                                                                                                                                                                                                                                                                    differentiated cells and supporting the growth and maintenance of differentiated cells, including the redifferentiation of transformed cells. These morphogens may also be capable of inducing redifferentiation of committed cells under appropriate environmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Morphogen; homodimer; stimulate; proliferation; progenitor cell; differentiation; growth; redifferentiation; transformation; human; mouse; Drosophila; Xenopus; committed cells; hippocampus; growth/differentiation factor 1; GDF-1; ss.
  25-AUG-1994
                                                    Q58055 standard; cDNA; 1247
                                                                                                                                                                                                                                                                                                                                  Sequence 1247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Screening cpds. to determine ability to modulate effective concnof a morphogen - by assaying test tissue type cells for parameter indicative of a prodn. level change of morphogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 116-118; 132pp; English
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68; Conserv
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04-MAR-1993;
31-MAR-1993;
31-JUL-1992;
16-SEP-1992;
                                                                                                                                                                                                                              Human GDF-1 (fx) morphogen and proteins having at least 70% homology with it are preferred morphogens for inclusion in new morphogen-enriched nutritional formulations. The formulations are dietary compositions suitable for people at risk for tissue damage due to protein energy malnutrition or to altered metabolism function and infant formulations to enhance tissue development in an infant or juvenile.
                                                                                                                                                                                                                                                                                                                                                       Morphogen enriched dietary compositions and infant formula capable of enhancing tissue morphogenesis, development and viability, e.g. in infants, aged individuals and metabolic disorders, e.g. anorexia nervosa, etc
                                                                                                                                                                                                           Sequence 1247 BP;
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P-PSDB; R46750.
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                                                                                                                                                                                                                                                                                                                                Disclosure and Claims 25-26; Page 139-141; 160pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jones WK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9403075-A
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92US-0946235.
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/note= "GDF-1(FX) cDNA"
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52.3%;
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Pred. No. 4.5;
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Pang RHL,
                                                                                                                                                                                                                                                 Morphogens comprising an amino acid sequence sharing at least 70% homology with OP-1, OP-2, CBMP2, Vg1(fx), Vgr(fx), DPP(fx), GDF-1(fx), 60A(fx) and at least homology with BMP3(fx), BMP5(fx) and BMP6(fx) are useful for integrating an implanted tooth in a tooth socket and for inhibiting tissue loss associated with periodontal disease or injury.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OP-1; OP-2; CBMP2; Vgl(fx); Vgr(fx); DPP(fx); GDF-1(fx); 60A(fx); BMP3(fx); BMP5(fx); BMP5(fx); btooth socket; alveolus; osteogenic protein; morphogen; morphogenic protein; periodontal tissue; regeneration; tooth implant; integration; inhibition; ss.
                                                                                                                                                                                                                                                                                                                                                                     Morphogen-induced periodontal tissue regeneration - used in integrating as implanted tooth in tooth socket or to inhibit tissue loss associated with periodontal disease or injury
                                                                                                                                                                                                                          Sequence 1247 BP; 127 A; 494 C; 451 G; 175 T; 0 other;
                                                                                                                                                                                                                                                                                                                                              Claim 28-29; Page 114-116; 132pp; English.
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04-MAR-1993;
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cggccgcggc 840
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milarity 52.3%;
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Rueger DC, Smari
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93US-0029335.
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Pred. No. 4.5;
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28	28	28	28	28.2	28.2	28.2	28.2	28.2	28.2	28.2	28.2	28.2	28.2	28.2	28.2	28.2	28.2
17.3	17.3	17.3	17.3	17.4	17.4	17.4	17.4	17.4	17.4	17.4	17.4	17.4	17.4	17.4	17.4	17.4	17.4
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US-09-248-026-3	US-08-136-742A-3	US-07-853-913-3	US-09-071-434-2	US-09-427-048A-3	US-08-836-022A-3	5240846-4	US-08-469-617-16	US-08-030-081-1	US-07-890-609-1	US-08-469-461-1	US-08-604-488-1	US-08-466-886-16	PCT-US93-11667-1	US-09-248-026-1	US-08-691-605-1	US-08-951-912-5	US-08-951-912-1
Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 2, Appli	Sequence 3, Appli	Sequence 3, Appli	Patent No. 5240846	Sequence 16, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 16, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 5, Appli	Sequence 1, Appli

## ALIGNMENTS

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US-08-278-729A-32
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                                                                                                           TELEFAX: (508) 435-6951
INFORMATION FOR SEQ ID NO: 32
SEQUENCE CHARACTERISTICS:
LENGTH: 1247 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/278,729A
FILING DATE: 20-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER ESq., EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-058CPFW
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 435-901
TELEPHONE: (508) 435-901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
2IP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPAS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES STREET: 45 SOUTH STREET
              FEATURE:
NAME/KEY: CDS
LOCATION: 84..1199
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                          MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 45 SOUTH
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RUEGER, DAVID C.
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OZKAYNAK, ENGIN
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              /product= "GDF-1"
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; NAME/KEY: CDS
; LOCATION: 84..1195
; OTHER INFORMATION:
US-08-155-343A-32
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US-08-155-343A-32
                             Query Match
Best Local Similarity
Matches 68; Conserv
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Best Local Similarity
Matches 68; Conserv
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                                                                                                                                                                                                                                                                               TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                        NAME: FENTON ESQ., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7560
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0:
FILING DATE: 15-NOV-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                     MOLECULE TYPE: CDNA
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31 ccgagaacccaccgcctgcccaaggagatgacgcctgtggaacctgctgccttcgccgcc 90
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                                                                                                                                                                                                                   STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: HOPKINTON
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45 SOUTH STREET
                                     Conservative
                                                                                                                                         84..1199
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                                                                                                                                                                                                                 single
                                                  19.0%;
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                                                Score 30.8; DB 1; Pred. No. 0.82;
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                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                  62;
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                                                             Length 1247;
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US-08-406-672-32
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Query Match
Best Local Similarity 52.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 32 Patent No.
                                                                                                                                                                                                                                  TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO: 3 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                              FEATURE:
                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: CRP-060CN TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                      FILING DATE: 11-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: FENTON ESq., GILLIAN M.
                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 30-AUG-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: TREATMENT TO PREVENT LOSS OF AND/OR TITLE OF INVENTION: INCREASE BONE MASS IN METABOLIC BONE DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                              NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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                                                                                                    OTHER INFORMATION:
                                                                                                                                                                             TOPOLOGY: 111
                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 20-MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 7 FILING DATE: 30-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
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                                                                                                                                                                                                                      LENGTH:
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84..1199
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OZKAYNAK, ENGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RUEGER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COHEN, CHARLES M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KUBERASAMPATH,
                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
                                                                                                                                                                                                                                                                              (617) 248-7560
                                                                                                                                                                                      single
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                            19.0%;
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                                                                                                  /product= "GDF-1"
                                                                                                                                                                                                                                                                                                                                                                                  US 667,274
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             Score 30.8; DB 1;
Pred. No. 0.82;
0; Mismatches 62;
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                                         Length 1247;
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            Gaps
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                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (508) 435-695
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        quence 32, Application US/08643563A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 06-MAY-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES STREET: 45 SOUTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                         NAME: TWOMEY ESq., MICHAEL J.
REGISTRATION NUMBER: 38,349
REFERENCE/DOCKET NUMBER: CRP-058CN2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1247 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                             MOLECULE TYPE:
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                                711 CCGCGCAGCCTCCGCCTGGCGCTGGCGCTACGCCCCGGGCCCCTGCCGCCTGCCGCGCGC 770
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   91
                                                           31 ccgagaacccaccgcctgcccaaggagatgacgcctgtggaacctgctgcctccgccgcc 90
                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: 84..1199
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
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gageteateteeaggetggagaaactgaaactggagetggaaageegeeatagtetggag 150
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                                                                                                                                                                                                                                                                                                           nucleic acid
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OZKAYNAK, ENGIN
KUBERASAMPATH, TI
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ilarity 52.3%;
Conservative
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                                                                                                                                                                                                                                                                         ; NAME/KEY: CDS; LOCATION: 84..1199; OTHER INFORMATION: US-08-643-763A-32
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                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (617) 248-71 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: FENTON ESQ., GILLIAN M. REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 06-MAY-19
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NUMBER OF SEQUENCES: 33
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ATTORNEY/AGENT INFORMATION:
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831 CGGCCGCGGC 840
                              151 gagcggctgc 160
                                                                                                                              31 ccgagaacccaccgcctgcccaaggagatgacgcctgtggaacctgctgccgtccgcc 90
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 01748
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
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                                                                                     gagctcatctccaggctggagaaactgaaactggagctggaaagccgccatagtctggag 150
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                                                               CTGGCCGAGGCCTCGCTGCTGCTGGTGACCCTCGACCCGCGCCTGTGCCACCCCCTGGCC 830
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45 SOUTH STREET
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; OTHER INFORMATION: //
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 22-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: TETWING.
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APPLICANT: COHEN, CHARLES M.
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NFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
   831
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ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES STREET: 45 SOUTH STREET
                             151 gagcggctgc 160
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TELECOMMUNICATION INFORMATION:
                                                         771 CTGGCCGAGGCCTCGCTGCTGCTGGTGACCCTCGACCCGCGCCTGTGCCACCCCCTGGCC 830
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                                                                                    91 gagctcatctccaggctggagaaactggaaactggagctggaaagccgccatagtctggag 150
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CGCCCCCGC 840
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OZKAYNAK, ENGIN
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US-08-451-953A-32
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 435-9001
                                                                                                                                                                                                                                                                                                              FEATURE:
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NUMBER OF SEQUENCES:
                                                                                                                  APPLICANT:
831 CGGCCGCGC 840
                          151 gagcggctgc 160
                                                         771 CTGGCCGAGGCCTCGCTGCTGCTGGTGACCCTCGACCCGCGCCCTGTGCCACCCCCTGGCC
                                                                                 91 gagotcatotcoaggotggagaaactgaaactggagctggaaagcogcoatagtotggag 150
                                                                                                                                   31 ccgagaacccaccgcctgcccaaggagatgacgcctgtggaacctgcttcccttcgccgcc 90
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LOCATION: 84..1199
OTHER INFORMATION:
                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: PITCHER ESQ., EDMUND R. REGISTRATION NUMBER: 27,829
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OZKAYNAK, ENGIN
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RUEGER, DAVID C.
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                                                                                                                                                                                                                                                                                                                                          Linear
                                                                                                                                                                                                                                                                                                                            CDNA
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, CHARLES M.
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                                                                                                                                                                                          Score 30.8; DB Pred. No. 0.82;
                                                                                                                                                                             Mismatches
                                                                                                                                                                                                        DB 1;
                                                                                                                                                                             62;
                                                                                                                                                                                                       Length 1247;
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                                                                                                                                                                             Gaps
                                                                                                                     770
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US-08-445-468A-32 ; Sequence 32, Application US/08445468A

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RESULT

Patent No. 5849686

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RESULT 9
US-08-461-397A-32
: Sequence 32, Application US/08461397A
: Patent No. 5972884
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                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 68; Conserv
                               GENERAL INFORMATION:
APPLICANT: CHARETI
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: FENTON ESQ., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-072FW2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,468A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: MORPHOGEN-INDUCED LIVER REGENERATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 84..1199
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1247 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: UZIP: 01748
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STATE: MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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COHEN, CHARLES M.
CHARETTE, MARC F.
KUBERASAMPATH, THANGAVEL
RUEGER, DAVID C.
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                                                                                                                                                                                                                                                                                                                                                                                                          19.0%;
52.3%;
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                                                                                                                                                                                                                                                                                                                                                                                          62;
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; LOCATION: 84..1199
; OTHER INFORMATION: /product= "GDF-1"
US-08-461-397A-32
                                                                                                                                                                                     RESULT 10
US-08-912-088-32
                                                                                                                                                     Sequence 32,
Patent No. 5
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Best Local Similarity
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                                                                                                                   GENERAL INFORMATION:
APPLICANT: SMART, JOHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1247 base pairs
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REFERENCE/DOCKET NUMBER: CRP-074FW2
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                     APPLICANT:
                                                                                 APPLICANT:
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                   APPLICANT:
                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: sing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68; Conservative
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INVENTION:
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                                                                                                                                                                   Application US/08912088
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                                              OPPERMANN, HERMAN
OZKAYNAK, ENGIN
KUBERASAMPATH, THANGAVEL
RUEGER, DAVID C.
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OZKAYNAK, ENGIN
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                                 ROY H.L.
CHARLES M. : MORPHOGENIC PROTEIN SCREENING METHOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62;
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NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:

STREET:

HOPKINTON

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ADDRESSEE:

B: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES 45 SOUTH STREET

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Best Local Similarity 52.3
Matches 68; Conservative
                                                                                                                                                                                  Sequence 32, Application US/08278730A
Patent No. 6022853
                                                                                                              GENERAL INFORMATION:
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: COHEN, CHARLES M.
APPLICANT: RUBGER, DAVID C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (508) 435-69 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: UL/40
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1247 base pairs
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APPLICATION NUMBER: |
FILING DATE:
                             NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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                                                                  TITLE OF INVENTION:
                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                      151 gagcggctgc 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 84..1199 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
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OPERATING SYSTEM:
SOFTWARE: Patent!
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ZIP: 01748
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REFERENCE/DOCKET NUMBER: CRP-
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 STREET:
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                   ADDRESSEE:
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2: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
45 SOUTH STREET
                                                                                OPPERMANN, HERMAN PANG, ROY H.L.
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                                                                  MORPHOGENIC-ENRICHED DIETARY COMPOSITION
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; OTHER INFORMATION: /product= "GDF-1"
US-08-278-730A-32
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SEQUENCE CHARACTERISTICS:
LENGTH: 1247 base
Typer
                                                                                                                                                                                                                                          Sequence 32,
Patent No. 6(
GENERAL INFO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local Similarity
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: CR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)*248-7560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                             TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                      APPLICANT:
                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                              831 CGGCCGCGGC 840
                                                                                                                                                                                                                                                                                                                                                                     151 gagcggctgc 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 ccgagaacccaccgcctgcccaaggagatgacgcctgtggaacctgctgccttcgccgcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 20-JU CLASSIFICATION: 43
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ZIP: 01748
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COUNTRY: USA
ZIP: 01748
                               STATE:
                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                     CTGGCCGAGGCCTCGCTGCTGGTGACCCTCGACCCGCGCCTGTGCCACCCCCTGGCC 830
                                                                                                                                                                                                                                             INFORMATION:
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                                        HOPKINTON
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                                                                                                                                                    RUEGER, DAVID C
COHEN, CHARLES M
OZKAYNAK, ENGIN
                                                                                                                                                                                                                                                                      Application US/08445467
                                                        35 SOUTH STREET
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                                                                                                                                           SMART, JOHN E
                                                                                                                                                                                                               KUBERASAMPATH, THANGAVEL PANG, ROY HL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                    OPPERMANN,
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                                                                        CREATIVE BIOMOLECULES, INC
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                                                                                                   INFLAMMATORY RESPONSE 33
                                                                                                                              MORPHOGEN-INDUCED MODULATION
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    Mismatches

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OTHER INFORMATION: /F.
OTHER INFORMATION: /n
US-08-445-467-32
                                                                                US-08-480-515A-32

; Sequence 32, Application US/08480515A

; Patent No. 6090776
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                                                                                                                                   RESULT
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Best Local Similarity
Matches 68; Conserv
                               GENERAL INFORMATION:
APPLICANT: KUBERA
APPLICANT: PANG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 1247 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 0 FILING DATE: 30-AUG-1991 ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 07/753,059
ETLING DATE: 30-AUG-1991
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                 APPLICANT:
                                                                                                                                                                                     831 CGGCCGCGGC 840
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                                                                                                                                                                                                                                                        771 CTGGCCGAGGCCTCGCTGCTGGTGACCCTCGACCCGCGCCTGTGCCACCCCCTGGCC 830
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                                                                                                                                                                                                                                                                                      91 gagctcatctccaggctggagaaactgaaactggagctggaaagccgccatagtctggag 150
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LOCATION: 84..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 27,829.
REFERENCE/DOCKET NUMBER: CRP-059CP.APP
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            KUBERASAMPATH, THANGAVEL PANG, ROY H.L. OPPERMANN, HERMANN
RUEGER, DAVID C
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11-MAR-1991
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/note= "GDF-1 CDNA"
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RESULT 14
PCT-US93-07190-32
; Sequence 32, Application PC/TUS9307190
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/480,5
FILING DATE: 07-JUN-1995
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FENTON Esq., GILLIAN M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
                                                                                                     TITLE OF INVENTION: MORPHOGEN-ENRICHED I NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS: ADDRESS: CREATIVE BIOMOLECULES, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: MORPHOGEN TREATMENT OF ORGAN TRANSPLANTS NUMBER OF SEQUENCES: 33
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COMPUTER READABLE FORM:
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LOCATION: 84..1199
OTHER INFORMATION:
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                                                 CITY: HOPKINTON
STATE: MA
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                COUNTRY: UZIP: 01748
                                                                                  STREET: 35 SOUTH STREET
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SMART, JOHN E.
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.52.3%;
                                                                                                                                                          MORPHOGEN-ENRICHED DIETARY COMPOSITION
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MEDIUM TYPE:

Floppy disk

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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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ORIGINAL SOURCE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
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OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION:
                                                                                                                                                               COUNTRY: UZIP: 01748
                                                                                                                                                                                                 CITY: HOPKINTON
STATE: MASSACHU
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                 CLASSIFICATION:
                                                APPLICATION NUMBER:
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                                                                                                                                                                                                                                              ADDRESSEE:
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LOCATION: 84..1199
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STRANDEDNESS: sing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: HOMO SAPIENS
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                                                                                                                                                                                              MASSACHUSETTS
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INFORMATION
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33
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/note= "GDF-1 CDNA"
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                                              PCT/US93/07231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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Search completed: June 7, 2001, 00:26:34 Job time: 19737 sec
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                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: CR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1247 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                        831 CGGCCGCGGC 840
                                                                                                  151 gagcggctgc 160
                                                                                                                                771 CTGGCCGAGGCCTCGCTGCTGCTGACCCTCGACCCGCGCCTGTGCCACCCCCTGGCC 830
                                                                                                                                                                                          91 gagctcatctccaggctggagaaactgaaactggagctggaaagccgccatagtctggag 150
                                                                                                                                                                                                       31 ccgagaacccaccgcctgcccaaggagatgacgcctgtggaacctgctgcccttcgccgcc 90
                                                                                                                                                                                                                                                            Match 19.0%;
Local Similarity 52.3%;
                                                                                                                                                                                                                                                                                                                                   LOCATION: 84..1199
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE TYPE: BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : YDOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH:
                                                                                                                                                                                                                                                68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KELLEY, ROBIN D.
                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       617,
                                                                                                                                                                                                                                                                                                                                                                                                                           HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /248-7100
                                                                                                                                                                                                                                                                                                                                   /product= "GDF-1"
/note= "GDF-1 CDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32:
                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRP-070
                                                                                                                                                                                                                                                              Score 30.8; DB Pred. No. 0.82;
                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                          DB 5;
                                                                                                                                                                                                                                                62;
                                                                                                                                                                                                                                                                           Length 1247;
                                                                                                                                                                                                                                                Indels
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Gaps

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Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length: 0
length: 2000000000
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(without alignments)
463.402 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9623517 seqs, 4368049070 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-587-574-8
162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gccaatggccaagtgtctct.....gtctggaggagcggctgcag 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gb_est1:*
gb_est2:*
gb_est3:*
                                                                                                                                                                                                                                                                                                                                                                                                                                               gb_est6:*
gb_est7:*
gb_est8:*
gb_est9:*
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9b_est14:*
9b_est16:*
9b_est16:*
9b_est19:*
9b_est21:*
9b_est21:*
9b_est23:*
9b_est23:*
9b_est33:*
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9b_est36:*
9b_est38:*
9b_est38:*
9b_est38:*
9b_est38:*
9b_est38:*
9b_est38:*
em_esthum2:*
em_esthum3:*
em_esthum4:*
em_esthum5:*
em_esthum6:*
em_esthum7:*
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gb_est11:*
gb_est12:*
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em\_estom1:
em\_estov1:
em\_estov2:
em\_estp11:
em\_estp11:
em\_estp13:
em\_estp14:
em\_estp15:
em\_estp15:
em\_estp17:

em\_estpl8:\*
em\_estpl9:\*
em\_estpl10:\*

em\_estrol: \*

em\_estin1:\*
em\_estin2:\*
em\_estin3:\*
em\_estin4:\*
em\_estin5:\*

em\_esthum26:\*
em\_esthum27:\*
em\_esthum28:\*

em\_esthum21:\*
em\_esthum22:\*
em\_esthum23:\*

em\_esthum24:\* em\_esthum25:\* em\_esthum18:\*
em\_esthum19:\*
em\_esthum20:\*

em\_esthum16:\*
em\_esthum17:\*

em\_esthum10:\*
em\_esthum11:\*
em\_esthum12:\*
em\_esthum13:\*
em\_esthum14:\*
em\_esthum15:\*

98: 99: 100: 101: 102: 103: 104: 105:

em\_estro20:\*
gb\_est25:\*
gb\_est26:\*
gb\_est27:\*
gb\_est27:\*
gb\_est29:\*
gb\_est30:\*
gb\_est31:\*
gb\_est31:\*
gb\_est41:\*
gb\_est44:\*
gb\_est44:\*
gb\_est44:\*

em\_estro12:\*
em\_estro13:\*
em\_estro14:\*
em\_estro15:\*
em\_estro17:\*
em\_estro18:\*
em\_estro18:\*

em\_estro6:\*
em\_estro7:\*
em\_estro8:\*
em\_estro9:\*

em\_estrol0:\* em\_estrol1:\* em\_estro2:\*
em\_estro3:\*
em\_estro4:\*
em\_estro5:\*

gb\_est48:\* gb\_est49:\*

```
Result
No.
                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
Score
                                                                                                                                                                   Match
em_gss_pln1:*
em_gss_pln2:*
em_gss_pro:*
em_gss_rod1:*
em_gss_rod2:*
                                                                                                                                                                    Length
 DВ
 102
.103
13
119
119
19
8
8
13
13
23
155
112
117
                                                                                                        18
18
8
20
17
3 AA937585

8 AI307112

8 AI307112

0 AI419942

7 AI220032

7 AI220032

02 AIB18109

03 AI858567

04 AW762829

04 AI336613

05 AA489748

07 AA489748

07 AA91599

07 AI360139

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                                                                                                                                                                                              SUMMARIES
AA937585 Of71h02.s
AI272864 q143h03.x
AI307112 q189f01.x
AA489644 aa43d02.s
AI419942 tg4d011.x
AI419942 tg4d011.x
AI1818109 wk27c05.x
AI1818109 wk7c05.x
AI884421 am16b12.s
AW762829 ur66f04.y
AI336613 q062c07.x
AA489748 aa43d02.r
AA489748 aa43d02.r
AA489748 aa456f01.s
AI660139 we61a09.x
R33823 yh78f12.r1
AW207598 UI-H-BI1-
AW566657 fk03a11.y
AI1742962 wg76d09.x
                                                                                                                                                                    Description
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gb\_est78: gb\_est79:

gb\_est80

161: 162: 163: 164: 165: 166: 166: 167: 168: 169: 170: 171: 172: 173: 174: 175:

> gb\_est70: gb\_est71: gb\_est72: gb\_est73:

gb\_est67

gb\_est74:

gb\_est91: gb\_est92: gb\_est93: gb\_est94: gb\_est95: gb\_est96:

gb\_est97

gb\_est98:\*
em\_gss\_fun1:\*
em\_gss\_hum1:\*
em\_gss\_hum2:\*
em\_gss\_hum3:\*
em\_gss\_hum3:\*
em\_gss\_hum6:\*
em\_gss\_hum6:\*
em\_gss\_hum6:\*
em\_gss\_hum6:\*
em\_gss\_hum6:\*
em\_gss\_hum6:\*

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REFERENCE
AUTHORS
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AA937585/c
                                                                                                                                                                                                                                                              COMMENT
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ORGANISM
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VERSION
KEYWORDS
                                                                                                              FEATURES
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                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA937585
of71h02.s1 |
similar to '
AA937585
                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 444) NCI-CGAP http://www.ncbi.nlm.nih.gov/nclcgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                           Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                       CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                               Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                  Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                       AA937585.1
                                                                                                                        Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                 human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Robert_Strausberg@nih.gov
/note-"Organ: colon; Vector: p7773D-Pac (Pharmacia) with modified polylinker; 1st strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I -
                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1435827"
/clone_lib="NCI_CGAP_Co8"
                                   /lab_host-"DH10B"
                                             /tissue_type="adenocarcinoma"
                                                                                                           ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                           444 bp mRNA EST 24-AUG-1998 NCI_CGAP_CO8 Homo sapiens cDNA clone IMAGE:1435827 3', TR:042400 042400 AXIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                       GI:3095696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144
19
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169
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AW661648
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AI363868
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AI629343
BF812711
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BG169700
AZ484715
BF442400
BF120462
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BF896910 CM2-MT015
BG109910 602279583
BE138253 ug50d03.y
AV392939 AV392939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI363868 qy60a10.x
AL223062 Tetraodon
D24290 RICR1662A R
AU173197 AU173197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE394032 601312390
AI629343 fc10h02.y
BF812711 RC3-CI019
BE379078 601237710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA913015 ol28e11.s
AA238939 my36b07.r
BF133900 601779134
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AW476930 ga39c05.y
BG169700 602324691
AZ484715 1M0311G20
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BG103866 RHIZ2_37,
AV642870 AV642870
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BF120462
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KEYWORDS
SOURCE
ORGANISM
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCCCCGTGGAACCCGCCACCTTTGCAGCTGAGCTGATCTCGAGGCTGGAAAAGCTGAAG
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similar to
                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-GGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI272864
                                                                                                                                                                                                                                                                                                                                                                              Tissue Procurement: Christopher Moskaluk, M.D., Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AI272864
                                                                                                                                                                                                                                                                                                                                                        Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 459)
                                                                                                                                                                                                                                                                                                               quality sequence stop: 387.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Robert_Strausberg@nih.gov
/note="Organ: colon; Vector: pT/T3D-Pac (Pharmacia) with modified polylinker; 1st strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Ecc RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library is normalized. Library was constructed bento Soares and M. Fatima Bonaldo. "
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                                                                                                                                                                      /tissue_type="adenocarcinoma"
/lab_host="DH10B"
                                                                                                                                                                                                                               /clone="IMAGE:1875125"
                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                           /clone_lib="NCI_CGAP_Co8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   459 bp mRNA EST 29-JAN-1999 NCI_CGAP_CO8 Homo sapiens cDNA clone IMAGE:1875125 TR:042400 042400 AXIN. ;, mRNA sequence.
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88.3%;
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AI307112/c
                                                                                                         BASE COUNT
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                                    Query Match
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ctggagctggaaagccgccatagtctggaggagcggctgcag 162
 143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI307112
q189f01.x1;
3' similar '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Insert Length: 534 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 487)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP care institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST
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   Conservative
                                                                                                         71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quality sequence stop: 471.
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                                                                                                  (Pharmacia) with a modified polylinker; Site_1: Not I; SIte_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.N.A.G.E. clones 260232-265223, 34048B-345479, and 48448B-489479."
                                                                                                                                                                                                                                                                                                                                     pregnant uterus"
                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Soares_NhHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                                                                                                                                                                                                                                                                                                                 /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:1879513"
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88.3%;
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Score 131.6; DB: 
Pred. No. 1.5e-27
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                                DB 18;
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2 ccaatggccaagtgtctctacctcattttccgagaacccaccgcctgcccaaggagatga 61

Matches Query Match Best Local

Similarity

80.6%;

Score 130.6; 1 Pred. No. 2.8e 0; Mismatches

; DB 8; 1.8e-27; les 19;

Indels Length 409;

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Gaps

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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: estewatson.wustl.edu

Email: estewatson.wustl.edu

This clone is available royalty-free through LLNL; contact the

This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WashU-Merck EST Project 1997
Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMAGE Consortium (info@image.linl.gov) for Possible reversed clone: polyT not found Seq primer: -41m13 fwd. ET from Amersham High quality sequence stop: 389.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
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Mammalia; |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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              /note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and sc circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 3 20232-265223, 340488-345479, and 484488-489479."
                                                                                                                                                                                                                                                                                                                               pregnant uterus"
                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:823683"
/clone_lib="Soares_NhHMPu_S1"
                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Pooled human melanocyte, fetal heart,
                                                                                                                                                                                                                                                                                                       lab_host="DH10B"
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                                                                                GCCAATGGCCAAGTGTCTCTACCTCATTTCCCGAGAACCCACCGCCTGCCCAAGGAGATG
                                                                                              gccaatggccaagtgtctctacctcattttccgagaacccaccgcctgcccaaggagatg
ACCCCGTTGGAACCCGCCACCTTTGCAGCTGAGCTGATCTCGAGGCTGGAAAAGCTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 740 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AI419942 460 bp mRNA EST 30-MJ tg40dll.xl Soares_NFL_T_GBC_Sl Homo sapiens cDNA clone IMAGE:2111253 3' similar to TR:042400 042400 AXIN. ;, r
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Seq primer: -40UP from Gibco
High quality sequence stop: 421.
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                                                                                                                                                                                                                                                                              I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction b Soares and M. Fatima Bonaldo. " 124 c 162 g 107 t
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/lab_host-"DH10B"
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/clone="IMAGE:2111253"
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Pred. No. 4.2e-27;
0; Mismatches 20;
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AI818109/c
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                                                                                                                                                                                                                                               gccaatggccaagtgtctctacctcattttccgagaacccaccgcctgcccaaggagatg
                                                                                                                                                  ACCACCGTGGAAGCCGCCACCTTTGCAGCTGAGCTGATCTCGAGGCTGGAAAAGCTGAAG
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High quality sequence stop: 224.
Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.
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Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 (bases 1 to 543)
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/db_xref="taxon:9606"
/clone="IMAGE:1841331"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                   79.3%;
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Pred. No. 1.2e-26;
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                                                                                                                                                                                                                                                                  GCCAATGGCCAAGTGTCTCTACCTCATTTCCCGAGAACCCACCGCCTGCCCAAGGAGATG
AI858567 418 bp mRNA EST 07-MAR-2000 w164d08.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2429679 3'
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Location/Qualifiers
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DNA Sequencing by: washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/ILNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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National Cancer Institute / National Institute of Neurological Discorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
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1 (bases 1 to 591)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                            78.3%; ilarity 86.4%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                       T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

a 159 c 192 g 138 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="IMAGE:2413544"
/clone_1ib="WCI_CGAP_Brn25"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                             Score 126.8; DB 10z, Pred. No. 3.6e-26; Indels
                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing (information
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                                                                                                                                                                                                                                                                                                                                                                                 591;
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                                      DEFINITION
                                                                         AA884421/c
                                                                                             RESULT
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298
                 124 gagctggaaagccgccatagtctggaggagcggctgcag 162
                                                                                                                   64 cctgtggaacctgctgccttcgccgccgagctcatctccaggctggagaaactgaaactg 123
                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                          4 aatggccaagtgtctctacctcattttccgagaacccaccgcctgcccaaggagatgacg
                                                                                                                                                                  AAGGGCGAAGTGTCTCTACCTCATTTCCCCGAGAACCCACCGCCTGCCAAGTGAGATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Home 1 (Dases 1 to 418)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurola Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 402.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 541 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AI858567.1 GI:5512183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similar to TR:088566 O88566 CONDUCTIN. ;, mRNA sequence AI858567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: -40UP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                     62
                                                                                                                                                                                                                                                                                                                                                                            T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

115 c 149 g 89 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:2429679"
/clone_lib="NCI_CGAP_Brn25"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
                                                                                                                                                                                                                                                                          72.5%;
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Primates;
                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                          Score 117.4; DB Pred. No. 1.7e-23
                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                              DB 103; Length 418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soares,
                                                                                                                                                                                                                                                      26;
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AA884421 391 bp mRNA EST 27-W am16b12.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:1466975 3' similar to TR:042400 042400 AXIN. ;, r

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REFERENCE
AUTHORS
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Best Local
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                                         ORGANISM
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                                                                                                                                                                                                                                                                                                              136
                                                                                                                                                                                                                                                                                                                                                                                                                              391
                                                                                                                                                                                                                                                                           271
                                                                                                                                                                                                                                                                                                                                                  331 CCCACCTTTGCAGCTGAGCTGATCTCGAGGCTGGAAAAGCTGAAGCTGGAGTTGGAGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                16 tctctacctcattttccgagaacccaccgcctgcccaaggagatgacgcctgtggaacct 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                            cgccatagtctggaggagcggctgcag 162
                                                                                                                                                                                                                                                                                                                                                                    gctgccttcgccgagctcatctccaggctggagaaactgaaactggagctggaaagc 135
                                                                                                                                                                                                                                                                           CGCCACATCCTGGAGGAGCGCCTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                            TCTCTACCTCATTTCCCGAGAACCCACCGCCTCCCAAAGGAGATGACCCCCGTGAACCCCG 332
Mus musculus
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                             AW762829 508 bp mRNA EST 04-MAY-2000 ur66f04.yl NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:3155263 similar to TR:088566 088566 CONDUCTIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyT not found
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 391)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
                                                                               EST.
                                                                                               AW762829
AW762829.1
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Mammalia; Eutheria;
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                                                           house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHLIM, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:1466975"
/clone_lib="Soares_NFL_T_GBC_S1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B"
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                                                                                                 GI:7694771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.0%;
83.0%;
   Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 107; DB 13;
Pred. No. 1.5e-20;
); Mismatches 25;
 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 391;
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AI336613/C
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REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 CGCCTGCCCAAGGAGATGACGCCTGTGGAACCTGCTGCCTTCGCCGCCGCCGAGCTCATCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGCTGGAGAAACTGAAACTGGAGCTGGAAAGCCGCCATAG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101;
Mammalia; Eutheria; Primates; Catarrhini; Hon 1 (bases 1 to 413)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat Tumor Gene Index Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
Other_ESTs: ur66f04.x1
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                              AI336613
                                                                                                                                                                                                                                                                                                                                          similar to
                                                                                                                                                                                                                                                                                                                                                             qo62c07.x1
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                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                        AI336613.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGI:1058019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          image.llnl.gov/image/html/iresources.shtml
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: mammary Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 37-43 (1999) 9 128 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism-"Mus musculus"
/strain-"129 - C57/B6 - FVBN"
/db_xref-"taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH10B"
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/clone_lib="NCI_CGAP_Mam3"
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CO8 Homo sapiens cDNA clone IMAGE:1913100
O42400 AXIN. ;, mRNA sequence.
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                                                                                       l (bases 1 to 399)

I (bases 1 to 399)

Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylle, T., Waterston, R. and Wilson, R. Washu-Merck EST project 1997

Unpublished (1997)

Contact: Wilson RK

Washington University School of Medicine

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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BA489748 EST 11-AUG-1997

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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Seg primer: -40UP from Gibco.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Emmert-Buck, M.D., Ph.D.
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est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Procurement: Christopher Moskaluk, M.D., Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified polylinker; ist strand CDNA was prepared from colon adenocarcinoma, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT?T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
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/lab_host="DH10B"
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/clone_lib="NCI_CGAP_Co8"
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Pred. No. 5.1e-18;
0; Mismatches 18;
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         CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 524 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA915999 546 bp mRNA EST 29-APR-1998 oh86g11.sl NCI_CGAP_CO8 Homo sapiens cDNA clone IMAGE:1473956 similar to TR:042400 042400 AXIN. ;, mRNA sequence.
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97; Conserv
                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                  Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 546)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                   Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                    Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: mixed (see below); Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus)
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/tissue_type="Pooled human melanocyte, fetal heart,
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88.2%;
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                                                                                                                                                                                                                                                                                                                              Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 8;
.9e-15;
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RESULT 14
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VERSION
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TITLE
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ggagctggaaagccgccatagtctggaggagcggctgca 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGAGTTGGAGAGCCCCACCAGCCTGAGGAGGATCCTGCA 290
                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
Unpublished (1997)
Contact: Robert Strau
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A1660139 408 bp mRNA EST 18-DEC-1999 we61a09.xl Soares_thymus_NHFTh Homo sapiens cDNA clone IMAGE: 2345560 3' similar to TR:088566 088566 CONDUCTIN. ;, mRNA
                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 788 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                         quality sequence stop: 333.
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                                                                                                                                                                                                                                                                                                                                                        Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-*Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. **

a 133 c 186 g 131 t 1 others
/clone="IMAGE:2345560"
/clone_lib="Soares_thymus_NHFTh"
/dev_stage="fetal"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: thymus, pooled; Vector: pT7T3D-pac
(pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not
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/lab_host="DH10B"
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/clone="IMAGE:1473956"
/clone_lib="NCI_CGAP_Co8"
                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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74.8%;
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Pred. No. 4.1e-14;
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ACCESSION
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ORGANISM
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JOURNAL
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chiasoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkin, M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Mardis, E., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 361)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
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                                                                                                                                                                      High quality sequence stop: 235.
Location/Qualifiers
                                                                                                                                                                                                                    Seq primer: M13RP1
                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information... insert Length: 445 Std Error: 0.00
                                                                                                                                                                                                                                                                                                        High quality sequence stops: 235 Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      constructed by Bento Soares and M. Fatima Bonaldo. _{\rm 1} 110 c 152 g 85 t
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/clone="IMAGE:135887"
                                                                                                        /organism="Homo sapiens"
/db_xref="GDB:541873"
                                           /clone_lib="Soares placenta Nb2HP"
'dev_stage="placenta obtained at birth (full term)"
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76.5%;
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Pred. No. 1
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1.5e-13;
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Search completed: June 6, 2001, 23:00:46 Job time: 15530 sec
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Location/Qualifiers
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Birchmeier, W. and Behrens, J.
CONDUCTINE PROTEIN AND A RELATED AGENT FOR DIAGNOSING
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Behrens,J., Jerchow,B.-A., Wurtele,M., Grimm,J., Asbrand,C., Wirtz,R., Kuhl,M., Wedlich,D. and Birchmeier,W.
Functional interaction of an axin homolog, conductin, with beta-catenin, APC, and GSK3beta
Science 280 (5363), 596-599 (1998)
                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Birchmeier, W. and Behrens, J.
CONDUCTINE PROTEIN AND A RELATED AGENT
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BIRCHMEIER WALTER (DE); BEHRENS JUERGEN (DE)
Location/Qualifiers
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2 (bases
                    Zhang,T., Fagotto,F., Hsu,W., Zeng,L., Gilbert,D., Copeland,N.G., Jenkins,N.A., Warburton,D. and Costantini,F. Properties of mouse Axin2 and human AXIN2: chromosomal location,
                                                                                                                                                                                                                                         Mus musculus Axin2
AF205889
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Submitted (22-JUN-1998) Cellular Biology, M
                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 3016)
                                                                                                                                                      Mus musculus
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expression pattern,
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REMHRSYKANGQVSLCHFPRTHRLPKEMTPVEPAFARAELISRLEKLKLELESHHSLE
ERLQQIREDEEKEGSEQALSSRDGAPVQHFLALLPSGSYEEDPQTILDDHLSRVLKTP
GCQSPGVGRYSPRSRSPDHHHQHHHHQQCHTLLSTGGKLPPVAACPLLGGKSFLTKQT
TKHVHHHYIHHAVPKTKEELEAATQRVRCLCPGGTDYYCYSCKCKSHPKAPEPLPGE
QFCGSRGGTLPKRNAKGTEPGLALSANDGGMSAAGGPDLYGEEGDRSQDVWQWMLES
GRQSKSKPHSAQSIRKSYFLESARAAFGERVSHHLLGASGHSRSVARAHPTQDPAM
PPLTPNTLAQLEEACRRLAFVSKPOKORCCVASQORDRNHSAAGGAGASPFANPSLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MSSAVLYTLLPDPSSSFREDAPRPPVPGEEGETPPCQPSVGKVQ
STKPMEVSSNARRNEDGIGEPEGRASEDSPLTRWTKSLHSLLGDQDGAYLFRTFLERE
KCVDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKRYIENNSVVSKQLKPATKTYING
IKKQQIGSVMEDQAQTEIQAVMEENAYQVFLTSDIYLEYVRSGEENTAYMSNGGLGSL
KVLCGYLPTLNEEEEWTCADLKCKLSPTVVGLSSKTLRATASVRSTETAENGFRSFKR
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/protein_id="AAC26047.1"
/db_xref="GI:3309247"
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  interaction with Axin and
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 191041)
                                                                               AC024114.8 GI:11094615
HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                              Mus musculus chromosome 11 clone RP23-278J12, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (16-NOV-1999) Genetics & Development, Columbia University, 701 W168th St. HHSC 1416, New York, NY 10032,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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                                              Mus musculus
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                                                                house mouse.
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PEDHKEPKKLASVHALQASELVVTYFFCGEEIPYRRMLKAQSLTLGHFKEQLSKKGNY
RYYFKKASDEFACGAVFEEIWDDETVLPMYEGRILGKVERID*
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QFCGSRGGTLPKRNAKGTEPGLALSARDGGMSSAAGAPQLPGEEGDRSQDVWQWMLES
ERQSKSKPHSAQSIRKSYPLESARAAPGERVSRHHLLGASGHSRSVARAHPFTQDPAM
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55. .2577
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                                                                                                                            30 unordered pieces
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REFERENCE

AUTHORS

JOURNAL REFERENCE

AUTHORS TITLE JOURNAL

COMMENT

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Direct Submission

Direct Submission

Submitted (24-FEB-2000) Human Genome.Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Nov 4, 2000 this sequence version replaced gi:9929587.

Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: MACA
Center clone name: MACA
Center clone name: RP23-278J12
Center clone name: RP23-278J12
Chemistry: Dye-tor: M13; L08821
Chemistry: Dye-terminator Big Dye: 5% of reads
Chemistry: Dye-terminator Big Dye: 5% of reads
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Chemistry: Dye-terminator Big Dye: 5% of reads
Chemistry: Dye-terminator Big Dye: 5% of reads
Chemistry: Dye-terminator Big Dye: 5% of reads
Chemistry: 158769 bases at least Q40
Consensus quality: 172780 bases at least Q30
Consensus quality: 172780 bases at least Q20
Estimated insert size: 180377; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 3.2x in Q20 bases; sum-of-contigs estimation
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Gorrell,J.H., Gunaratne;P., Haller,G., Hernandez,J., Hogues,M.,
Hosak,H., Hou,X., Huber,J., Jackson,L., Jia,Y., Kelly,J., Kelly,S.,
Kovar,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Martin,R.,
Massey,E., McLeod,M.P., Mei,G., Moore,S., Morgan,M., Morris,S.,
Meal,D., Nelson,A., Nguyen,R., Nguyen,N., Oguh,M., Parish,B.,
Perez,L., Reiter,D., Say,J., Shen,H., Vasquez,L., Watlington,S.,
Williamson,A., Wrensford,G., Zhou,X., Bouck,J., Hodgson,A.,
Williamson,A., Scherer,S., Sodergren,E., Weinstock,G.,
Muzny,D.M., Rives,M., Scherer,S., Sodergren,E., Weinstock,G.,
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                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: Estimated insert size may differ from sequence length (see http://www.lbgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'vorking draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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                      gtgggtcgctacagcccacggtcccgc 207
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GTGGGCCGCTACAGCCCACGCTCCCGC 1479
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Direct Submission
Submitted (08-AUG-1997) Biochemistry, Hiroshima University,
Submitted (08-AUG-1997) Biochemistry, Hiroshima, Hiroshima
Of Medicine, 1-2-3 Kasumi, Minami-ku, Hiroshima, Hiroshima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of Xenopus embryos
Mol. Cell. Biol. 18 (5), 2867-2875 (1998)
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Rattus norvegicus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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DHKEPKRLASVHALQASELIVTYFFCGEEIPYRRMLKAQSLTLGHFKEQLSKKGNYRY
YFKKASDEFACGAVFEEIWDDETYLPMYEGRILGKVERID"
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STKPMPVSSNARRNEDGIGEPEGRASPDSPLTRWTKSLHSLLGQDGAYLFRTFLERE
KCVDTLDFWFACNGFRGNULKDTKTLEVAKAIY KRY IENUSVVSKQLKPATKTY IND
IKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDIYLEYVRSGENTAKMSNGGLGSL
KKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDIYLEYVRSGENTAKMSNGGLGSL
KVLCGYLPTLMEEEBWTCADLKCKLSPTVVGLSSKTLKATASVRSTFTAENGFRSFKR
KVLCGYLPTLMEEEBWTCADLKCKLSPTVGGLSSTLKATASVRGIPPYRMGSKKOLQ
REMHRSVKANGQVSLPHFPRTHRLPKEMTPVEPAAFAAELISRLEKLKLELESSHSQLQ
REMRSVKANGQVSLPHFPRTHRLPKEMTPVEPAAFAAELISRLEKLKLELESSHSLGL
ERLQQIREDEEKEGSEQALSSRDGAPYQHPLALLPSGSYEEDPQTILDDHLSRVLKTP
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HVHHHYIHHAVPKTKEEIEAEATQRVRCLCPGGTDYYCYSKCKSHSKPPEPLPGEQF
CGSRGGTLPKRNTKGTEPGLALPAREGGMSSAAGAPQLPGEEGDRSQDVWQWMLESER
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/db_xref="taxon:10116"
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/db_xref="GI:3080759"
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GTAGGCCGCTATAGCCCTCGCTCCCGC
                  gtgggtcgctacagcccacggtcccgc 207
                                                                         ACGATACTGGACGATCACCTGTCCAGGGTCCTCAAGACCCCTGGCTGCCAGTCTCCGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'-& 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (9-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., ikema,r., Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S. NEDO human cDNA sequencing project
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2 (bases 1 to 2104)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Agency).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           University of Tokyo (partly supported by Science and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="HepG2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="highly similar to AF078165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="HEP"
/note="cloning vector pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="hepatoma"
/clone="HEP10566"
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77.88;
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                                                                                                                                                                                                                                                                                                                            Score 133.4; DB 8
Pred. No. 9.3e-24;
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706
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ORGANISM
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                                                                            1355
                                                                                                                                                         1295 CAGATCCGAGAGGATGAAGAGAGAGAGGGCTCCGAGCTCACACTCAATTCGCGGGAGGGG 1354
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121 accattttggacgaccacctctccagggtcctcaagacccccggctgtcaatcccctggt 180
                                                                                                                      61
                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                              Н
                                                                                            gcaccggtccagcacccctggccctcctaccctccggcagctatgaagaggacccacaa 120
                                                                                                                                                                                     cagatcogggaggatgaagaaaaggaggggtctgagcaggccctgagctcacgggatgga 60
                                                                     GCGCCCACGCACCCCCCCCCCCCCACTGCCCCTCCGGCAGCCACGAGGAAGACCCCGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens AXIN2
AF205888
AF205888.1 GI:6653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (16-NOV-1999) Genetics & Development, Columbia University, 701 W168th St. HHSC 1416, New York, NY 10032, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhang, T., Fagotto, F., Hsu, W., Zeng, L., Gilbert, D., Copeland, N.G. Jenkins, N.A., Warburton, D. and Costantini, F. Properties of mouse Axin2 and human AXIN2: chromosomal location,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhang, T., Fagotto, F., Hsu, W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression pattern, interaction with Axin and effects on embryonic
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                                                                                                                                                                                                                                                                                                                                                                                             617
                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     formation
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                                                                                                                                                                                                                                                                                                                                                                                          KASDEFACGAVFEEIWEDETVLPMYEGRILGKVERID"
1724 c 724 g 473 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKQQIDSIMFDQAQTEIQSVMEENAYQMFLTSDIYLEYVRSGGENTAYMSNGGLGSLK VVCGYLPTLNEEEEWTCADFKCKLSPTVVGLSSKTLRATASVRSTETVDSGYRSFKRS DPVNPYHIGSGYVFAPATSANDSEISSDALTDDSMYDDSSVOEIPPYRVGSKKQLQR EMHRSVKANGRVSLPHFFRTHKLPKEMTPVEPATFANSTEISRLEKLKLELESRHSLEE RLQQIREDERREGSELTLNSREGAPTQHPLSLLPSGSYEEDPOTILDDHLSRYLKVEE RLQQIREDERREGSELTLNSREGAPTQHPLSLLPSGSYEEDPOTILDDHLSRYLKVETG CQSPGVGRYSPRSRSPDHHHHHHSQYHSLLPPGGKLPPAAASPGACPLLGGKGFVTKQ TTKHYHHHYLHHHANPKTKEEIEAEATQRVHCFCPGGGSEYYCYSKCKSHSKAPETMPS
                                                                                                                                                                                                                                                                                                                                                                                                                                  EPKKLAGVHALQASELVVTYFFCGEEIPYRRMLKAQSLTLGHFKEQLSKKGNYRYYFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PNTLAHLEEACRRLAEVSKPPKORCCVASQORDRNHSATVOTGATPFSNPSLAPEDHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQFGAQSTKKAYPLESARSSPGERASRHHLWGGNSGHPRTTPRAHLFTQDPAMPSLTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CVDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKRYIENNSIVSKQLKPATKTYIRDGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MSSAMLYTCLPDPSSSFREDAPRPPYPGEEGETPPCHHGGOGPG
HQTHYCLFQHQAERRWYGEPEGRASPDSPLTRWTKSLHSLLGDQDGAYLFRTFLEREK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAF22799.1"
/db_xref="GI:6653584"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product-"AXIN2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="AXIN2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissue_type="brain; lymphoblast"
/note="similar to ESTs 823683 and 446378"
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                                                                                                                                                                                                                                                                           64.4%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AXIN2) mRNA, complete cds.
                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                        Score 133.4; DB 8 Pred. No. 8.9e-24;
                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA
                                                                                                                                                                                                                                                                                                  DB 88;
                                                                                                                                                                                                                                                      46;
                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                             Length 2538;
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                                                                                                                                                                                                                                                 Gaps
                                                                     1414
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121 accattttggacgaccacctctccagggtcctcaagacccccggctgtcaatcccctggt 180

61 gcaccggtccagcacccctggccctcctaccctccggcagctatgaagaggacccacaa 120

GCGCCCACGCAGCACCCCCTCTCCCTACTGCCCTCCGGCAGCTACGAGGAAGACCCGCAG 1397

1 cagatccgggaggatgaagaaaaggagggtctgagcaggccctgagctcacggggatgga 60

CAGATCCGAGAGGATGAAGAGAGAGAGGGCTCCGAGCTCACACTCAATTCGCGGGAGGGG 1337

Matches Query Match

161;

Conservative

0;

Mismatches

Indels Length 3072;

0;

Gaps

0

DB 88; 46;

Local Similarity

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BASE COUNT
ORIGIN
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AUTHORS
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ORGANISM
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VERSION
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (15-JUL-1998) Lab Medicine and Pathology, Mayo clinic, 200 First Street SW, Rochester, MN 55905, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mai, M., Qian, C., S
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mai,M., Qian,C., Yokomizo,A., Smith,D.I. and Liu,W. Cloning of the human homolog of conductin (AXIN2), to chromosome 17923-924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens conductin mRNA, complete cds. AF078165
AF078165.1 GI:4454790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomics 55 (3), 341-344 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Primates;
1 (bases 1 to 3072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                               PAMPPLTPPNTLAQLEEACRRLAEVSKPPKQRCCVASQQRDRNHSATVQTGATPFSNP
SLAPEDHKEPKKLAGVHALQASELVVTYFFCGEEIPYRRMLKAQSLTLGHFKEQLSKK
GNYRYYFKKASDEFACGAVFEEIWEDETVLPMYEGRILGKVERID"
                                                                                                                                                                                                                          {	t ESERQSKPKPHSAQSTKKAYPLESARSSPGERASRHHLWGGNSGHPRTTPRAHLFTQD}
                                                                                                                                                                                                                                                 SEQFGGSRGSTLPKRNGKGTEPGLALPAREGGAPGGAGALQLPREEGDRSQDVWQWML
                                                                                                                                                                                                                                                                     QTTKHVHHHYIHHHAVPKTKEEIEAEATQRVHCFCPGGSEYYCYSKCKSHSKAPETMP
                                                                                                                                                                                                                                                                                               GCQSPGVGRYSPRSRSPDHHHHHHSQYHSLLPPGGKLPPAAASPGACPLLGGKGFVTK
                                                                                                                                                                                                                                                                                                                    REMHRSVKANGQVSLPHFPRTHRLPKEMTPVEPATFAAELISRLEKLKLELESRHSLE
ERLQQIREDEEREGSELTLNSREGAPTQHPLSLLPSGSYEEDPQTILDDHLSRVLKTP
                                                                                                                                                                                                                                                                                                                                                                          SDPVNPYHIGSGYVFAPATSANDSEISSDALTDDSMSMTDSSVDGIPPYRVGSKKQLQ
                                                                                                                                                                                                                                                                                                                                                                                              IKKQQIDSIMFDQAQTEIQSVMEENAYQMFLTSDIYLEYVRSGGENTAYMSNGGLGSL
KVVCGYLPTLNEEEEEWTCADFKCKLSPTVVGLSSKTLRATASVRSTETVDSGYRSFKR
                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="mssamlyTclpdpsssfredaprppypgeegetppcqpgygkgq
VTKPMSVSSNTRRNEDGLGEPEGRASPDSPLTRWTKSLHSLLGDQDGAYLFRTFLERE
KCYDTLDFWFACNGFRQMNLKDTKTLRYAKAIYKRYIENNSIYSKQLKPATKTYIRDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="conductin"
/protein_id="AAD20976.1"
/db_xref="GI:4454791"
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/db_xref="taxon:9606"
/chromosome="17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="AXIN2"
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64.48;
77.88;
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Score 133.4; DB 8
Pred. No. 8.6e-24;
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AB032263
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839 c 864 g
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/protein_i0="BAA92440.1"
/db_xref="GI:729080"
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PVKTIMADLRCSTARRDEDGLGEPEGSASPDSPLARWTKSLHFILGDQDGAQLFRAYL
EREKCUTLDFWFACNGFRQMDLKDTKTHRVAKAIXFT ENDETVAKQLKPAFYTFI
EREKCUTLDFWFACNGFRQMDLKDTKTHRVAKAIXFT FYDETFI
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GGLKLVCGYLFTLNEEEEWSCNDFKAKALATVGISAKTLSFPLRAVEALEKGYRSY
RRSDDGNPNRFTSGYSFAPATSANDSEVSSDALTDDSMSMTDSSVDALFPYKLGSKKO
LOREMORNMRMNGOVSLPFFPRTRRPPKEMTPVEPAAFAAOLIARLERLKREOETMSS
LEERLOQIOEEEERDESEMSSSSASHSLFLLPGTCEEDPQAILDEHLSRVLKTFGCO
SPGLLRHSPRERSPEORPLPRGGLSTFSOSSSMGYVPAKTFISROSTRHIHHYIHH
HAGGPKSKEQIEVEATORVQCLCHGTSECCTAPYIRSRSLGRDQCASPAEVALGHSSTL
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Matches Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hirano, Biomedical research center, Osaka Univ. Med. scool, Department of Molecular Oncology; 2-2, Yamadaoka, Sulta, Os 565-0871, Japan (E-mail:hirano@molonc.med.osaka-u.ac.jp, URL:http://www.med.osaka-u.ac.jp/pub/molonc/www/index.html, Tel:81-6-879-3880, Fax:81-6-879-3889)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (09-SEP-1999) to the DDBJ/EMBL/GenBank databases. Toshio Hirano, Biomedical research center, Osaka Univ. Med. scool.
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Danio rerio mRNA for axin1, complete cds.
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                             859
                                                                               EMREPLPADDMERNQKILQMMMEGEKEAGRYKRSPYGSISGPKKAQGHEPARPSSVER
LGAVHPWVTAQLRNNVQPSHPFIQDPTMPPNPAPNPLTQLEEARRRLEEERRKSGTLQ
AKQRHKNMKKQPCENITVAYYFCGEPIPYRTSVKGRIVTLGQFKELLTKKGSYKYYFK
                                                                                                                                                            ROIKPATKSFIKDCVMKLHIDPAMFDQAĞTEIQTMMEENTYPLFLKSDIYLEYTRTGG
ESPKLESDQSSYSGNGKVLPGYLFDYLEDVEWRCDQEEQIAESDGTPSNRLTQKLLL
ETVPQRYANSKRYQDMREYHHASMEREPVNPYVNGSYALPATSANDSEQQMSGSDAD
TLSLTDSSVDGVPPYRYRKPHREIHESAKVNGRVPLPHIPRTNRIPKDIHVEPEKFA
AELISRLEGVLREREAQEKLEERLKRVRLEEECDDADISTGPSLANHRVPPAVHVQHY
GGRYSEMSYNGLOLDAHEENPESILDEHVQRWKTPGCQSPGTGRHSFKSRSPDGL
GGRYSEMSYNGLOLDAHEENPESILDEHVQRWKTPGCQSPGTGRHSFKSRSPDGLPA
GGRYSEMSYNGLOLDAHEENPESILDEHVQRYSSKGSTLSKRPVRKEGEQAEAEAAR
MGGFAMNTEOHYGPKSRNYADGMSVGFNTMDPMGYSSKGSTLSKRPVRKEGEGGRNF
                             KVSYEFDCGVVFEEVREDDAILPIFEEKIIGKVEKVD"
769 c 874 g 564 t
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IHLFRTFLKQEECADMLDFWFACSGFRKQEANDGNEKMLKLAKAIYKKYILDNNGIVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="axin1"
25. .2532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="BAA92439.1"
/db_xref="GI:7229078"
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/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="axin1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene-"axin1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MSMSVNEKGICYLPDLGSSFTEDAPRPPVPGEEGDLVSSDGRQY/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus Axin mRNA, AF009012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (13-JUN-1997) Genetics and Development, Columb University, 701 W. 168th Street, New York, NY 10032, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zeng,L., Zhang,T., Perry,W.L. III, Lee,J.J. and Costantini,F. Direct Submission
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                                                                                Similarity
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                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                YSSKSDAVRNETSTATPËRSDLDLGYEPËGSASPTPPYLKWAESLHSLLDDQOGINLE
RTFLKQEDCADLLDTWFACSGFRKLEPCVSNEEKRLKLAKAIY KKYLLDNOGIVSRQI
KPATKSFI KDCVMKLQI DPDMFDQAQTE I QCMI EDNIY PLFLK SDI YLEYTRITGGESP
KI YSDPSSGSGTGKGLPGY LEYTLNEDEEWKCDQDTEPEASRDSAPSSRLTQKLLLETA
TQRATSTRYSEGREFRHGSWREPVNEYYVNTGYAMAPATSANDSEQQSMSSDADTMS
TQRATSTRYSEGREFRHGSWREPVNEYYVNTGYAMAPATSANDSEQQSMSSDADTMS
LTDSS LDG I PPY RLFKQHREEWLESKAKANGRVPLPH I PRTYRKMPSAQPFHHFAPR
YSEMGCAGMQMRDAHEENFES I LDEHYQRVMKTPGCOSPGPGHSPKCRSPESGHLGK
LGGTLGT I PPGHGKHTTKSGMKLDAANLYHKHYNHI I HHSMMKFKEQ I EAEATQRV
LKGTLGT I PPGHGKHTTKSGMKLDAANLYHKHYNHI I HHSMMFKEQ I EAEATQRV
                                                                                                                                                                                                                              YRYYFKKVSDEFDCGVVFEEVREDDTILPIFEEKIIGKVEKID"
                                                                                                                                                                                                                                                                             PVAVHPWVSAQLRNVVQPSHPFIQDPTMPPNPAPNPLTQLEEARRRLEEEEKRAGKLP
                                                                                                                                                                                                                                                                                                                                 QNSFAWNVDSHNYATKSRNYSENLGMAPVPMDSLGYSGKASLLSKRNIKKTDSGKSDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAC60245.1"
/protein_id="AAC60245.1"
/db_xref="GI:2252818"
/db_xref="GI:2252818"
/translation="MNIQGKGFPLDLGRSFTEDAPRPPVPGEEGELVSTDPRPVSHGF
/translation="MNIQGKGFPLDLGRSFTEDAPRPPVPGEEGELVSTDPRPVSHGF
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                                                                                                                                                                                                                                                      LKQRLKPQKRPGSGASQPCENIVVAYYFCGEPIPYRTLVKGRVVTLGQFKELLTKKGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="Axin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function="may inhibit embryonic axis formation"
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/db_xref="taxon:9031"
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                                                                                        1392 CCACGAGGAAAATCCGGAATCTATTCTGGATGAACACGTGCAGCGTGTTATGAAAAACCCC 1451
1452 GGGCTGCCAGTCCCCTGGGACTGGACGTCATTCCCCCAAAATCCCGC 1497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
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                                      162 cggctgtcaatcccctggtgtgggtcgctacagcccacggtcccgc 207
                                                                                                                                102 ctatgaagaggacccacaaaccattttggacgaccacctctccagggtcctcaagacccc 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 gctgtcaatcccctggtgtgggtcgctacagcccacggtcccg 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTGTCAGTCTCCAGGCCCCGGCCGCCACTCTCCCAAGCCACG 1753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGAAGAAAACCCAGAAAGCATCCTGGACGAACACGTGCAGCGTGTGATGAAAACACCAG 1710
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Hedgepeth,C.M., Deardorff,M.A. and Klein,P.S.
Xenopus axin interacts with glycogen synthase kinase-3 beta and
expressed in the anterior midbrain
mech. Dev. 80 (2), 147-151 (1999)
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Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (06-OCT-1998) Medicine,
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Hedgepeth,C.M., Dear
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                                                                                                                                                          761
                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                     PQKQRLKPQKKNVSAPSQPCDNIVVAYYFCGEPIPYRTMVKGRVVTLGQFKELLTKKG
NYRYYFKKVSDEFDCGVVFEEVREDDMILPIYEEKIIGQVEKID"
1 602 c 635 g 531 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KNYSDQSSGSGTGKGPSGYLPTLNEDEEWRCDQGGEHERERECIPSSLFSQKLALDSS
SHCAGSNRRLSDGREERPGTWREDVNPYYNTGYARAPYTSANDSEQQSMSSDADTMS
LITDSSVDGIPSYRLKKIYRREMQESANANGRGPLPHIPTYMMPKDIHVDPEKFAAEL
ISRLEGVLROREAEQKLEERLKRVRAEEEGDDGDVSSGPSVISHKLPSGPPMHHENSR
YSETGCVGMQIRDAHEENPESILDEHVQRVMKTPGCQSPGTGRHSPKSRSPDGHLSKT
                                                                                                                                                                                                                                                                                                                                                                                          PGAVHPWVSAQLRNVVQPSHPFIQDPTMPPNPAPNPLTQLVSKPGARLEEEEKKAAKM
                                                                                                                                                                                                                                                                                                                                                                                                                  ASHEMPVVPEDSERHQKILQWIMEGEKEIIRHKKSNHSSSSAKKQPPTELARPLSIER
                                                                                                                                                                                                                                                                                                                                                                                                                                     QTNFPWNVESHNYATKSRNYAESMGMAPNPMDSLAYSGKVSMLSKRNAKKADLGKSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPGSLGTMQTGHGKHSSKSTAKVDSGNLHHHKHVYHHVHHHGGVKPKEQIDGESTQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RTFLQQENCADLLDFWFACSGFRKLEPNDSKVEKRLKLAKAIYKKYVLDSNGIVSRQI
KPATKSFIKDCVLRQQIDPAMFDQAQMEIQSMMEDNTYPVFLKSDIYLEYTTIGGESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="axin"
/protein_id="AAC71036.1"
/db_xref="GI:3834643"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YSLKNDGIKNETSTATPRRPDLDLGYEPEGSASPTPPYLKWAESLHSLLDDQDGIHLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Xenopus laevis"
/db_xref="taxon:8355"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MSVKGKGFPLDLGGSFTEDAPRPPVPGEEGELITTDQRPFSHTY"
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                                                                                                                                                                             Score 42; DB 8
Pred. No. 0.76;
0; Mismatches
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Best Local
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                       162 cggctgtcaatcccctggtgtgggtcgctacagccc 197
                                                                                                                                                                                            Local Similarity
                                                                                                             TGGCTGCCAGTCACCTGGCCCAGGCCACCGCTCTCC 1867
                                                                                      CCATGAGGAGAATCCTGAGAGCATCCTGGATGAGCACGTGCAAAGGGTCATGAGGACACC
                                                                                                                                                                            60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zeng, L., Fagotto, F., Zhang, T., Hsu, W., Vasicek, T.J., Perry, W.L. 3rd, Lee, J.J., Tilghman, S.M., Gumbiner, B.M. and Costantini, F. The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling pathway that regulates embryonic axis formation Cell 90 (1), 181-192 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (13-JUN-1997) Genetics and Development, Columb University, 701 W. 168th Street, New York, NY 10032, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zeng,L., Zhang,T., Perry,W.L. III, Lee,J.J. and Costantini,F. Direct Submission
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EIRVEPQKFAEELIHRLEAVQRTREAEEKLEERLKRVRMEEEGEDGEMPSGPMASHKL
PSVPAMHHFPPRYVDMGCSGLRDAHEENPESILDEHVQRVMRTPGCQSPGPGHRSPDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="LGSGSRLREALAAAAAAGACWGRAGAWFQRGLVRVSSRFWRRSAA
CLAPPPGHGSPSRRRRDGGPPGPRPRRGPPAEPPLSAWASPGREPGPGPRLHSRRAL
ERLIPLGAVSTEVLGCSAHCSLWQSPKNNVQEQGFPLDLGASFTEDAPRPPVPGEEGE
                                                                                                                                                                                                                                                                                                                                   DEPVLPVFEEKIIGKVEKVD"
                                                                                                                                                                                                                                                                                                                                                     KQRYVQAVMQRGRTCVRPACAPVLSVVPAVSDLELSETETKSQRKAGGGSAPPCDSIV
VGYYFCGEPIPYRTLVRGRAVTLGQFKELLTKKGSYRYYFKKVSDEFDCGVVFEEVRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YILDSNGIVSROTKPATKSFIKDCVMKOQIDPAMFDQAQTEIQSTMEENTYPSFLKSDIVLEYTRTGSESPKVCSDQSSGSGTGKGMSGYLPTLNEDEEWKCDQDADEDDGRDPLPPSRLTQKLLETAAPRAPSSRRYNEGRELRYGSWREPVNPYYVNSGYALAPATSANDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="17"
                                                                                                                                                                                                                                                                                                                                                                                                 GAVHPWVSAQLRNSVQPSHLFIQDPTMPPNPAPNPLTQLEEARRRLEEEEKRANKLPS
                                                                                                                                                                                                                                                                                                                                                                                                                         NAEVPSTTEDAEKNQKIMQWIIEGEKEISRHRKAGHGSSGLRKQQAHESSRPLSIERP
                                                                                                                                                                                                                                                                                                                                                                                                                                              RRVQSSFSWGPETHGHAKPRSYSENAGTTLSAGDLPFGGKTSAPSKRNTKKAESGKNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GHVAKTAVLGGTASGHGKHVPKLGLKLDTAGLHHHRHVHHHVHHNSARPKEQMEAEVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVSTDSRPVNHSFCSGKGTSIKSETSTATPRRSDLDLGYEPEGSASPTPPYLRWAESL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAC53285.1"
/db_xref="GI:2252816"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSLLDDQDGISLFRTFLKQEGCADLLDFWFACSGFRKLEPCDSNEEKRLKLARAIYRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product-"Axin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="Axin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"Fused
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="Axin"
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Pred. No. 5.6;
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                                                                                                                                                                                                                   DB
                                                                                                                                                                            36;
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AC011505/c
LOCUS
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Consensus quality: 165118 bases at least Q30
Consensus quality: 165125 bases at least Q20
Consensus quality: 166195 bases at least Q20
Estimated insert size: 169620; agarose-fp estimation
Quality coverage: 4.78 in Q20 bases; sagrose-fp estimation
Quality coverage: 4.78 in Q20 bases; sum-of-contigs estimation.
**NOTE: This is a 'working draft' sequence. It currently
**consists of 19 contigs. The true order of the pieces
**is not known and their order in this sequence record is
** arbitrary, Gaps between the contigs are represented as
**runs of N, but the exact sizes of the gaps are unknown.
**This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (07-OCT-1999) Production Sequencing Facility, I Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 9 On May 4, 2000 this sequence version replaced gi:6604364.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 171415)
DOE Joint Genome Institute.
Sequencing of Human Chromosome
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DOE Joint Genome Institute.
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Web site: http://www.jgi.doe.gov
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Summary Statistics
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                                                 f unknown length
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                                                                                                   of 7613 bp
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                                                                                                                                                                 of 4889
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94598, USA
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FEATURES
Source
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ORIGIN
Search completed: June 7, 2001, 00:36:12 Job time: 20986 sec
                                                                                                                                                                                                                                                                                                                                                           Query Match 18.0%; Score 37.2; DB 62; Length 171415; Best Local Similarity 51.9%; Pred. No. 4.8; Matches 84; Conservative 0; Mismatches 78; Indels 0;
                                                                                                       4416 CCAGTGCCCCACCAGGTCCCGTAACTCACCTAGCAGTGAAGAGCCTGCACTCACACCATG 4357
                                                                                                                                                                                                                   69 ccagcacccctggccctcctaccctccggcagctatgaagaggacccacaaaccatttt 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers

1. 171415

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="19"

/clone="CTD-2081K17"

/clone_lib="CalTech human BAC library D"

43300 a 41368 c 40333 g 44601 t 1813 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88458
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151018
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88457: contig of 12877 bp in length
88557: gap of unknown length
101414: contig of 12857 bp in length
101514: gap of unknown length
115884: contig of 14370 bp in length
115984: gap of unknown length
135910: contig of 17526 bp in length
133510: contig of 17526 bp in length
131017: contig of 17407 bp in length
151017: contig of 17407 bp in length
151117: gap of unknown length
171415: contig of 20298 bp in length
171415: contig of 20298 bp in length
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                Score
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1: /SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT:*

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23: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:*
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Murine axin gene.
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Human axin gene.
Human imidazoline
Aspergillus niger
DNA encoding a hum
DNA sequence of th
HCV NS2-NS4 clone
                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                     Human conductin cD
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eryA region of S.	Q46806	14	29879	14.3	9.	44
fusi	X84593	20	6056	14.3	9.	43
616	X84592	20	5828	٠	9.	42
Ċ	X84594	20	4226	14.3	29.6	41
protein	x84595	20	4024	•	9.	40
Human pancreatic c	C99118	21	498	٠	9	39
Nucleic acid seque	V81865	20	10279		9	38
SIVmac239 proviral	Q22487	13	10279	14.4	9	37
SIVmac239 nef-dele	Q24802	13	10097	14.4	9	36
0	Q43374	14	2045	14.4	9.	
d seq	X89693	20	1352	14.4	9.	34
DNA encoding a GDP	Z45317	21	1340	14.4	9	ω ω
HCV NS2-NS4 clone	Q32442	13	3564			32
HCV NS2-NS4 clone	Q32479	13	1280	14.5	30	31
HCV NS2-NS4 clone	Q32472	13	849		30	30
Human G-protein co	Z20298	20	3852		•	29
×	C77294	21	3362			28
protei	290525	21	1520		٠	27
Human G-protein co	220297	20	1212	14.6	30.2	26
Neisseria gonorrhe	Z53531	21	960			25
Neisseria meningit	Z53533	21	957		•	24
	253530	21	720		•	23
	253528	21	720	14.6	•	22
EST clone EC302.	V87645	20	421		•	21
HCV antigen clone	Q32436	13	7911	14.7		20
AB005297 cDNA clon	C90314	22	5535	14.7	•	19
Human BAI1 gene.	X21355	20	5535	14.7	•	18
Human METH2 relate	Z32057	20	5535	14.7	•	17
Human ORFX ORF1991	C76436	21	4447	14.7	•	16
HCV NS2-NS4 clone	Q32501	13	3564	14.7	•	15
se Voltag	Z49454	21	1518	14.7	•	14
NS2-NS4 c	Q32495	13	1280	14.7	30.4	13
HCV NS2-NS4 clone	032494	13	1280	14.7	30.4	12

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## ALIGNMENTS

17-JUN-1999 (first entry)

x23370;

X23370 standard; cDNA; 2523 BP

Human conductin cDNA.

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Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour; therapy; cytoplasmic degradation; blockade; Wnt signalling pathway; Wingless signalling pathway; Adenomatous Polyposis Coli; APC; tumour suppressor; ss.
Tumor-suppressing protein conductin diagnosis of tumors
                           WPI; 1999-214706/18.
P-PSDB; W93570.
                                                      Behrens J, Birchmeier W;
                                                                                           02-SEP-1997;
                                                                                                              01-SEP-1998;
                                                                                                                                 11-MAR-1999
                                                                                                                                                  W09911780-A2
                                                                                                                                                                    Homo sapiens
                                                                         (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX
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                                                                                                               98WO-DE02621.

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Best Local S
Matches 207
                                     misc_feature
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                                                                                  protein_bind
                                                                                                                                 protein_bind
                                                                                                                                                                               misc_signal
                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                   Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour; therapy; cytoplasmic degradation; blockade; Wnt signalling pathway; Wingless signalling pathway; Adenomatous Polyposis Coll; APC;
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                                                                                                                                                                                                                                                                                                                                                                                      x23369;
                                                                                                                                                                                                                                                                                                                                                                                                           X23369 standard; cDNA; 2825
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anti-tumour
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207; Conserv
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                                 /bound_moiety= |
/note= "as desc:
2561..2713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          describes a novel human conductin protein which has
                                                                                                                                                                               /product= "Conductin" 446..814
                                                                                                                                                                                                                 Location/Qualifiers 215..2737
                                                                                            /bound_moiety= GSK-3beta
/note= "as described in o
                                                                                                                                1241..1402
                                                                                 1403..1609
                        /*tag=
                                                                       /*tag=
                                                                                                                                      /note= "regulator of G-protein signalling region described in Claim 19"
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 "Dishevelled homology region
Claim 22"
                                           sty= beta-catenin
described in Claim
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Pred. No. 1.7e-48;
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Best Local
CDS
                                                                                                                                              Axin; cancer; breast cancer; colorectal cancer; gastrointestinal cancer; esophageal cancer; carcinoma; melanoma; diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1523
                                                                           Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1403
                                                                                                                           beta-catenin;
                                                                                                                                                                                                                                                       Murine axin gene
                                                                                                                                                                                                                                                                                                                14-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                 X09013 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anti-tumour activity. Detecting the presence or amount of conductin, at protein or nucleic acid levels, is used to diagnose tumours, while agents that (re)activate conductin are used for tumour therapy. Conductin binds to beta-catenin and induces its cytoplasmic degradation, resulting in blockade of the Wnt/Wingless signalling pathway in vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2825 BP; 703 A; 815 C; 813 G; 494 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor-suppressing protein conductin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB;
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Location/Qualifiers
1..2981
                                                                                                                                                                                                                                                                                                           entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acts as a tumour suppressor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for treatment
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Best Local S
Matches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                    1772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       type Axin and homologues of Axin are useful for treating subjects who are likely to develop cancer (thyroid carcinomas). The nucleic acids are also useful for diagnosing cancer and for detecting mutations in cancerous cells. Wild type Axin, its antisense molecule and identified compounds form pharmaceutical compositions in the treatment of cancer. The compositions are also useful for treating cancer by inhibiting tumorigenesis (by inducing degradation of beta-catenin). The nucleic acid encoding Axin acts through
         Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathc; antiparkinsonian; timunosuppressant; cardiant immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antimnal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypottension neurodegenerative disorder; osteoarthritis; graft was host disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding mutant and wild type Axin and oligonucleotides derived from them are useful for detecting mutations in the Axin gene and for determining whether a subject is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                likely to develop cancer (including breast, colorectal, gastrointestinal, esophageal, carcinomas or melanomas). The wild
                                                                                                                                                                                                                                            C75493;
                                                                                                                                                                                                                                                                           C75493 standard; cDNA; 402
                                                                                                                                                                                                                                                                                                                                                                 1832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3761 BP; 890 A; 1012 C; 1088 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Figure 9A-9B; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Constantini F,
                                                                                                                                                                       Human ORFX ORF1048
                                                                                                                                                                                                          08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Newly isolated nucleic acid encoding "axis inhibition" protein (Axin) - useful for detecting, diagnosing and treating cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9902179-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            negative regulation of the Wnt pathway in the Nieuwkoop Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                                                                                                                                                                                                                                                                                              162 cggctgtcaatcccctggtgtgggtcgctacagccc 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 ctatgaagaggacccacaaaaccattttggaacgaccacctctccagggtcctcaagacccc 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                            tggctgccagtcacctggcccaggccaccgctctcc 1867
                                                                                                                                                                                                                                                                                                                                                                                                                                ccatgaggagaatcctgagagcatcctggatgagcacgtgcaaagggtcatgaggacacc 1831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60;
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                                                                                                                                                                                                      (first entry)
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/product= Axin
                                                                                                                                                                      polynucleotide sequence SEQ ID NO:2095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.6%;
62.5%;
diabetes mellitus;
                                                                                                                                                                                                                                                                           ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38.4;
Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB
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X09012 ID XI XX

X09012 standard; DNA;

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                                                                                                                                                                                                                                                       represent the human OREX open reading frames 1 to 3161. The OREX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; mootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antifungal; antifungal; antithromoty; antibacterial; antivital; antifungal; antifungal; anticonvold; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an OREX-associated disorder. The nucleic acids can be used to express orex proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, disorders, asthma, altergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuta, antiinflammatory disease; to
                                                                                                                                                           Matches
                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAR-1999; 99US-0127607
02-APR-1999; 99US-0127636
05-APR-1999; 99US-0127728
30-MAR-2000; 2000US-0540763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cholesterol ester storage; systemic lupus erythematosus; infection severe combined immunodeficiency; malaria; autoimmune disorder; as allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulati
                                                                                                                                                                                                                                                     Sequence 402 BP; 77 A; 126 C; 107 G; 92 T; 0 other;
                                                                                                                                                                                                                                                                                           enhance coagulation; to inhibit thrombosis; and as a contraceptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C74446 to C77606 encode the proteins given in B40237 to B43397, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 1573; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-2000; 2000WO-US08621.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CURA-) CURAGEN CORP.
                                                                              131
      191
                      113 acccacaaaccattttggacgaccacctctccagggtcctcaagacccccgg 164
                                                                                                                  53
                                                                                                                                                                           Local Similarity
ctcttgtgctgcaagtgaaagaagccctccccagtgtcctcaccacccatgg
                                                                          gcgtgggttcagtgggcacccactccctggtactgctactgtccggccccaatgatgaac 190
                                                                                              gggatggagcaccggtccagcaccccctggccctcctaccctccggcagctatgaagagg 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-602362/57.
)B; B41284.
                                                                                                                                                         64;
                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leach
                                                                                                                                                                       17.0%;
57.1%;
                                                                                                                                                       Score 35.2; DB Pred. No. 0.5; 0; Mismatches
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                                                                                                                                                                                               В
                                                                                                                                                         48;
                                                                                                                                                                                             Length 402;
                                                                                                                                                           Indels
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X09012

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RESULT
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                                                                                                                                                                                                                                                                                                              Nucleic acids encoding mutant and wild type Axin and coligonucleotides derived from them are useful for detecting mutations in the Axin gene and for determining whether a subject is likely to develop cancer (including breast, colorectal, gastrointestinal, esophageal, carcinomas or melanomas). The wild type Axin and homologues of Axin are useful for treating subjects who are likely to develop cancer (thyroid carcinomas). The nucleic acids are also useful for diagnosing cancer and for detecting mutations in cancerous cells. Wild type Axin, its antisense molecule and identified compounds form pharmaceutical compositions in the treatment of cancer. The compositions are also useful for treating cancer by inhibiting tumorigenesis (by inducing degradation of beta-catenin). The nucleic acid encoding Axin acts through cancer negative regulation of the Wnt pathway in the Nieuwkoop Center.
                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                              Matches
                                                                                                                                                    1503
            X28371 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Axin; cancer; breast cancer; colorectal cancer;
gastrointestinal cancer; esophageal cancer; carcinoma; melanoma;
diagnosis; treatment; therapy; thyroid carcinoma; tumorigenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                      Sequence 3411 BP; 752 A; 1010 C; 1066 G; 582 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Figure 10A-10B; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Newly isolated nucleic acid encoding "axis inhibition" protein (Axin) - useful for detecting, diagnosing and treating cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Constantini F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JAN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              beta-catenin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human axin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-JUN-1999
                                                                                                      164 gctgtcaatcccctggtgtgggtcgctacagccc 197
                                                                                                                                                                  104 atgaagaggacccacaaaccattttggacgaccacctctccagggtcctcaagacccccg 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                                                                                            Local Similarity
                                            σ
                                                                                      gccgccagtcgcctgggcctggccatcgctcccc 1596
                                                                                                                                                  acgaggagaaccctgagagcatcctggacgagcacgtacagcgtgtgctgaggacaactg 1562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1999-120510/10.
                                                                                                                                                                                                              56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful for detecting, diagnosing and treating
                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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              CDNA; 15202 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= Axin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                            16.0%;
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                                                                                                                                                                                                              0;
                                                                                                                                                                                                           Score 33.2; DB Pred. No. 2.8; 0; Mismatches
                                                                                                                                                                                                                                            В
                                                                                                                                                                                                            38;
                                                                                                                                                                                                                                          20;
                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                              Indels
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W AC XX
                                                                                                 RESULT 7
F11514/c
ID F11514 standard;
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                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                               This sequence encodes an imidazoline receptor of the invention. Host cells expressing the polypeptides are useful for screening for ligands of an imidazoline receptor. Restriction fragments of the polynucleotide are useful as labeled probes for isolating and identifying DNA material encoding polypeptides that are receptive to imidazoline compounds. The isolation of polynucleotides encoding the imidazoline receptive polypeptides have immunological and ligand binding properties, which enable identification of agents having greater potency and/or more selectivity for these receptors.
Multiple gene expression; filamentous fungal cell; EST;
                                                  13-MAR-2001
                                                                                                                                                                9872
                                                                                                                                                                                                                 9932
                                                                                                                                                                                                                                                                 9992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides encoding imidazoline receptive polypeptides useful for screening for ligands of imidazoline receptors, and isolating and identifying polynucleotides encoding imidazoline
                        Aspergillus niger EST SEQ ID NO:4037.
                                                                          F11514;
                                                                                                                                                                                                                                                                                                                                                                           Sequence 15202 BP; 2844 A; 4417 C; 4444 G; 3479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 72-79; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptive polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-214698/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human imidazoline receptor coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           x28371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ivanov TR, Piletz JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UMIS ) UNIV MISSISSIPPI MEDICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Imidazoline receptor; human; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JUN-1999
                                                                                                                                                                                        121 acca 124
                                                                                                                                                                                                                                        61
                                                                                                                                                              GCCA
                                                                                                                                                                                                                 gcaccggtccagcaccccctggccctcctaccctccggcagctatgaagaggacccacaa 120
                                                                                                                                                                                                                                                                 cagatccgggaggatgaagaaaaggagggtctgagcaggccctgagctcacgggatgga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens
                                                                                                                                                                                                                                                                                                                67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y05244
                                                                                                                                                                9869
                                                                                                                                                                                                                                                                                                                Conservative
                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97WO-US15695.
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                                                                                                  CDNA; 438
                                                                                                                                                                                                                                                                                                                            15.8%;
                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                            Score 32.8; Di
Pred. No. 4.8;
                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CENT.
                                                                                                                                                                                                                                                                                                                                       ВВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genomic clone
                                                                                                                                                                                                                                                                                                                 57;
                                                                                                                                                                                                                                                                                                                                       20;
                                                                                                                                                                                                                                                                                                                                                                            Τ,
                                                                                                                                                                                                                                                                                                                                       Length 15202;
                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                           18 other;
                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                               Gaps
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RESULT
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                                                                                                                                                                                                                                  5
                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
                                                                                                                                                                                                                                                                                                                                                                             Sequence 438 BP; 84 A; 92 C; 91 G; 170 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 87; Page 1782; 3161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a substrate of expressed sequence tags -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Berka RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200056762-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-MAR-2000; 2000WO-US07781.
                                                                                                                                                                                                                                                                                                                                                                                                                specifically claimed in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NOVO ) NOVO NORDISK BIOTECH INC (NOVO ) NOVO NORDISK AS.
                                                                                                                  100
                                                                                                                                           160 cccggctgtcaatcccctggtgtgggtcgctacagcccacggtcc 204
                                                                                                                                                                                                160
                                                          œ
                                                                                                                                                                                                                   agctatgaagaggacccacaaaaccattttggacgaccacctctccagggtcctcaagacc 159
                                                                                                                  TCCGCATAAATAGCCTCTAATTTCCGGATCTGCAGTCCAAGACCC
                                                                                                                                                                                              AGGAAAGAAAAGGATTAAAGAAGCATTTTGAACTAACACTTCTCCAACCGCTTCCTCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rey MW,
                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                              15.2%;
                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                              Score 31.4; D
Pred. No. 5.8;
                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                                                                           46;
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                                                                                                                                                                                                                                                                                                              Length 438;
                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                           0,
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X86273 standard; DNA; 2326 BP

22-FEB-2000

(first entry)

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RESULT
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                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                            The specification describes the use of p53 transcription tags for developing products to determine p53 status, to diagnose cancer and to evaluate cytotoxicity or carcinogenicity of a test agent. A method for diagnosing cancer or determining p53 status in a sample suspected for being neoplastic comprises comparing the level of transcription of an RNA transcript in a first sample (s1) of a first tissue (t1) to the level of transcription of the transcript in a second sample (s2) of a second tissue (s2), where s1 is suspected of being neoplastic and s2 is a normal human tissue (of the same type) and the transcript is identified by a tag; and categorizing s1 as neoplastic or as having a mutant p53 when transcription is found to be the same or lower in the first, than in s2. The methods and products can be used to determine p53 status, to diagnose cancer and to evaluate cytotoxicity or carcinogenicity of a test agent. X86265-75 encode human PIG proteins.
Z36256
                              Z36256 standard;
                                                                                                                                                                                                                                                                                                                                                                    Sequence 2326 BP; 544 A; 635 C; 637 G; 510 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 64-65; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of p53 transcription cancer diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-443793/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kinzler KW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-1998;
17-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding a human PIG protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-SEP-1999
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                                                                                                       121
                                                                                                                                                                  61
                                                                                                                                                                                                                                             23 aggaggggtctgagcacgggcctgagctcacgggatggagcacccggtccagcacccctgg
                                                          9
                                                                                                                                                                                    ccctcctaccctccggcagctatgaagaggacccacaaaccattttggacgaccacctct 142
                                                                                                    cgcggcgcctgcagtggcacggattgctctgccctaccgtgacgcgctccgg
                                                                                                                                 ccagggtcctcaagacccccggctgtcaatcccctggtgtgggtcgctacag 194
                                                                                                                                                                  gccgccggcacacaaggcgctttctagctccctcccccgagcgcacagcccgcctccttc
                                                                                                                                                                                                                             aggccggagaggaggcggtgcggtggccgtgcggagacccggtccagacgcctggcg
                                                                                                                                                                                                                                                                                          84;
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                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOHNS HOPKINS
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97US-0059153
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                              DNA;
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                              10384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tags to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          status;
                              ВP
                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                     Score 31.2; DB Pred. No. 9.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             determine p53 status in, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer; cytotoxicity; carcinogenicity;
                                                                                                                                                                                                                                                                                                                        DB
                                                                                                                                                                                                                                                                                          ; 88
                                                                                                                                                                                                                                                                                                                        20;
                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                      Length 2326;
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Best Local S
Matches 69
Hepatitis C virus
                         Clone; polypeptide; NS2-NS4;
transcriptase; cDNA; primer;
                                                                  HCV NS2-NS4 clone MX25-2.
                                                                                             26-APR-1993
                                                                                                                                                 Q32483 standard; DNA; 849
                                                                                                                                                                                                                     1912
                                                                                                                                                                                                                                                                                                                                2032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents the human longevity assurance gene 1 (LAGI), designated LAGIHs. The LAGIHs cDNA was isolated from total brain mRNA. The LAGI protein, or proteins with at least 25-30% homology to the LAGIHs protein, is administered to increase the longevity of a human cell: Expression of these polypeptides is used to increase tolerance of human cells to cellular stresses, such as starvation or acidic pH (5-5.5). The LAGI proteins are also used for increasing reproductive capacity of human cells. LAGI polynucleotides can be used as probes for detecting LAGI from different species, as the LAGI gene is highly conserved across the spectrum of eukaryotes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10384 BP; 2135 A; 2839 C; 3598 G; 1812 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human homologue for increasing longevity, tolerance and reproductive capacity of a cell -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-053098/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jazwinski SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (RESE ) RESEARCH CORP TECHNOLOGIES
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                                                                                                                                                                                                                                               193
                                                                                                                                                                                                                                                                                                                                                         73
                                                                                                                                                                            10
                                                                                                                                                                                                                                                                                           gaccacctctccagggtcctcaagacccccggctgtcaatcccctggtgtgggtcgctac 192
                                                                                                                                                                                                                                                                                                                                          caccccctggccctcctaccctccggcagctatgaagaggacccacaaaccattttggac 132
                                                                                                                                                                                                                    AGCCCGAGGCCCC 1900
                                                                                                                                                                                                                                           agcccacggtccc 205
                                                                                                                                                                                                                                                                         AGGGGGCGCGCGGCCCGAGAGACCTTATCCTGGGGCTCCAACGTCCTGGGCCTCTCC
                                                                                                                                                                                                                                                                                                                            CTCACCCCAGCCCGCCACACCCCCGCATCTACCCGGGTTCCCCCCACGCAGCACTGTCTGA 1973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reproductive capacity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tolerance;
                                                                                                                                                                                                                                                                                                                                                                                    69; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            longevity assurance gene 1; LAG1; LAG1Hs; cell longevity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 92-99; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kirchman P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0075014.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US10160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cellular stress;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the human longevity assurance gene 1 (LAG1).
                                                                                                                                                                                                                                                                                                                                                                                              14.8%;
                                                                                                                                                   BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jiang J;
                                                                                                                                                                                                                                                                                                                                                                                   0;
                         Hepatitis allele; ss
                                                                                                                                                                                                                                                                                                                                                                                              Score 30.6;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 starvation; acidic pH;
                                      c;
                                                                                                                                                                                                                                                                                                                                                                                                18;
                                                                                                                                                                                                                                                                                                                                                                                                            DB
                                       Virus;
                                                                                                                                                                                                                                                                                                                                                                                 64;
                                                                                                                                                                                                                                                                                                                                                                                                            21;
                                       HCV;
                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Length 10384;
                                       serum;
                                                                                                                                                                                                                                                                                                                                                                                0;
                                       HC
                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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07-OCT-1991;
16-DEC-1991;
20-APR-1992;
             16-DEC-1992
                                      EP518313-A.
                                                             Hepatitis C
                                                                                                   Clone;
                                                                                                                        HCV NS2-NS4 clone MX25-1.
                                                                                                                                                                         Q32482;
                                                                                                                                                                                              12/c
Q32482 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 849
                                                                                                                                                                                                                                                                                                                                                                                                                                            sequences given in Q32578-79. The sequences were then amplified using primer pairs. The cDNA sequences isolated represent different alleles of the same region of the HCV gene. Sequence comparisons of these clones showed that it is possible for a patient to carry more than one HCV strain at one time. See also Q32436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequences given in Q32483-501 are various clones which were used in the isolation of the NS2-NS4 regions of the Hepatitis C Virus (HCV) gene of the invention (see also Q32442 and Q32472-82). These sequences were isolated from the serum of a patient suffering from hepatitis C (HC). The isolated RNA sequences were converted into CDNA using transcriptase in the presence of one of the primer sequences given in 032578-79. The sequences were then amplified
                                                                                     transcriptase; cDNA;
                                                                                                                                                  26-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 147-49; 305pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New hepatitis C virus gene and its encoded protein - used for diagnosing and vaccinating against hepatitis C virus infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1992-417213/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hayashi N,
Teranishi Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP518313-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MITU ) MITSUBISHI KASEI CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JUN-1991;
                                                                                                                                                                                                                                                                                                            123
                                                                                                                                                                                                                                                                                                                                   16
                                                                                                                                                                                                                                                             63
                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                             CACCAGGTTCTCCAAGGCGGCCTCAGCT
                                                                                                                                                                                                                                                                            cccctggccctcctaccctccggcagct 103
                                                                                                                                                                                                                                                                                                            GAAGAACACAAGGAAAGAGAGGATGCCATGCGCTCCCCCCCATGGATGCTGCATTGAGGAC
                                                                                                                                                                                                                                                                                                                         gaagaaaaggagggtctgagcaggccctgagctcacgggatggagcaccggtccagcac
                                                                                     polypeptide; NS2-NS4;
riptase; cDNA; primer;
                                                                                                                                                                                                                                                                                                                                                           52;
                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                               virus
                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Honda Y,
                                                                                                                                                                                                                                                                                                                                                                                                                       вÞ;
                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91JP-0139268.
91JP-0172794.
91JP-0287008.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91JP-0332329.
92JP-0099957.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92EP-0109812
                                                                                                                                                                                                DNA; 849 BP
                                                                                                                                                                                                                                                                                                                                                                                                                     150 A; 250 C;
                                                                                                                                                                                                                                                                                                                                                                      14.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murakami T,
                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                     Hepatitis C; Virus; HCV; serum;
allele; ss.
                                                                                                                                                                                                                                                                                                                                                                      Score 30.4;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                     247 G;
                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                             36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seki M,
                                                                                                                                                                                                                                                                                                                                                                                                                       202
                                                                                                                                                                                                                                                                                                                                                                                  DВ
                                                                                                                                                                                                                                                                                                                                                                                                                       T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Takahashi
                                                                                                                                                                                                                                                                                                                                                           36;
                                                                                                                                                                                                                                                                                                                                                                                  13;
                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                             64
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RESULT 12
Q32494/c
Q32494 standard; DNA; 1280 BP.
XX
AC
Q32494;
XX
DT
26-APR-1993 (first entry)
XX
DE
HCV NS2-NS4 clone MX25026A-1.
XX
DE
KW Clone; polypeptide; NS2-NS4; Hep
KW transcriptase; CDNA; primer; all
XX
OS
Hepatitis C virus.
XX
FH
Key
FT
CDS
FT
CDS
FT
CDS
FT
CDS
PN
EP518313-A.
XX
PD
16-DEC-1992.
XX
PF
11-JUN-1992; 92EP-0109812.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JUN-1991;
12-JUL-1991;
07-OCT-1991;
16-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the invention. These sequences were isolated from the serum of a patient suffering from hepatitis C (HC). The isolated RNA sequences were converted into CDNA using transcriptase in the presence of one of the primer sequences given in 03253-64. The sequences were then amplified using primer pairs. The cDNA sequences isolated represent different alleles of the same region of the HCV gene. Sequence comparisons of these clones showed that it is possible for patient to carry more than one HCV strain at one time. See also
                                                                                                                                                                                   Clone; polypeptide; NS2-NS4; Hepatitis C; Virus; transcriptase; cDNA; primer; allele; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequences given in Q32472-82 and Q32442 are various clones which encode the NS2-NS4 regions of the Hepatitis C Virus (HCV) gene of the invention. These sequences were isolated from the serum of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New hepatitis C virus gene and its encoded protein - used for diagnosing and vaccinating against hepatitis C virus infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 849 BP; 146 A; 245 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 146-47; 305pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1992-417213/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashi N,
Teranishi Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MITU ) MITSUBISHI KASEI CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123
                                                                                                                                                                                                                                                                                                                                                                                                        ဌ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16
                                                                                                                                                                                                                                                                                                                                                                                                                                   76
                                                                                                                                                                                                                                                                                                                                                                                                                     cccctggccctcctaccctccggcagct 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gaagaaaaggagggtctgagcaggccctgagctcacgggatggagcaccggtccagcac 75
                                                                                                                                                                                                                                                                                                                                                                                                       CACCAGGTTCTCCAAGGCGGCCTCAGCT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAGAACACAAGGAAAGAGAGGATGCCATGCGCTCCCGCCATGGATGCTGCATTGAGGAC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.7%;
ilarity 59.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Honda Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91JP-0139268.
91JP-0172794.
91JP-0287008.
91JP-0332329.
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                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murakami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 30.4;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'n,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seki M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Takahashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36;
                                                                                                                                                                                                     HCV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                     serum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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RESULT 13
Q32495/C
ID Q32495
XX Q32495
AC Q32495
XX Q32495
AC Q32495
XX C10ne;
CY 26-APR
XX C10ne;
KW C10ne;
KW C10ne;
KW C10ne;
KW C10ne;
KW C10ne;
KW C10ne;
KW C10ne;
KW C10ne;
KW C10ne;
KW C10ne;
KW C10ne;
LY C10 C10;
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Best Local S
Matches 52
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12-JUL-1991;
07-OCT-1991;
16-DEC-1991;
20-APR-1992;
                         11-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q32495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA using transcriptase in the presence of one of the primer sequences given in Q32578-79. The sequences were then amplified using primer pairs. The cDNA sequences isolated represent different alleles of the same region of the HCV gene. Sequence comparisons of these clones showed that it is possible for a patient to carry more than one HCV strain at one time. See also Q32436.
                                                                                                                                                                                                                                                                        Hepatitis C
                                                                                                                                                                                                                                                                                                                       Clone; polypeptide; I
transcriptase; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q32495 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1280 BP; 222 A; 385 C; 376 G; 297 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New hepatitis C virus gene and its diagnosing and vaccinating against
                                                                           16-DEC-1992
                                                                                                                       EP518313-A.
                                                                                                                                                                                                                                                                                                                                                                                                  HCV NS2-NS4 clone MX25026B-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HCV) gene of the invention (see also Q32442 and Q32472-82). These sequences were isolated from the serum of a patient suffering from the patitis C (HC). The isolated RNA sequences were converted into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequences given in Q32483-501 are various clones which in the isolation of the NS2-NS4 regions of the Hepatitis C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 165-67; 305pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MITU ) MITSUBISHI KASEI CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cccctggccctcctaccctccggcagct 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gaagaaaaggagggtctgagcaggccctgagctcacgggatggagcaccggtccagcac 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CACCAGGTTCTCCAAGGCGGCATCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAGAACACAAGGAAAGAGAGGATGCCATGCGCTCCCGCCATGGATGCTGCATTGAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity 59.: 52; Conservative
                                                                                                                                                                                                                                                                           virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Honda Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91JP-0139268.
91JP-0172794.
91JP-0287008.
91JP-0332329.
92JP-0099957.
                         92EP-0109812.
                                                                                                                                                                                                Location/Qualifiers
1..1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
                                                                                                                                                                                                                                                                                                                    NS2-NS4;
h; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murakami T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30.4; D
Pred. No. 14;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                       Hepatitis C; allele; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encoded protein - hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seki M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                                                                    Virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Takahashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36;
                                                                                                                                                                                                                                                                                                                                                    HCV; serum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                used for infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             were used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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RESULT 14
Z49454
ID Z49454
AC Z49454
AC Z49454
AX VOLUSE
DE MOUSE
XX VOLUSE
KW PSYCHO
KW PSYCHO
KW PSYCHO
KW PSYCHO
KW PTIMET
XX MUS SP
FH KEY
FT MAL_PE
FT MISC_f
FT MISC_f
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Best Local
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12-JUL-1991;
07-OCT-1991;
16-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequences given in Q32483-501 are various clones which were used in the isolation of the NS2-NS4 regions of the Hepatitis C virus (HCV) gene of the invention (see also Q33442 and Q32472-80). These sequences were isolated from the serum of a patient suffering from hepatitis C (HC). The isolated RNA sequences were converted into cDNA using transcriptase in the presence of one of the primer sequences given in Q32578-79. The sequences were then amplified using primer pairs. The cDNA sequences isolated represent different alleles of the same region of the HCV gene. Sequence comparisons of these clones showed that it is possible for a patient to carry more than one HCV strain at one time. See also Q32436.
                            misc_feature
                                                                                                                                                                                 resting potential; alpha subunit; modulator; hearing/vision problem; migraine; central nervous system; CNS; seizure; neuroprotective agent; psychotic disorder; reporter; treatment; detection; antibody; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashi N,
Teranishi
                                                                                                                                                                                                                                                                                                                                                    249454 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1280 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New hepatitis C virus gene and its encoded protein - diagnosing and vaccinating against hepatitis C virus
                                                                                           mat_peptide
                                                                                                                                       Mus sp.
                                                                                                                                                                    primer;
                                                                                                                                                                                                                                                            Mouse Voltage-gated Potassium channel monomer, Kv6.2 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MITU ) MITSUBISHI KASEI CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16
                                                                                                                                                                                                                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                                                                                                                                                                                                                                            76
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                                                                                                                                                                                                                                                                                                                                                                                                                                CACCAGGTTCTCCAAGGCGGCATCAGCT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                cccctggccctcctaccctccggcagct 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAGAACACAAGGAAAGAGAGGATGCCATGCGCTCCCGCCATGGATGCTGCATTGAGGAC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gaagaaaaggagggtctgagcaggccctgagctcacgggatggagcaccggtccagcac 75
                                                                                                                                                                      ds
                                                                                                                                                                                                                               gated potassium channel; Kv6.2; mouse; excitability; ion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 167-69; 305pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Honda Y,
                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91JP-0287008.
91JP-0332329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91JP-0139268.
91JP-0172794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92JP-0099957.
                             /label= Mouse_Kv6.2_polypeptide
/note= "Voltage gated potassium
1381..1389
                                                                                                         Location/Qualifiers
/note= "This region encodes the amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              222 A; 385 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.7%;
59.1%;
                                                                                                                                                                                                                                                                                                                                                        1518
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                                                                            D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
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Pred. No. 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           376 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seki M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              297 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takahashi K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36;
                                               channel subunit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     used for
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RESULT
Q32501/c
ID Q33501/c
ID Q33
XX
AC Q33
XX
DT 26
XX
DT 26
XX
TX
DE HCV
XX
C10
KW tra
XX
OSS Hep
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is the gene encoding the mouse Kv6.2 monomer, which is an alpha subunit of heteromeric voltage-gated potassium channel. It is isolated from brain tissue and maintains the resting potential and controls the excitability of a cell. Kv6.2 polypeptide can be used to identify compounds, that modulate the ion flux through heteromeric voltage-gated potassium channels. Such modulators are used as neuroprotective agents and for treating CNS disorders, such as migraines, hearing and vision problems, psychotic disorders and seizures. It can also be used as reporter molecules in assays and to produce antibodies. Kv6.2 DNA sequence can be used to produce specific primers or probes
                                          Clone; polypeptide; NS2-NS4; Hepatitis C; transcriptase; cDNA; primer; allele; ss.
                                                                                                                                              Q32501;
                                                                                                                                                                          )1/c
Q32501 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New voltage-gated potassium channel alpha subunit, useful for identifying modulators of voltage-gated channel activity usefureating central nervous system disorders e.g. migraines and neuroprotective agents
             Hepatitis C virus
                                                                                    HCV NS2-NS4 clone N25N15-1.
                                                                                                                  26-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1518 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for detection purposes.
                                                                                                                                                                                                                                                 296
                                                                                                                                                                                                                                                                           122 ccattttggacgacca 137
                                                                                                                                                                                                                                                                                                                                                                 176 agatectagtgaatgtgggtggeeageggtacetgetgeeetggageaceetggatgeet 235
                                                                                                                                                                                                                                                                                                                         62 caccggtccagcaccccctggccctcctaccctccggcagctatgaagaggacccacaaa 121
                                                                                                                                                                                                       15
                                                                                                                                                                                                                                                                                                                                                                                                                                        Toca<sub>T</sub>
                                                                                                                                                                                                                                                                                                                                                                                   2 agatccgggaggatgaagaaaaggagggtctgagcaggccctgagctcacgggatggag
                                                                                                                                                                                                                                                                                                        tcccgctgagccgcctgagcaggctccggctgtgccgcagccatgaggagatcacgcagc
                                                                                                                                                                                                                                              tctgcgatgactacga 311
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                                                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity
70; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 65-66; 80pp;
                                                                                                                                                                                                                                                                                                                                                                                                                           14.7%;
nilarity 51.5%;
Conservative
                                                                                                                 (first entry)
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                                                                                                                                                                            DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271 A; 467 C;
                                                                                                                                                                            3564 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELK, which is represented in the specification as the typographical error KV6.2 (an insertion of the protein name)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 30.4;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   470 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 T;
                                                          Virus; HCV; serum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                                                                                                                                              66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful
                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                            HC;
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Search completed: June Job time: 8637 sec
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Best Local Similarity 59.1%;
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUN-1991;
12-JUL-1991;
07-OCT-1991;
16-DEC-1991;
20-APR-1992;
                                                                                                                                                                                                                                                                                                           The sequences given in Q32483-501 are various clones which were used in the isolation of the NS2-NS4 regions of the Hepatitis C virus (HCV) gene of the invention (see also Q32442 and Q32472-82). These sequences were isolated from the serum of a patient suffering from hepatitis C (HC). The isolated RNA sequences were converted into CDNA using transcriptase in the presence of one of the primer sequences given in Q32578-79. The sequences were then amplified using primer pairs. The CDNA sequences isolated represent different alleles of the same region of the HCV gene. Sequence comparisons of these clones showed that it is possible for a patient to carry more than one HCV strain at one time. See also Q32436.
                                                                                                                                                                                                                                                                                    Sequence 3564 BP; 668 A; 1064 C; 1046 G; 786 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 186-92; 305pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New hepatitis C virus gene and its encoded protein - used for diagnosing and vaccinating against hepatitis C virus infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1992-417213/51.
P-PSDB; R29870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashi N,
Teranishi Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP518313-A.
                                                                                                                                         123 GAAGAACACAAGGAAAGAGGATGCCATGCGCTCCCGCTATGGATGCTGCATTGAGGAC 64
                                                                                             76 cccctggccctcctaccctccggcagct 103
                                                                                                                                                                          16
                                                                            63 CACCAGGTTCTCCAAGGCGGCCTCAGCT 36
                                                                                                                                                         gaagaaaaggaggggtctgagccaggccctgagctcacgggatggagcaccggtccagcac 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91JP-0139268.
91JP-0172794.
91JP-0287008.
91JP-0332329.
92JP-0099957.
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              7, 2001, 00:31:59
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                                                                                                                                                                                                     Score 30.4; DI
Pred. No. 17;
0; Mismatches
                                                                                                                                                                                                     0
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                                                                                                                                                                                                                                     DB 13;
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                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                   Length 3564;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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          seq length:
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Match
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfilesl.seq:*
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14.3
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           302621 seqs, 87301344 residues
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Gapop 10.0 , Gapext 1.0
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207
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          2000000000
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US-08-937-972-4
US-07-642-734C-3
US-08-439-009A-3
US-08-460-900C-42
US-08-460-900C-42
US-08-540-406-5
US-08-656-055-5
US-08-656-055-5
PCT-US95-13233-5
US-09-954-668-5
PCT-08-510-6468-14
US-09-918-953-3
US-08-081-661-3
US-09-18-953-12
US-07-918-953-12
US-07-918-953-12
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Sequence 21, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 42, Appli
Sequence 42, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 1, Appli
Sequence 14, Appli
Sequence 14, Appli
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Sequence 16, Appli
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Sequence 19, Appli
Sequence 28, Appli
                                                                                                                                                                                                                                                                                                                                                                                                  Description
    ; Sequence 4, Application US/08937972
Patent No. 5932443
; GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
                                                                           RESULT 2
US-08-937-972-4
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Oy Oy Oy Oy	A S S A S	RESULT US-08- US-08- ; Sequ ; Pate ; GENE ; APP ; APP ; APP	n
1 9992 61 9932 121 121 9872	FILE REFER FILE REFER PATENT AP CURRENT FI EARLIER AP EARLIER AP EARLIER FI NUMBER OF SOFTWARE SEQ ID NO 2 LENGTH: 1 TYPE: DNA ORGANISM: 3-08-922-635 Query Match Best Local Matches 6	SULT 1 -08-92-635 Sequence 21 Patent No. GENERAL IN: APPLICANT: APPLICANT: APPLICANT:	4444444 000000000000000000000000000000
)		ULT 1 08-922-635-21/c 08-922-635-21/c equence 21, Applica atent No. 6033871 ENERAL INFORMATION: APPLICANT: IVANOV, APPLICANT: IVANOV, APPLICANT: IVANOV, APPLICANT: IVANOV, APPLICANT: IVANOV, APPLICANT: IVANOV, APPLICANT: IVANOV, APPLICANT: IVANOV, APPLICANT: IVANOV, APPLICANT: IVANOV, APPLICANT: IVANOV, APPLICANT: OF INVENTION:	28.2 28.2 28.2 28.2 28.2 28.2 28.2 28.2
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atgaag       grgarg acccc       ngcaac	Corrected Seque Corrected Seque TON NUMBER: US/ ATE: 1997-09-03 ATE: 1997-09-05-20 TON NUMBER: 60/ TON NUMBER: 60/ ATE: 1996-03-01 NOS: 22 IN Ver: 2.0  sapiens sapiens 15.8%; rity 54.0%; nservative 0	ation US	359 359 510 510 515 515 515 515 615 2156 4895 1302 6312 2451 2451 2451 2451 2451 2467 2487
TAG	Seque 3. 080 3. 080	/08 /DECI	44118442448284684
agggtctgagcagg	ence Listing /08/922,635A 3 /650,766 /012,600 1 Score 32.8; DB 3; L Pred. No. 1.5; Pred. No. 1.5; Pred. No. 1.5;	ALIGNMENTS US/08922635A E. R. R. R. ROLECULES ENCODEN IMIDALINE DOLYDEPTIDES ENCODED THEREBY	US-08-784-582-3 US-06-785-271-3 US-08-781-661-7 US-08-589-028-1 US-08-785-271-1 US-08-785-271-1 US-08-785-271-1 US-08-99-514-1 US-08-99-514-7 US-08-913-050A-2 US-09-011-745-7 US-08-716-351A-1 US-08-716-351A-1 US-09-273-565-29 US-09-273-565-29 US-09-273-565-32 US-09-055-699-32 US-09-055-699-32 US-09-055-699-32 US-09-055-699-32
igctcacgggatgga 60                 GCAGGGGGGGGGGGGG 9933 	Length 15202;	RECEPTIVE POLYPEPTIDES	Sequence 3, Appli Sequence 7, Appli Sequence 7, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 29, Appli Sequence 29, Appli Sequence 29, Appli Sequence 29, Appli Sequence 29, Appli Sequence 32, Appli

CORRESPONDENCE ADDRESS

ADDRESSEE:

E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive

TITLE OF INVENTION: ANTIGENS UMBER OF SEQUENCES: 6

Corley, Neil C. Shah, Purvi

Abbott Laboratories D377/AP6D-2 One Abbott

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Best Local Similarity
Matches 67; Conserv
                                                                                                                                                Sequence 3, Application US/07642734C Patent No. 5824513
                                                                                                                                                                              ·07-642-734C-3
                                                                                                                               GENERAL INFORMATION:
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                                            APPLICANT: Mcalpine
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                1245
                                                                                                                                                                                                                                                                                                                                                                            1125 CAGGAGCTGAGGGCACCACCCAGCAACCTGGGGCCTGCATTCCATCCGCTCTGCAGCCCCA 1184
                                                                                               APPLICANT: Katz, L
APPLICANT: Donadio, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1352 base pairs
TYPE: nucleic acid
                                NUMBER OF SEQUENCES:
                                                                                                               APPLICANT:
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/937,972 FILING DATE: Herewith CLASSIFICATION: 424 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                               157 accccggc 165
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ELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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                                                                                                                                                                                                                                                                                                                                     ggcagctatgaagaggacccacaaaccattttggacgaccacctctccagggtcctcaag 156
                                                                                                                                                                                                                                                                                                                                                                                                 caggccctgagctcacgggatggagcaccggtccagcaccccctggccctcctaccctcc 96
                                                                                                                                                                                                                                                                                                             AGCATCTTTCCAGTGGGGCCCCCATTCACGTTGGTCCTCAGGGAAACCAGGGTCCGGGGC 124
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                                                                            Mcalpine, J B
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Edward H. Gorman
                ADDRESS:
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                                Erythromycin
27
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                                                             Recombinant DNA Method for Producing
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                                             Analogs
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INFORMATION FOR SEQ ID NO: 3:
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ORIGINAL SOURCE:
ORGANISM: Sacc
                                                                                                      FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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HYPOTHETICAL:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-9396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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ATTORNEY/AGENT INFORMATION:
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LOCATION:
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STREET:
CITY: A
STATE:
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                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature LOCATION: 1693..2670 OTHER INFORMATION: /fur
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OTHER INFORMATION:
OTHER INFORMATION:
NAME/KEY: misc_feature
                                   OTHER INFORMATION:
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                                                                                                                                                      LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
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REGISTRATION NUMBER: 32652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US, FILING DATE: 17-JAN-91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
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    Saccharopolyspora erythraea
NRRL 238

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                                                                  misc_feature
4471..10722
                                                                                                                                                        misc_feature
4171..4428
                                                                                                                                                                                                                                            misc_feature
3406..3921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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beta-ketoreductase domain of module 3"
                                  module
                                                                                                                      acyl carrier
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beta-ketoacyl ACP synthase of module 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start= 19
/function= "gene eryA"
/product= "eryA ORF2 encoding modules 3 & 4
6-deoxyerythronolide B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function= "approximate span
module 3"
                                                                                                                      /function= "approximate span of acyl carrier domain of module 3"
                                   /function=
module 4"
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                                                  "approximate span of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of,
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NAME/KEY: misc_feature LOCATION: 10831.12174
OTHER INFORMATION: /func OTHER INFORMATION: beta-FEATURE:
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LOCATION: 14857..15114
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain of module 5
FEATURE:
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LOCATION: 10723..20
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 10723..15165
OTHER INFORMATION: /fun
OTHER INFORMATION: modu
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LOCATION: 14062..14610
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoreductase of module 5"
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: acyltransferase domain of module
                                                              NAME/KEY: misc_feature
LOCATION: 16768..17721
OTHER INFORMATION: /fur
OTHER INFORMATION: acyl
                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 15172..1659
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylaCPsynthase domain of modul"
                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 15166..20235
OTHER INFORMATION: /fur
OTHER INFORMATION: modu
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LOCATION: 12379..13350
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LOCATION: 9433..9984
                      NAME/KEY:
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misc_feature
18379..18921
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beta-ketoacylACPsynthase domain of modul"
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module 5"
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module 6"
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/function= "gene -eryA"
/product= "orf3 encoding modules 5 & 6
f-deoxyerythronolide B formatio"
                                                                   /function= "approximate span of acyltransferase domain of module
                                                                                                                                                                                                                                                                                                                                "approximate span
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LOCATION: 19492..20235
; OTHER INFORMATION: /function= "approximate span of
; OTHER INFORMATION: thioesterase domain of module 6"
US-07-642-734C-3
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Best Local Similarity
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                                                                                                                                                                                      TELEPHONE: 847-938-3137 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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NAME: CASULO, DIANNE
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 499
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                   HYPOTHETICAL: 1
ANTI-SENSE: NO
ORIGINAL SOURCE
                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 20235 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Katz, L
APPLICANT: Mcalpine,
                                                                      MOLECULE TYPE:
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LOCATION: 19149..19398
OTHER INFORMATION: /function= "a
OTHER INFORMATION: acyl carrier
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CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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acyl carrier domain of module 6"
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Pred. No. 13;
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NAME/KEY: misc_feature
LOCATION: 7165..9216
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: dehydratase and encylreductase domains
FEATURE:
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FEATURE:
NAME/KEY:
LOCATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 4471..10722
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: module 4"
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LOCATION: 4171.428
OTHER INFORMATION: function= "approximate span of OTHER INFORMATION: acyl carrier domain of module 3"
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LOCATION:
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LOCATION:
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LOCATION: 10225..10483
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OTHER INFORMATION: /fun OTHER INFORMATION: modu
                                                                                                                                    LOCATION:
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LOCATION: 9433..9984
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OTHER INFORMATION:
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10723..20235
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97..1482
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                                                    /function= "gene =eryA"
/product= "orf3 encoding modules
6-deoxyerythronolide B formatio"
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acyl carrier domain of module 4"
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acyltransferase domain of module
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beta-ketoacyl ACP synthase of module
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beta-ketoreductase domain of
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/product= "eryA ORF2 encoding modules 3 & 4
6-deoxyerythronolide B"
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RESULT 5
US-08-356-060A-42/c; Sequence 42, Application US/08356060A
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Best Local Similarity
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LOCATION:
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LOCATION:
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LOCATION: 19492..20235
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OTHER INFORMATION: module 6"
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LOCATION: 14857..15114
OTHER INFORMATION: /function= "approximate span o
OTHER INFORMATION: acyl carrier domain of module
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LOCATION:
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19149..19398
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16768..17721
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18379..18921
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15172..16569
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15166..20235
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10831..12174
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beta-ketoreductase domain of
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Pred. No. 13;
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Patent No. 584\*...
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                                                                                                                                                                 Sequence 42, Application US/08460900C Patent No. 6165747 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                  APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,00
FILING DATE: 14-DEC-1994
                                           APPLICANT: Bumcrot, David A.
APPLICANT: Marti-Gorostiza, Elisa
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
TITLE OF INVENTION: Proteins and Uses Related Thereto
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                                                                                                                     APPLICANT:
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FILING DATE: 30-DEC-1993
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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                                NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                             124 attttggacgaccacctctccagggtcctcaagacccc 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Vincent, Matthew P. REGISTRATION NUMBER: 36,709 REFERENCE/DOCKET NUMBER: HM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH:
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                                                                                                                  McMahon, Andrew
Tabin, Clifford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                    Ingham, Phillip W. McMahon, Andrew P. Tabin, Clifford J.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.18;
HOAG & ELIOT LLP
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Pred. No. 12;
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                                                                                                                                                                                                       Sequence 5, Application US/08540406 Patent No. 5837538 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (617) 832-700 INFORMATION FOR SEQ ID NO:
                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 3900 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: HN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
FILING DATE: 14-DEC-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/435,093
FILING DATE: 4-MAY-1995
PRIOR APPLICATION DATA:
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                                                                                                                               NUMBER OF SEQUENCES:
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                                                                                                                                              TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                     120 CTGATCGAGCGCCACTTGGGCGTCCACCCAGCTGGTGCGTATGTAAAGATCCGAGAATAA 61
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                       64 ccggtccagcaccccctggccctcctaccctccggcagctatgaagaggacccacaaacc 123
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0:
FILING DATE: 5-JUNE-1995
                                                STATE:
                                                             CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
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TOPOLOGY: li
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USA
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                                 SD
                                                                                                                                           GOODRICH, LISA V
JOHNSON, RONALD L
VENTION: Patched Genes and their Use
                                                                                                                                                                                           SCOTT, MATHEW P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (617) 832-7000
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30-DEC-1993
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Pred. No. 12;
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us-08-656-055-5/c
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Matches 55; Conservative
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                                 ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, BETTLAM I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: a60190-1
                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/656,055
                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SCOTT MATHEW P
APPLICANT: GOODRICH, LISA V
APPLICANT: JOHNSON, ROMALD L
TITLE OF INVENTION: Patched Genes and their Use
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 4434 base pairs
TYPE: nucleic acid
STRANCEUNESS: single
                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
ELECOMMUNICATION INFORMATION: TELEPHONE: 415-781-1989
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                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
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CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
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COMPUTER: II
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 12
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; TOPOLOGY: 1
; MOLECULE TYPE:
US-08-954-668-5
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US-08-954-668-5/c
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   Matches
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                  Best Local
                                Query Match
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                               SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/954,668
FILLNG DATE: 20-0ct-1997
CLASSIFICATION: 530
                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 617-832-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SCOTT, MATHEW P
APPLICANT: GOODRICH, LISA V
APPLICANT: JOHNSON, RONALD L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Patched Genes and their Use NUMBER OF SEQUENCES: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 TTTCTCATCGACCACATCGCCGTGTGTGTCCGGAACGC 224
                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                              NAME: Vincent, Matthew P. REGISTRATION NUMBER: 3670 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 coggtccagcaccccctggccctcctaccctccggcagctatgaagaggacccacaaacc 123
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                                                                                                                                                                 LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
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                  Similarity
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 Conservative
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                 14.18;
56.18;
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56.1%;
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                  Score 29.2;
Pred. No. 12;
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Pred. No. 12;
 Mismatches
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                                DB 4;
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 43;
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Indels
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Gaps
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64 ccggtccagcaccccctggccctcctaccctccggcagctatgaagaggacccacaaacc 123

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321 CTGATCGAGCGCCACTTGGGCGTCCACCCAGCTGGTGCGTATGTAAAGATCCGAGAATAA 262

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                  Sequence 2, Application US/07953230A
Patent No. 5476779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-398-3249 INFORMATION FOR SEQ ID NO:
                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 4434 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                      APPLICANT: CHEN, Thomas T
APPLICANT: SHAMBLOTI, MICHAEL J
TITLE OF INVENTION: INSULIN-LIKE GROWTH FACTORS ISOLATED
TITLE OF INVENTION: FROM RAINBOW TROUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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                                    CORRESPONDENCE ADDRESS
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                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                              261 TTTCTCATCGACCACATCGCCGTGTGTGTCCGGAACGC
                                                                                                                                                                                                                                                                                                   124 attitggacgaccacctctccagggtcctcaagacccc 161
                                                                                                                                                                                                                                                                                                                                                        321 CTGATCGAGCGCCACTTGGGCGTCCACCCAGCTGGTGCGTATGTAAAGATCCGAGAATAA 262
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                                                                                                                                                                                                                                                                                                                                                                                     64 ccggtccagcacccctggccctcctaccctccggcagctatgaagaggacccacaaacc 123
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 56.1 es 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 20 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/
FILING DATE: 06-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94111
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Four Embarcadero Center, Suite 3400
Burns, Doane, Swecker & Mathis
George Mason Bldg., Washington & Prince Sts.
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Pred. No. 12;
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US-07-953-230A-2
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Best Local Similarity
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                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
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LENGTH: 732 base pairs
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NAME: Crane-Feury, Sharon
REGISTRATION NUMBER: 36,1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 836-6620
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               CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                    TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              594 CAGGGCCCGGAAGTTCCGGAGGCAGGCGGTGAAGATCAAGGCCCCAAGAGCAGGCGATGTT 653
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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STATE: Virginia
COUNTRY: United
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 30-SEI CLASSIFICATION: 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 gcaccggtccagcaccccctggccctcctaccctccggcagctatgaagaggacccacaa 120
                                                                                                                ZIP: 46268
                                                                                                                                COUNTRY:
                                                                                                                                                    STATE:
                                                                                                                                                                   CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 cagatcogggaggatgaagaaaaggagggtotgagcaggcoctgagctcaogggatgga 60
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                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                     OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                          , Application US/09036987A 6143526
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22313-1404
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                                                                                                                                                    Indiana
                                                                                                                                                                                 E: Dow AgroSciences LLC Patent Department 9330 Zionsville Road
                                                                                                                                    USA
                                                                                                                                                                                                                                                                                    Waldron,
                                                                                                                                                                                                                                                                                  Treadway, Patti J.
Turner, Jan R.
Waldron, Clive
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                                                                                                                                                                                                                                                                                                                                                       Crawford, Kathryn P. Madduri, Krishnamurthy
                                                                                                                                                                                                                                                                                                                                                                                     Broughton, Mary C.
                               PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                          Baltz,
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                                                                                                                                                                                                                                      Production : 39
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                                                                                                                                                                                                                                                                      Biosynthetic Genes For Spinosyn Insecticide
US/09/036,987A
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Pred. No. 10;
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ATTORNEY/AGENT INFORMATION: NAME: Stuart, Donald R

REGISTRATION NUMBER:

NFUN.... Donald R 28,479

50,608

0;

FILING DATE: 0

09-MAR-1998

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RESULT 13
US-09-010-928B-3/c
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Best Local Similarity
~~+~hes 63; Conserv
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APPLICANT: Lewis, Randolph
APPLICANT: Hayashi, Chery
                                                                                                                                                                         REFERENCE/DOCKET NUMBER: NFORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28977
                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 22-JAN-19
CLASSIFICATION: 435
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MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (317)337-4816
TELEFAX: (317)337-4847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 tatgaagaggacccacaaaccattttggacgaccacctctccagggtcctcaagaccccc 162
                                                                                   TOPOLOGY:
                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: UZIP: 22042
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CITY: FALLS CHURCH
             NAME/KEY:
                                                                                                                                      ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
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                                                                                                                                      2824 base pairs
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8110 GATEHOUSE RD. SUITE 500E
                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                             UNITED STATES OF AMERICA
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Best Local Similarity
Matches 55; Conserv
                                                             TELEFAX: (202) 408-4400 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL
                                                                                                         REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
PRIOR APPLICATION UNMEER: PCT/FR 93/00923
                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                         FILING DATE: 25-SEP-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                            FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: TITLE OF INVENTION:
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 STRANDEDNESS:
                                                                                             TELEPHONE:
                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                              ENGTH:
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             nucleic acid
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                              474 base pairs
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double
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10-MAY-1995
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                                                                                           408-4000
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Biosynthesis Of Streptogramins,
Coding For These Polypeptides Av
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                                                                                                                           03806.0054-00000
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Pred. No. 16;
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                                                                                                                                     CUMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN Release #1.0, Ver.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,646B
FILING DATE: 03-AUG-1995
CLASSIFICATION: 435
PRIOR ADDITION: 435
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ORIGINAL SOURCE:

~~~anISM: S.pristinaespiralis
          APPLICATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-193
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CITY: Washington
STATE: D.C.
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LOCATION: 1.474
OTHER INFORMATION:
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De Crecy-Lagard, Valerie
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MBER: FR 92/11441
25-SEP-1992
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Blosynthesis Of Streptogramins, Nucleotide Sequences
Coding For These Polypeptides And Their Use
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Pred. No. 12;
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Search completed: June 7, 2001, 00:26:48 Job time: 19751 sec
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 03806.0054-01000 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CI
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LOCATION: 1...
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                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: S.pristinaespiralis
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Pred. No. 12;
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Gapop 10.0 , Gapext 1.0
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first 45 summaries
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64: em_esthum21:*
65: em_esthum21:*
66: em_esthum21:*
67: em_esthum21:*
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69: em_estro11:*
69: em_estro11:*
69: em_estro11:*
69: em_estro12:*
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69: em_estro13:*
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gb\_est53:\*
gb\_est54:\*
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gb\_est48:\*
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gb\_est56:\*
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gb\_est58:\*
gb\_est60:\*
gb\_est61:\*
gb\_est61:\*
gb\_est62:\*
gb\_est65:\*\*

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Result
No.
       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
     133.4
133.4
133.4
133.8
130.8
130.8
130.1
122
122
121.4
121.4
121.4
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111.6
110.8
110.8
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                                                                                                                                                                                                             Query
Match
      em_gss_vrt3:*
gb_gss1:*
gb_gss4.*
gb_gss6:*
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gb_gss7:*
gb_gss10:*
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em_gss_pln2:*
em_gss_pro:*
em_gss_rod1:*
em_gss_rod2:*
em_gss_rod3:*
em_gss_rod4:*
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em_gss_vrt2:*
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AI660139
AI220032
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AI858567
AI8585613
AI3728613
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A1742962 wg76d09.x
A1660139 we661a09.x
A1220032 qg78h02.x
A1818109 wk27c05.x
A1818109 wk27c05.x
A18419942 tg40d11.x
A1858567 w164d08.x
AW207598 UI-H-BI1-
AN336613 qc62c07.x
A1272864 q144h03.x
A1307112 q189f01.x
A1307112 q189f01.x
A130712 q189f01.x
AA918299 ch86g11.s
AW4742151 xs23a05.x
AA489644 aA43d02.s
AA497585 cf71h02.s
AAW17276 xj36f12.x
AA884421 am16b12.s1
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153: 154: 155: 156: 157: 157: 158: 159: 160: 161: 161:

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9b\_est86:\*
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9b\_est86:\*
9b\_est88:\*

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gb\_est99:

gb\_est66:\*
gb\_est75:\*
gb\_est77:\*
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gb\_est69: gb\_est70: gb\_est71:

9b\_est73:\*
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9b\_est96:\*
9b\_est97:\*
9b\_est98:\*
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em\_gss\_hum5:\*
em\_gss\_hum6:\*
em\_gss\_hum6:\*
em\_gss\_hum6:\*
em\_gss\_hum6:\*
em\_gss\_hum6:\*
em\_gss\_hum8:\*

em\_gss\_other:\*

8 AA489644 13 AA937585 111 AW172276 13 AA884421 155 R33824

Description

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AT742962 345 bp mRNA EST 20-DEC-1999 wg76d09.11 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3371025 3' similar to TR:070240 070240 AXIL. ;contains TAR1_t1 MER22 repetitive element ;, mRNA sequence.
                                                                                                                                                                                                                             Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg,
Tel: (301) 496-1550
                                                                                                                                                                                  Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length; 457 Std Error: 0.00
                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 345)
                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                       AI742962
                                                                                                                                                                          Seq primer: -40UP from Gibco.
                                                                                                                                                                                                                                                                       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                              AI742962.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NbHSF pool 1:
                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2371025"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
                                                                                                                                                               Location/Qualifiers
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608
361
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301
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561
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577
640
858
950
454
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AV611922
BE546616
AI878841
AL523470
CNS0133Z
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AI437053
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BE196680
AL047246
BE379078
BF629803
BF509525
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CNS0091P
BF867287
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BF712351
AI873834
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BE431012
BE427144
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                                                                                                                                                                                                                                                                                                        Hominidae;
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BF712351 MI-P-A3-a
A1873834 wm42c05.x
BF189495 235091 MA
AL053013 Drosophi1
BF867287 963088C11
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AV611922 AV611922
BE546616 601075659
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AL523470
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BE431012 SUN010.C1
BE427144 PSR6660 I
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R33823 yh78f12.r1
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HVSMEh009
DKFZp586A
601237710
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AI660139/c
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 gtgggtcgctacagcccacggtcccgc 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI660139 408 bp mRNA EST 18-DEC-1999 we61a09.x1 Soares_thymus_NHFTh Homo sapiens cDNA clone IMAGE:2345560 3' similar to TR:088566 088566 CONDUCTIN.;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 408)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 333.
Location/Qualifiers
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National Cancer Institute, Cancer Genome Ana
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/lab_host="DHIOB (phage-resistant)"
/lab_host="DHIOB (phage-resistant)"
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/note="Organ: thymus, pooled; Vector: pT7T3D-Pac
/note="Organ: thymus, pooled; Vector: pT7T3D-Pac
/note="Organ: thymus, pooled; Vector: ptiled in it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it is it 
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/clone_lib="Soares_thymus_NHFTh"
/dev_stage="fetal"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 752 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI220032 543 bp mRNA EST 30-NG 9978h02.xl Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone MAGE:1841331 3' similar to TR:042400 042400 AXIN. ;, r
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Ana
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AI220032
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1 (bases 1 to 543)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               quality sequence stop: 224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (301) 496-1550
1: Robert_Strausberg@nih.gov
/note="Organ: pooled; vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729996-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
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                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:1841331"
/clone_lib="Soares_NFL_T_GBC_S1"
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Pred. No. 4.3e-26;
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Location/Qualifiers
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                                                                                                                                                                                                                                                                      found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CGAP/BTGAP), Tumo
Unpublished (1998)
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National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
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മ
                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                              /tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
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                                     /note="Organ: pooled; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
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159 c 192 g 138 t
   Soares and M. Fatima Bonaldo.
1 124 c 162 g 107 t
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:2111253"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host-"DH10B"
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AI858567.1
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                                                                                                                                                                                                                                                                                                                                      DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 541 Error: 0.00
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Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
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NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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Seg primer: -40UP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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/tissue_type="anaplastic oligodendroglioma"
/lab_host="DH10B"
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/clone_lib="NCI_CGAP_Brn25"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg@nih.gov
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: NCI-CGAP clone distribution
information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 383 bp. mRNA EST 02-DEC-1999 UI-H-BII-afk-g-08-0-UI.sl NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722358 3', mRNA sequence.
AM207598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLYA-No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 383)
/organism="Homo sapiens"
/organism="Homo sapiens"
/olone="Image:2722358"
/clone=lib="NCI_CGAP_Sub3"
/clone=lib="NCI_CGAP_Sub3"
/lab_bost="PH10B (Life Technologies)"
/lab_bost="PH10B (Life Technologies)"
/lab_bost="PT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not i, Site_2: Eco RI; The
NCI_CGAP_Sub3 library is a subtracted library derived from
the NCI_CGAP_Sub1 library, which is a subtracted library
derived from BI. BI constitutes a mixture of 21
normalized or subtracted NCI_CGAP libraries: NCI_CGAP_CO4
,NCI_CGAP_F22, NCI_CGAP_F28, NCI_CGAP_CO10,
NCI_CGAP_CO10, NCI_CGAP_K1013, NCI_CGAP_K1011, NCI_CGAP_L1012,
NCI_CGAP_Br2, NCI_CGAP_K1011, NCI_CGAP_L1012,
NCI_CGAP_Br2, NCI_CGAP_CO8, NCI_CGAP_L1012,
NCI_CGAP_Br3, NCI_CGAP_G04, NCI_CGAP_L024,
NCI_CGAP_L1019, NCI_CGAP_GC4, NCI_CGAP_L024,
NCI_CGAP_L1019, NCI_CGAP_GC4, NCI_CGAP_L026
NCI_CGAP_Br025. These 21 libraries were pooled and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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1 115 c 149 g 89 t
                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.0%;
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Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 130.4;
Pred. No. 2.8e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .8e-25;
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Дb Qy 밁 ρ B Q B Qy

105

165

225

61

COMMENT

Sequencing Center

JOURNAL

REFERENCE

TITLE

AUTHORS

SOURCE VERSION ACCESSION DEFINITION AI336613/c

ORGANISM

KEYWORDS

Locus

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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCGCCCACGCAGCACCCCCTCTCCNTACTGCCCTCCGGCAGCTACGAGGAAGACCCGCAG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gcaccggtccagcacccctggccctcctaccctccggcagctatgaagaggacccaca 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACGATACTGGACGATCACCTGTCCAGGGTCCTCAAGACCCCTGGCTGCCAGTCTCCGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qo62c07.x1
similar to
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequences.
                                                                                                                                                                            Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg,
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                           1 (bases 1 to 413)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI336613
                                                                                                                                             Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AI336613.1
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NCI_CGAP_Kid3 pool 1 LLAM 334-3337, 3682-3683, 3798-3803 (IMAGE CloneIDs 1322376-1323911, 1456008-1456775, 1500552-1502855); NCI_CGAP_Kid5 pool 1 LLAM 3338-3342, 145052-1472903, 1492104-1493255); NCI_CGAP_Lu5 pool 1 LLAM 3575-3582, 3851-3854 (IMAGE CloneIDs 1323912-1325831, 1471368-1472903, 1492104-1493255); NCI_CGAP_Lu5 pool 1 LLAM 3757-3582, 3851-3854 (IMAGE CloneIDs 1414930-1417991, 1520904-1522439); NCI_CGAP_GC4 pool 1 LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE CloneIDs 1414930-1417991, 1469064-1470983, 1475522-1476743); NCI_CGAP_PC2 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDs 985608-986759, 1101192-1101959, 1217928-1220615); NCI_CGAP_COLD pool 1 LLAM 2644-2653, 2871-2872 (IMAGE CloneIDs 1057416-1061255, 1144584-1145351). Subtraction was performed as previously described (Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAG_LIB=NCI_CGAP_Lu5
TAG_TISSUE-lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           413 bp mRNA EST 13-FEB-1999 NCI_CGAP_CO8 Homo sapiens cDNA clone IMAGE:1913100 TR:042400 042400 AXIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:4073540
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Pred. No. 5.2e-23;
O; Mismatches 46;
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                                                                                                                                                                                                                                                                                           Anatomy Project (CGAP),
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                                                                                                                     Michael
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ORIGIN

Matches

BASE COUNT

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BASE COUNT
ORIGIN
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AUTHORS
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ORGANISM
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AI272864/c
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                                                                                                                                                                                                   COMMENT
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                                                                                                                                                                                                                                                                  TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCGCCCACGCAGCA - CCCCTCTCCCTACTGCCCTCCGGCAGCTACGAGGAAGACCCCGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGATCCGAGAGGATGAAGAGAGAGAGGGCTCCGAGCTCACACTCCAATTCGCGGGAGGGG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACGATACTGGACGATCACCTGTCCAGGGTCCTCAAGACCCCTGGCTGCCAGTCTCCGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 761 Std Error: 0.00
Seq primer: -40UP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similar to
AI272864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q143h03.x1
                                                                                                                                                                        Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 459)
                                                                                                            Tissue Procurement: Chri
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                         Robert_Strausberg@nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="adenocarcinoma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:1913100"
/clone_11b="NCI_CGAP_CO8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        459 bp mRNA EST 29-JAN-1999 NCI_CGAP_CO8 HOMO Sapiens cDNA clone IMAGE:1875125 TR:042400 042400 AXIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                           GI:3895132
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                                                                                                                                Christopher Moskaluk, M.D., Ph.D.,
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Pred. No. 7.0
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                                                                                                                                    Michael
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AI307112/c
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EST.
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                                                                  Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 534 Std Error: 0.00
Step primer: -400p from Gibco
                                                                                                                                                               Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 487)
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National Cancer Institute, Cancer Genome Ana
                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from colon adenocarcinoma, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
/clone="IMAGE:1875125"
/clone_1ib="NCI_CGAP_C08"
                                  Location/Qualifiers
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/lab_host="DH10B"
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∕organism≃"Homo sapiens"
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77.3%;
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Pred. No. 7.7e-23;
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Gy60a10.x1

similar to
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 504 Std Error: 0.00
                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 299)
NGI/NINDS-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index Unpublished (1998)
                                                                                                                                                                                                                             Tissue Procurement:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                    Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH9) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
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/tissue_type="Pooled human melanocyte, fetal heart,
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Pharmacia) with a modified polylinker; Site_1: Not I;
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BASE COUNT

JOURNAL COMMENT

REFERENCE AUTHORS

TITLE

SOURCE ORGANISM

KEYWORDS

/ERSION ACCESSION RESULT 11 AI363868/c

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DEFINITION

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similar to
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                                                                                                                                                     National Cancer Institute, Cancer Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nlh.gov
                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Primates; Catarrhini; Hor
1 (bases 1 to 546)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
                 CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                 Emmert-Buck, M.D., Ph.D.
                                                                                                                                   Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ww-bio.llnl.gov/bbrp/image/image.html
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/lab_host="DH10B"
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/clone_lib="NCI_CGAP_Brn25"
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76.0%;
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AW474251 282 bp mkna xs23a05.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2770448 similar to TR:070240 070240 AXIL.; mRNA sequence
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                                                                                                                                                                                                                             Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                     www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
                                                          cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D. CDNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                   Tissue Procurement: Chri
                                                                                                                                                                                    Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
                                                                                                                                                                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 282)
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High quality sequence stop: 209
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Location/Qualifiers
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/clone_lib="NCI_CGAP_Co8"
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/db_xref="taxon:9606"
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/lab_host="DH10B"
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Pred. No. 3.5e-20;
0; Mismatches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 13; Length 546;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 CTGGACGATCACCTGTCCAGGGTCCTCAAGACCCCTGGCTGCCAGTCTCCGGGCGTAGGC 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 ttggacgacctctccagggtcctcaagacccccggctgtcaatcccctggtgtgtgggt 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGGAGGGAAGGAGAGAGAAGGCTCAGAGNTTACANNNANTNGNGNGAGNGGNNGNNN 223
                                                                                       Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: polyT not found
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 389.
                                                                                                                                                                                                                                                                                                  Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wy. T., Waterston, R. and Wilson, R. Washu-Merck EST Project 1997 Unpublished (1997)
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AA489644
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aa43d02.sl Soares_NhHMPu_Sl
                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                            Washington University School of Medicine
                                                                                                                                                                                                                                                                                    Contact: Wilson RK
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a 72 c
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/Clone_lib="NCI_CGAP_Ut2"
/Clone_lib="NCI_CGAP_Ut2"
/Clone_lib="NCI_CGAP_Ut2"
/LISSue_type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
/lab_host="DH10B"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sali;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.85 kb. Life Technologies catalog #:
                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone="IMAGE:823683"
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Pred. No. 4.7e-20;
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AA937585/c
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source
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                                                                                                                                                                                                                          Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157;
                                        cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 537 Std Error: 0.00
Seq primer: -4m13 fwd. ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA937585 444 bp mRNA EST 24-AUG-1998 of71h02.sl NCI_CGAP_CO8 HOMO sapiens cDNA clone IMAGE:1435827 similar to TR:042400 042400 AXIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                    Location/Qualifiers
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108 c 152 g 89 t 1 others
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/lab_host="DH10B"
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75.8%;
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KEYWORDS ZERSION

JOURNAL TITLE

FEATURES

/organism="Homo sapiens"

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Matches 139; Conserv
                                              181 gtgg 184
                                                                                                                    121 accattttggacgaccacctctccagggtcctcaagacccccggctgtcaatcccctggt 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:1435827"
/clone_lib="NCI_CGAP_CO8"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
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Pred. No. 2.2e-17;
0; Mismatches 43;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

AF009674 Homo sapi	AF009674	88	3411	57.9	88.6	11 7
AF009012 C	AF009012	æ 6	3156	50 . D .	41.8	, 0
AF078165	AF078165	90	2075	70 7	121	٥
AF205888	AF205888	88	2538	79.1	121	œ
AK025718	AK025718	89	2104	79.1	121	7
AB052751	AB052751	85	1863	79.1	121	6
AF017757	AF017757	94	3216	93.7	143.4	œ
AF205889	AF205889	94	3016	100.0	153	4
AF073788	AF073788	94	2825	100.0	153	w
A98521 Seq	A98521	9	2825	100.0	153	N
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Birchmeter, W. and Behrens, J.
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Pred. No. 7.1e-38;
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                                                                                                          Mus musculus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae
1 (bases 1 to 2825)
Behrens, J., Jerchow, B.-A., Wurtele, M., Grimm, J., Asbrand, C.,
Wirtz, R., Kuhl, M., Wedlich, D. and Birchmeier, W.
Functional interaction of an axin homolog, conductin, with
beta-catenin, APC, and GSK3beta
Science 280 (5363), 596-599 (1998)
2 (bases 1 to 2825)
Behrens,J., Jerchow,B.-A. and Birchmeier,W.
Direct Submission
Submitted (22-JUN-1998) Cellular Biology, Max Delbrueck Center
Molecular Medicine, Robert-Roessle 10, Berlin 13122, Germany
Location/Qualifiers
                                                                                                                                                                                                                                                                                         AF073788.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TUMOR ILLNESSES
Patent: WO 9911780-A 6 11-MAR-1999;
BIRCHMEIER WALTER (DE); BEHRENS JUEI
LOCATION/Qualifiers
                                                                                                98221239
                                                                                                                                                                                                                                                          house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Birchmeier, W. and Behrens, J. CONDUCTINE PROTEIN AND A RELATED AGENT FOR DIAGNOSING AND TREATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unidentified unidentified
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/db_xref="taxon:32644"
815 c 813 g 49.
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                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 3016)
Zhang, T., Fagotto, F., Hsu, W., Zeng, L., Gilbert, D., Copeland, N.G., Jenkins, N.A., Warburton, D. and Costantini, F. Properties of mouse Axin2 and human AXIN2; chromosomal location, expression pattern, interaction with Axin and effects on embryonic
                                                                                                      Submitted (16-NOV-1999) Genetics & Development, Columbia University, 701 W168th St. HHSC 1416, New York, NY 10032, Location/Qualifiers
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                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                  Zhang, T.
                                                                                                                                                                                                                                         Unpublished
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TKHVHHY IHHHAVPKTKEEIEAEATQRVRCLCPGGTDYCYSKCKSHPKAPEPLPGE
OFCGSRGGTLEKRNAKGTEPGLALSATQRVRSLCPGEEGDTSQDVWQWMLES
ERQSKSKPHSAQSIRKSYPLESARAAFGERVSRHHLLGASGHSRSVARAHPFTQDPAM
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SDPVNPYHVGSGYVFAPATSANDSELSSDALTDDSMSMTDSSVDGVPPYRMGSKKQLQ
REMHRSVKANGQVSLPHFPRTHRLPKEMTPVEPAAFAAELISRLEKLKLELESRHSLE
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KCVDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKRYIENNSVVSKQLKPATKTYIRDG
IKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDIYLEYVRSGGENTAYMSNGGLGSL
                    /organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="11"
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815 c 813 g 494 t
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/db_xref="GI:3309247"
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215. .2737
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/map="between Wnt3 and Pkca"
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Pred. No. 1.1e-37;
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                                                              2 (bases 1 to 3216)
Yamamoto, H., Ikeda, S., Murai, H., Kishida, S. and Kikuchi, A.
Direct Submission
Submitted (08-AGG-1997) Biochemistry, Hiroshima University,
of Medicine, 1-2-3 Kasumi, Minami-ku, Hiroshima, Hiroshima
                                                                                                                                                                                                                                   and Kikuchi,A.

Axil, a member of the Axin family, interacts with both glycogen synthase kinase 3beta and beta-catenin and inhibits axis formation
                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                            Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF017757 3216 bp mRNA ROD 24-APR-1998 Rattus norvegicus GSK-3beta interacting protein Axil mRNA, complete
                                          Japan
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KKUCGYLPTLNEEEEBTCADLKCKLSPTVVGLSSKTLAATASVRSTETARNGFRSFK
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ERLQQIREDEEKEGSEDALSSRDGAPVQHPLALLPSGSYEEDPQTILDDHLSRVLKTP
GCQSFQKANGQVSLPHHQHHHQQCHTLLPTGGKLPPVAACPLLGGKSSLTKQT
TKHVHHYIHHAVFRTKEELEAEATQRVRCLCPGGTDYYCYSKCKSHFKAPEPLFGE
QFCGSRGGTLPKRNAKGTEPGLALSARDGGMSSAAAGAPALFGEECDRSQDVWQWMLES
ERQSKSKPHSAQSIRKSYPLESARAAPEERVSRHHLGASGHSRSYARAHFFTQDPAM
PPLTPPNTLAQLEEACRRLAEVSKPQKQRCCVASQQRDRNHSAAGQAGASFFANFSLA
PEDBKEPKKLASVHALGASELVTYFFCGEELPYRRMLKAGSLTLGHFKEQLSKKGNY
PEDBKEPKKLASVHALGASELVTYFFCGEELPYRRMLKAGSLTLGHFKEQLSKKGNY
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55. .2577
Location/Qualifiers
1. .3216
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/db_xref="GI:6653586"
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Pred. No. 1.1e-37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens Axin2 mRNA AB052751
                                                                                                            Submitted (16-DEC-2000) to the DDBJ/EMBL/GenBank databases. Yoichi Furukawa, Institute of Medical Science, Human Genome Center; 4-6-1 Shirokanedai, Minato-Ku, Tokyo 108-1639, Japan (E-mail:furukawa@ims.u-tokyo.ac.jp, Tel:81-35449-5373,
                                                                                                                                                                                                                            1 (sites)
Takahashi,M. and Furukawa,Y.
Takahashi,M. and Furukawa,Y.
Identification of 3' UTR of Axin2
Published Only in DataBase (2000) In press
Published I to 1863)
The Taylor Control of The Inches I to 1863
                                                                                                  Fax:81-35449-5406)
                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                              Nakamura, Y., Furukawa, Y. and Takahashi, M.
                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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DHKEPKRLASVHALQASELIVTYFFCGEEIPYRRMLKAQSLTLGHFKEQLSKKGNYRY
YFKKASDEFACGAVFEEIWDDETVLPMYEGRILGKVERID"
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GCQSPGVGRYSDRSRSDHHHHHHQCCHALLPTGGKLPPEACFULGGKSFLTKQTTK
HVHHHYIHHHAVPKTKEELEAEATQRVRCLCPGGTDYYCYSKOKSHSKPEPEILPGGG
GSRGGTLPKRNTKGTEPGLALPAREGGMSSAAGAPQLPGEEGDRSQDVWQWMLESER
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SEPVNPYHVGSGYVFAPATSANDSELSSDALTDDSMSMTDSSVDGIPPYRMGSKKQLQ
REMHRSVKANGQVSLPHFPRTHRLPKEMTPVEPAAFAAELISRLEKLKLELESRHSLE
            /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                           ocation/Qualifiers
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KCVDTLDFWFACNGFRQMNLKDTKTLRVAKAIYKRYIENNSVVSKQLKPATKTYIRDG
IKKQQIGSVMFDQAQTEIQAVMEENAYQVFLTSDIYLEYVRSGGENTAYMSNGGLGSL
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/translation="MSSAVLVTLLPDPSSSFREDAPRPPVPGEEGETPPCQPSVGKVQ
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/protein_id="AAC40089.1"
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/db_xref="taxon:10116"
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96.1%;
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Pred. No. 1.2e-34;
0; Mismatches 6
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for
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                                                                                                                               NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- a 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
Unpublished (2000)
2 (bases 1 to 2104)
Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T.,
"Anaka, T. and Nakamura, Y.
                                                                                                                                                                                                                                                                                                                             Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Cent Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AKU25718 2104 bp mRNA PRI 29-SEP-2000 Homo sapiens CNNA: FLJ22065 fis, clone HEP10566, highly similar to AF078165 Homo sapiens conductin mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sumio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y.,
Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oligo capping; fis (full insert sequence).
Homo sapiens hepatoma cell_line:HepG2 cDNA to mRNA, clone_lib:HEP
                                                                                                                                                                                                                                                                                                            Fax:81-3-5449-5416)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                   Location/Qualifiers
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SLAPEDHKEPKKLAGVHALQASELVVTYFFCGEEIPYRRMLKAQSLTLGHFKEQLSKK
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/gene="Axin2"
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Pred. No. 1.3e-27;
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1 (bases 1 to 2538)

Zhang, T., Fagotto, F., Hsu, W., Zeng, L., Gilbert, D., Copeland, N.G., Jenkins, N.A., Warburton, D. and Costantini, F.

Properties of mouse Axin2 and human AXIN2: chromosomal location, expression pattern, interaction with Axin and effects on embryonic
                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-NOV-1999) Genetics & Development, Columbia University, 701 W168th St. HHSC 1416, New York, NY 10032,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF205888.1
                                                                                                                                                                                                                                                                                                                                                                                                            Zhang, T. and Costantini, F. Direct Submission
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HOTHVCLFOHQAERRHVGEPEGRASPDSPLTRHTKSLHSLLGDODGAVLFRTFLEREK
CVDTLDFWFACNGFROMNLKDTKTLRVAKAIY KRYIENNSIVSKOLKPATKTYIRDGI
KKQQIDSIMFDQAQTEIQSYWEENAYOMFLTSDIYLEYVRSGEBNTAYWSNGGIGSKY
VVCGYLPTLNEEEEWTCADFKCKLSPTVVGLSSKTLRATASVRSTETVDSGYRSFKRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="HEP"
/note="cloning vector pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="hepatoma"
/clone="HEP10566"
                                                                    /protein_id="AAF22799.1"
/db_xref="GI:6653584"
/translation="MSSAMLVTCLPDPSSSFREDAPRPPVPGEEGETPPCHHGGQGPG
                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="highly similar to AF078165 Homo sapiens conductin
                                                                                                                       /codon_start=1
/product="AXIN2"
                                                                                                                                                                                                                             /tissue_type="brain; lymphoblast"
/note="similar to ESTs 823683 and 446378"
                                                                                                                                                                                                                                                                  /map="17q24"
                                                                                                                                                            /gene="AXIN2"
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red. No. 1.3e-27;
Mismatches 20;
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1 (bases 1 to 3072)

Mai,M., Qian,C., Yokomizo,A., Smith,D.I. and Liu,W.

Cloning of the human homolog of conductin (AXIN2), a gene mapping to chromosome 17q23-q24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (15-JUL-1998) Lab Medicine and Pathology, Mayo clinic, 200 First Street SW, Rochester, MN 55905, USA
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Direct Submission
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99168905
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RLOQI REDEEREGSELTLNSREGAPTOHPLSLLPSGSYEEDPOTI LIDDHLSRYLKTPG
CQS-FGVGRYS PRSRSPDHHHHHSQYHSLLPPGGKLPPAAASPGACPLLGGKGFTTKQ
TYKHVHHHY IHHHAVPKYKEE ILBAENORVHCRCPGGSEYYCYSKCKSHSKAPETMPS
EQFGAQSTKKAYPLESARSSPGERASRHHLWGGNSGHPRTTPRAHLTTQDPAMPSLTP
PNTLAHLEEACRRLAEVSKPPKORCCVASQQRDRNHSATVGTGATPFSNPSLAPEDHK
EPKKLAGVHALQASELIVTYFFCGEEIPYRRMLKAQSLTLGHFKEQLSKKGNYRYYFK
KASDEFACGAVFEEIWEDETVLPMYEGRILGKVERID*

8 724 c 724 g 473 t
/Protein_id="aad20976.1"
//protein_id="aad20976.1"
//db_xref="GI:4454791"
//db_xref="GI:445
                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="AXIN2"
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/chromosome="17"
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86.9%;
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Pred. No. 1.4e-27;
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Gallus ga
AF009012
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (13-JUN-1997) Genetics and Development, Co. University, 701 W. 168th Street, New York, NY 10032,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zeng,L., Zhang,T., Perry,W.L. III, Lee,J.J. and Costantini,F.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               signaling pathway that regulates embryonic axis formation Cell 90 (1), 181-192 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zeng,L., Fagotto,F., Zhang,T., Hsu,W., Vasicek,T.J., Perry,W.L. 3rd, Lee,J.J., Tilghman,S.M., Gumbiner,B.M. and Costantini,F. The mouse Fused locus encodes Axin, an inhibitor of the Wnt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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KIYSDPSSGSGTGKGLPGYLPTLNEDEEWKCDQDTEPEASRDSAPSSRLTQKLLLETA
TQRATSTRRYSEGREFRHGSWREPVNPYYVNTGYAMAPATSANDSEQQSMSSDADTMS
                                         /translation="MNIQGKGFPLDLGRSFTEDAPRPPVPGEEGELVSTDPRPVSHGF
YSSKSDAVRRETSTATPRRSDLDLGYEPEGSASPTPPYLKWAESHSLLDDQDGINLF
RTFLKQEDCADLLDFWFACSGFRKLEPCVSNEEKRIKLAKAIYKYILDNUGIVSROJ
KPATKSFIKDCVMKLQIDPDMFDQAQTEIQCMIEDNTYPLFLKSDIYLEYTRTGGESP
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SLAPEDHKEPKKLAGVHALQASELVVTYFFCGEEIPYRRMLKAQSLTLGHFKEQLSKK
GNYRYYFKKASDEFACGAVFEEIWEDETVLPMYEGRILGKVERID*
                                                                                                                                                                                                                                                                                 mutation due
                                                                                                                                                                       /product="Axin"
                                                                                                                                                                                                                                                                                                     /note="Fused
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ESERQSKPKPHSAQSTKKAYPLESARSSPGERASRHHLWGGNSGHPRTTPRAHLFTQD
                                                                                                                               /protein_id="AAC60245.1"
/db_xref="GI:2252818"
                                                                                                                                                                                             /codon_start=
                                                                                                                                                                                                                                         /gene="Axin"
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                                                                                                                                                                                                                                                                                                                           ′gene≖"Axin"
                                                                                                                                                                                                                                                                                                                                                                     organism="Gallus gallus"
/db_xref="taxon:9031"
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86.9%;
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Pred. No. 1.4e-27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114;
                                                                                                                                                                                                                                                                                                                                                            3rd, Lee,J.J., Tilghman,S.M., Gumbiner,B.M. and Costantini,F. The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling pathway that regulates embryonic axis formation Cell 90 (1), 181-192 (1997)
                                                                                                                                                                                                                                                                          Submitted (22-JUN-1997)
                                                                                                                                                                                                                                                                                                                        3 (bases 1 to 3411)
Vasicek, T.J., Tilghm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transposon insertions
Genetics (1997) In press
2 (bases 1 to 3411)
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                               and Zhang,T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia;
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AF009674
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                                                   mutation due
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/gene="AXIN"
/function="may inhibit embryonic axis formation"
                                                                   /note="Fused
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LSGTLGTIPPGHGKHTTKSGMKLDAANLYHHKHVYHHIHHHSMMKPKEQIEAEATQRV
QNSFAMNVDSHNYATKSRNYSENLGMAPVPMDSLGYSGKASLLSKRNIKKTDSGKSDG
                                                                                     /gene="AXIN"
                                                                                                                                                        /map="16p13.
                                                                                                                                                                        /chromosome="16"
                                                                                                                                                                                          /db_xref="taxon:9606"
                                                                                                                                                                                                        /organism="Homo sapiens"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 to 3411)
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LKQRLKPQKRPGSGASQPCENIVVAYYFCGEPIPYRTLVKGRVVTLGQFKELLTKKGN
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partial cds.
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                                                                                     Submitted (09-SEP-1999) to the DDBJ/EMBL/GenBank databases. Toshio Hirano, Blomedical research center, Osaka Univ. Med. scool, Department of Molecular Oncology; 2-2, Yamadaoka, Suita, Osaka 565-0871, Japan (E-mail:hirano@molonc.med.osaka·u.ac.jp, URL:http://www.med.osaka·u.ac.jp/pub/molonc/www/index.html, Tel:81-6-879-3880, Fax:81-6-879-3889)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shimizu,T., Yamanaka,Y., Ryu,S.L., Hashimoto,H., Yabe,T., Hirata,T., Bae,Y.K., Hibi,M. and Hirano,T. Cooperative roles of Bozozok/Dharma and Nodal-related proteins the formation of the dorsal organizer in zebrafish Mech. Dev. 91 (1-2), 293-303 (2000)
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AB032263
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Hirano, T., Hibi, M. and Shimizu, T.
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Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Danio rerio
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                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20171051
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LSETETRSQRKVGGGSAQPCDSIVVAYYFCGEPIPYRTLVRGRAVTLGQFKELLTKKG
SYRYYFKKVSDEFDCGVVFEEVREDEAVLPVFEEKIIGKVEKVD*
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//db_xref="G1:2252820"
//db_xref="G1:225282
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may inhibit embryonic axis formation"
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                                                  Location/Qualifiers
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nRNA for axin2,
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74.28;
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Pred. No. 2
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2.4e-17;
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2649

122

2589

62

BASE COUNT

SOURCE

ORGANISM

(EYWORDS VERSION ACCESSION DEFINITION

REFERENCE

AUTHORS

TITLE

**LOCUS** AB032263

RESULT 12

JOURNAL MEDLINE REFERENCE AUTHORS

TITLE

JOURNAL

FEATURES

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REFERENCE
AUTHORS
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112;
                                                                                                                                                                                                 l (bases 1 to 2529)
Hedgepeth,C.M., Deardorff,M.A. and Klein,P.S.
Xenopus axin interacts with glycogen synthase kinase-3 beta
expressed in the anterior midbrain
Mech. Dev. 80 (2), 147-151 (1999)
                                                                                                2 (bases 1 to 2529)
Hedgepeth.C.M., Deardorff,M.A. and Direct Submission
Submitted (06-OCT-1998) Medicine,
                                                                                                                                                                                                                                                                                                                          Xenopus laevis
Eukaryota; Metazoa; Chordata
Amphibia; Batrachia; Anura;
                                                                                                                                                                                                                                                                                                                                                                                                                                     AF097313.1
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                                                                                 Medical
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                                                                                                                                                                                                                                                                                                           enopodinae; Xenopus.
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                                                                                 School, 415 Curie
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LQREMQRNMRMIGQVSLLPFPRRFRPREMTPVEPARAPALLA RLERLKREGETMSS
LEERLOGIOEBEERDRSSEMSSSASHSLFLLPPGTCEEDPQAILDEHLSRVLKTPGCO
SPGLLRHSPRSRSPEQRPLPRGGLSTRSQSSSMIGYVPAKTFISROSTKHIHHHYIHH
HAGPKSKEDIEVEATORVOLLCHGTSECCTAPYIRSBLGRDCCASPAEVALCHSSTL
SKRLCKSGEEVNMEGLENSLLQLPADSTDRSQNWQMILSBDROTKHKPHSTQNVKKS
HSLEFTRTHWGGGGSSGHLRAHQPAHFFVQDPAMPPLPPPNTLAQLEEARRRLEEVS
KPSKQRHSTSSLQRDKSHPVPVQNGSSAFPMDERKDFKKMSGCHSSLGSETVYTYFFFC
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MYEGKILGKVDRMD"
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EREKCYDTLDFWFAC NG FROMDLKDTKTHRVAKALYKRY I ENNS IVAKQLLKPATKTF I
RDNIKRQQLDSAMFDQAMEIQTAMEENAXQNFELTSDIYLEYVRTGCENPSHVNRNGL
GGLKLYCGYLPTLNEEEEWSCNDFKAKALATVVGLSAKTLRS PPLRAVEALEKGYRSY
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297
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/db_xref="taxon:7955"
297. .2735
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/db_xref="GI:7229080"
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/product="axin2"
/organism="Xenopus laevis"
/db_xref="taxon:8355"
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                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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74.28;
                                                                                                                                              Deardorff, M.A. and Klein, P.S
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Pred. No. 2.4e-17;
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                                                                                 Philadelphia,
                                                                                 University of Pennsylvania
Philadelphia, PA 19104, USA
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ORIGIN
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Best Local :
                                                                                                                                                          JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2354 TAACCCTGGGACAGTTCAAGGAGCTGCTCACCAAGAAAGGAAACTATAGGTATTACTTCA 2413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (08-AUG-1997) Biochemistry, Hiroshima University of Medicine, 1-2-3 Kasumi, Minami-ku, Hiroshima, Hiroshima
                                                                                                                                                                                                                                                                      Axin, a negative regulator of the Wnt signaling pathway, forms a complex with GSK-3beta and beta-catenin and promotes GSK-3beta dependent phosphorylation of beta-catenin EMBO J. 17 (5), 1371-1384 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus
                                                                                                                                                                                    Direct Submission
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Ikeda, S., Kishida, S.,
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                                                                                                                                                                                                    Ikeda, S., Yamamoto, H., Murai, H., Kishida, S. and Kikuchi, A.
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/organism="Rattus norvegicus"
/db_xref="taxon:10116"
199. .2697
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LPGSLGTMQTGHGKHSSKSTAKVDSGNLHHKRVYHKYHHHGKVKEQLDGESTQRV
GTNRPWNVESHNYATKSRNYAESMGMAPNPDSLAYSGKYSMLSKRNAKKADLGKSES
ASHEMPVVPEDSERHQKILQWIMEGEKEIIRHKKSNHSSSSAKKQPPTELARPLSIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHCAGSNRRLSDGREFRPGTWREPVNPYYVNTGYAGAPVTSANDSEQQSMSSDADTMS
LTDSSVDGIPPYRLRKHYRREMQESANANGRGPLPHIPRTYHMPKDIHVDPEKFAAEL
ISRLEGVLRDREAEQKLEERLKRVRAEEEGDDGDVSSGPSVISHKLPSGPPMHHPNSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YSLKNOGIKNETSATPRRPDLDLGYEPEGSASPTPPYLKWAESLHSLLDDQDGIHLF
RTFLQQENCADLLDFWFACSGTRKLEPNDSKVEKRLKAKATKKYVLDSNGIVSRQI
KPATKSFIKDCVLRQQIDPAMFDQAMEIQSMEMEDNTYFVFLKSDIYLEYTTIGGESP
KPATKSFIKDCVLRQGIDPAMFDQAMEIQSMEDNTYFUFLKSDIYLEYTTIGGESP
KNYSDQSSGSGTGKGPSGYLPTLNEDEEWRCDQGGEHERERECIPSSLFSQKLALDSS
                                                                                      Location/Qualifiers
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PQKQRLKPQKKNVSAPSQPCDNIVVAYYFCGEPIPYRTMVKGRVVTLGQFKELLTKKG
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/protein_id="AAC71036.1"
/db_xref="GI:3834643"
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73.6%;
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Sciurognathi; Muridae; Murinae;
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Best Local
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                                                                                                       Zeng, L., Zhang, ...,
Zeng, L., Zhang, ...,
Direct Submission
Submitted (13-JUN-1997). Genetics and
University, 701 W. 168th Street, New
Location/Qualifiers
                                                                                                                                                                                                                                                                            Zeng,L., Fagotto,F., Zhang,T., Hsu,W., Vasicek,T.J., Perry,W.L. 3rd, Lee,J.J., Tilghman,S.M., Gumbiner,B.M. and Costantini,F. The mouse Fused locus encodes Axin, an inhibitor of the Wnt signaling pathway that regulates embryonic axis formation Coll 90(1), 181-192 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
AF009011
                                                                                                                                                                                                                                                                97373830
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 3761)
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                      /map="between <1. .3761
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KAGGGSAPPCDSIVVAYYFCGEPIPYRTLVRGRAVTLGQFKELLTKKGSYRYYFKKVS
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FPPRYVDMGCSGLRDAHEENPESILDEHVORVMETPGCQSGPGPGHRSPSGHVAKTAV
LGGTASGHGKHAPKLGLKLDSAGLHHBRHVHHHKHNHSAFKEQMEAEARRYVOSSES
WGPETHGHAKPRSYSESTGTNPSAGDLAFGGKASAPSKRNTKKAESGKNASAEVPSTT
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LLETAAPRAPSSRRYNEGRELRYGSWREPVNPYYVNSGYALAPATSANDSEQQSLSSD
ADTLSLTDSSVDG1PPYRIRKQHRREWQESVQVNGRVPLPHIPRTYRWPKEIRVEPQK
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GISLFRTFLKQEGCADLLDFWFACSGFRKLEPCDSNEEKRLKLARAIYRKYILDSNGI
VSRQTKPATKSFIKDCYMKQQIDPAMFDQAQTEIQSTMEENTYPSFLKSDIYLEYTRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAC40066.1"
/db_xref="GI:2982198"
                                                         /chromosome="17"
                                                                                /db_xref="taxon:10090"
                                                                                                   /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="rAxin"
/gene="Axin"
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72.2%;
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Pred. No. 7.7e-16;
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                                       Hba-ps4 and D17Leh54"
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                                                                                                                                                               New York,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42;
                                                                                                                                                               Development, Columb
York, NY 10032, USA
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'note="Fused is the classical dominant mouse tail

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Search completed: June Job time: 20991 sec
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ORIGIN
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Best Local Similarity 71.5
Matches 108; Conservative
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                                                                               2926 CCGTCTTGCCTGTCTTTGAAGAAAAGATCAT 2956
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                                                                                                                                                                                                                                                                                                                                                                                                                                               mutation due to an iap insertion in the Axin gene" <1...2981
                                                                                                                                                                                                                       DEPVLPVFEEKIIGKVEKVD"
                                                                                                                                                                                                                               VGYYFCGEPIPYRTLVRGRAVTLGQFKELLTKKGSYRYYFKKVSDEFDCGVVFEEVRE
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                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                                                            function="may inhibit embryonic axis formation"
        7, 2001, 00:36:17
                                                                                                                                                                                                               1012
                                                                                                                                                                 53.7%;
71.5%;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                              Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match Length
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153
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/SIDS2/gcgdata/geneseq/geneseqn/NA1987.DAT: *
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/SIDS2/gcgdata/geneseq/geneseqn/NA1982.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn/NA1983.DAT:*
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26.4	26.4	26.4	26.4	26.4	26.4	26.4	26.6	26.6	26.6	26.8	26.8	26.8	27	27.2	27.2	27.4	27.4	27.4	27.6	27.6	28	28	28.2	28.4	28.8	28.8	29.2	29.2	29.2	29.2	29.6	29.6	29.6
17.3	17.3	17.3	17.3	17.3	17.3	17.3	17.4	17.4	17.4	17.5	17.5	17.5	17.6	17.8	17.8	17.9	17.9	17.9	18.0	18.0	18.3	18.3				•	•	•		19.1	•		
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Z91253	X20550	Z91259	C35947	Z19228	Z19440	Z15585	C44660	Z30413	Z15741	X13181	Z16081	Z14749	A10595	F12525	C65784	V71742	A38860	A49788	Z52940	T93777	C48750	C40313	A67611	C37835	C74570	C79811	C36225	C47412	A52642	T19983	C35517	116	894
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Bacterium 2412	Polynucleotide	CoA ligase fcc	Arabidopsis	M. tuberculosis	M. tuberculosis	Human gene express	Arabidopsis	Arabidopsis	Human gene express	Enterococcus	Human gene o	Human gene express	Gene encoding a su	Aspergillus oryzae	Human lung cancer	Human V3 loop HIV	Arabidopsis wax s	Arabidopsis wax s	Human prostate	cDNA encoding	Arabidopsis	S	Eucalyptus grandis	S.	Human ORFX ORF125	Human secre	Arabidopsis	Arabidopsis	Eosinophil activat	Human gene	Arabidopsis	Arabidopsis	Arabidopsis

## ALIGNMENTS

RESULT X23370

x23370;

X23370 standard; cDNA; 2523

BP

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Tumor-suppressing protein conductin diagnosis of tumors
                                                                                                                                                                                                             Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour; therapy; cytoplasmic degradation; blockade; Wnt signalling pathway; Wingless signalling pathway; Adenomatous Polyposis Coli; APC; tumour suppressor; ss.
                                                                                                        02-SEP-1997;
                                                                                                                           01-SEP-1998;
                                                                                                                                                                                                                                                                Human conductin cDNA.
                                                                                                                                                                                                                                                                                    17-JUN-1999 (first entry)
                               WPI; 1999-214706/18.
P-PSDB; W93570.
                                                             Behrens J, Birchmeier W;
                                                                                                                                                 11-MAR-1999
                                                                                                                                                                    W09911780-A2
                                                                                                                                                                                                            tumour suppressor;
                                                                                  (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX
                                                                                                                                                                                         Homo sapiens
                                                                                                        97DE-1038205.
                                                                                                                            98WO-DE02621
             used for treatment and
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Score

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X23370 X23369 A77754

Human conductin cD Human conductin DN cDNA encoding huma cDNA encoding huma

Human axin gene. Murine axin gene.

Description

153 153 121 121 121 88.6 82.2 30.2 29.6 29.6

A77843 X09012 X09013 Q12839 Q36133

Variable region of MH4H7 MAb heavy ch Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia

100.0 100.0 79.1 79.1 57.9 53.7 21.6

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X23369
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Best Local Similarity
Matches 153; Conser
                      WO9911780-A2
                                                                               misc_feature
                                                                                                                             protein_bind
                                                                                                                                                                                                                        misc_signal
                                                                                                                                                                                                                                                                                                                        Conductin; tumour; diagnosis; treatment; beta-catenin; anti-tumour; therapy; cytoplasmic degradation; blockade; Wnt signalling pathway; Wingless signalling pathway; Adenomatous Polyposis Coli; APC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes a novel human conductin protein which has anti-tumour activity. Detecting the presence or amount of conductin, at protein or nucleic acid levels, is used to diagnose tumours, while agents that (re)activate conductin are used for tumour therapy. Conductin binds to beta-catenin and induces its cytoplasmic degradation, resulting in blockade of the Wnt/Wingless signalling pathway in vertebrates. Conductin also binds to Adenomatous Polyposis Coli (APC) fragments and, in conjunction with APC, acts as a tumour suppressor.
                                                                                                                                                                          protein_bind
                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                tumour suppressor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               X23369 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2407
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                                                                             /bound_moiety= beta-catenin
/note= "as described in Claim
2561..2713
                                                                                                                                                                                                                        /product= "Conductin"
446..814
                                                                                                                                                                         1241..1402
                                                                                                                          1403..1609
                                                                                                                                       /note= "as desc
                                                                                                                  /*tag=
                                                                                                                                                                                                /note≖ "regulator
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                                                                                                                                                                                                                                                         Location/Qualifiers
215..2737
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Claim 22"
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Pred. No. 5.1e-41;
                                                                                                                                                  GSK-3beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      723 G;
                                                                                                                                                                                   of G-protein signalling in Claim 19"
                                                      homology region
                                                                                                                                     in
                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      452 T; 0 other;
                                                                                        21"
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Best Local
                       23-DEC-1998;
02-JUL-1999;
22-SEP-1999;
19-NOV-1999;
                                                                                                                                   WO200037643-A2
                                                                                    23-DEC-1999;
                                                                                                           29-JUN-2000
                                                                                                                                                                             Human colon tumour polypeptide; tumour antigen; cancer; vaccine; immunotherapy; diagnosis; progression; ss.
                                                                                                                                                                                                                     cDNA encoding
                                                                                                                                                                                                                                                                                                                                                         2681
                                                                                                                                                                                                                                                                                                                                                                                                        2621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel human conductin protein which has anti-tumour activity. Detecting the presence or amount of conductin, at protein or nucleic acid levels, is used to diagnose tumours, while agents that (re)activate conductin are used for tumour therapy. Conductin binds to beta-catenin and induces its cytoplasmic degradation, resulting in blockade of the Wntr.Wingless signalling pathway in vertebrates. Conductin also binds to Adenomatcus Polyposis Coli (APC) fragments and, in conjunction with APC, acts as a tumour suppressor.
                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                             14-NOV-2000
                                                                                                                                                                                                                                                                      A77754;
                                                                                                                                                                                                                                                                                           A77754 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor-suppressing protein conductin diagnosis of tumors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2825 BP; 703 A; 815 C; 813 G; 494 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 18; Fig 2; 22pp; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                              61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birchmeier
                                                                                                                                                                                                                  human colon tumour polypeptide,
                       98US-0221298.
99US-0347496.
99US-0401064.
99US-0444242.
                                                                                   99WO-US30909
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                                                                                                                                                                                                                                                                                             CDNA; 401
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Pred. No. 5.3e-41;
; Mismatches 0;
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                                                                                                                                                                                                                    SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC cancer: T-cells specific for the polypeptide expressed by the APC are CC used to remove tumour cells from biological samples, especially blood or CC fractions thereof. The sample or the isolated T-cells specific for the CC polypeptide can then be used to inhibit cancer development. CD4+ and/or CC collect acid of the invention, or an APC expressing such a polypeptide, or CC nucleic acid of the invention, or an APC expressing such a polypeptide, or CC collect acid of the invention, or an APC expressing such a polypeptide, or CC concese the proliferation of specific T-cells. The T-cells can be CC cloned and then administered back to the patient to inhibit cancer CC development. Nucleic acids encoding the polypeptides and antibodies against the polypeptides may be used to determine the expression level CC of a tumour protein of the invention, and therefore to determine whether CC cancer cells are present. Such diagnostic methods may also be used to CC monitor the progression of a cancer by repeating the processes at time CC intervals, and comparing the current result to previous results. The present sequence represents a cDNA encoding a human colon tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 133; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xu J, I
Wang T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequences A77722-A78199 represent 478 cDNAs encoding proteins portions of proteins which are associated with human colon turbe invention also specifically discloses 8 human colon tumous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (B11897-B11904). The nucleic acids, the polypeptides they encode, and antigen presenting cells (APCs, preferably dendritic cells) expressing such polypeptides may be used in vaccines that target tumour cells, especially colon tumour cells, thereby inhibiting the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New colon tumor polypeptides used to inhibit the development of cancer, especially colon cancer, and for diagnosing and monitoring the progression of the cancer -
                                                                                                                                 cDNA encoding
                                                                                                                                                                                                                                              A77843 standard; cDNA; 1205 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 401
W0200037643-A2
                                                                                            Human colon tumour polypeptide; tumour antigen; cancer; vaccine;
                                                                                                                                                                    14-NOV-2000 (first entry)
                                                                        immunotherapy; diagnosis; progression;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Page 96-97; 229pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP;
                                                                                                                               human colon tumour polypeptide, SEQ ID NO:123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 A; 88 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Secrist H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 121;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>ი</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 T;
                                                                                                                                                                                                                                                                                                                                            350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Meagher MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       colon tumour
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tumours
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RESULT X09012

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X09012 standard; DNA; 3411

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                                                                                                                                                                                                                                                                                                                                                                            Sequences A77722-A78199 represent 478 cDNAs encoding proteins or corrections of proteins which are associated with human colon tumours. CC portions of proteins which are associated with human colon tumours. CC the invention also specifically discloses 8 human colon tumours proteins CC (B11897-B11904). The nucleic acids, the polypeptides they encode, and antigen presenting cells (APCs, preferably dendritic cells) expressing CC such polypeptides may be used in vaccines that target tumour cells, CC especially colon tumour cells, thereby inhibiting the development of concer. T-cells specific for the polypeptide expressed by the APC are CC used to remove tumour cells from biological samples, especially blood or CC concer. T-cells from a patient may be incubated T-cells specific for the polypeptide can be used to inhibit cancer development. CD4+ and/or CC cD8+ T-cells from a patient may be incubated with a polypeptide or nucleic acid of the invention, or an APC expressing such a polypeptide, coloned and then administered back to the patient to inhibit cancer development. Nucleic acids encoding the polypeptides and antibodies against the polypeptides may be used to determine the expression level cof a tumour protein of the invention, and therefore to determine whether CC ancer cells are present. Such diagnostic methods may also be used to intervals, and comparing the current result to previous results. The correct secunds secunds results. The ancer correct secunds are consequent a connect correct secunds and antibodies.
                                                                                                                                                                                                                        Matches 133;
                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JUL-1999;
22-SEP-1999;
19-NOV-1999;
02-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 progression of the cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New colon tumor polypeptides especially colon cancer, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-442671/38
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                                                                                                                                                                                                                                                                                                               Sequence 1205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xu J,
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                                                                                                                                                                                                                                                                                                                                                                     present sequence represents a cDNA encoding a human colon
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   324
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                                                                                                                                                                 1 ttgaccctgggccacttcaaggagcagctcagcaaaaaagggaaattacaggtattattc 60
                    acagtgctccccatgtacgaaggcaggatcctg
                                                                                       aagaaggcgagtgacgaatttgcctgcggagcagtttttgaggagatctgggacgacgag 120
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acggtgctcccgatgtatgaaggccggattctg
                                                                        aaaaaagcaagcgatgagtttgcctgtggagcggtgtttgaggagatctgggaggatgag
                                                                                                                                              ttgaccctgggccactttaaagagcagctcagcaaaaagggaaattataggtattacttc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 125-126; 229pp; English
                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                               BP; 316 A; 248
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99US-0444242.
99US-0454150.
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                                                                                                                                                                                                                                         79.1%;
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                                                                                                                                                                                                                                         Score 121; DB 21; Pred. No. 1.5e-30;
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                                                                                                                                                                                                                                                                                                               324 G;
                                     153
                                                                                                                                                                                                                                                                                                                 317 T; 0 other
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                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                          Matches
                                                                                                                              2529
 2649
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                                                                                                                                                                                                                                                                  Sequence 3411 BP; 752 A; 1010 C; 1066 G; 582 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Figure 10A-10B; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Newly isolated nucleic acid encoding "axis inhibition"
(Axin) - useful for detecting, diagnosing and treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Constantini F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYCO ) UNIV COLUMBIA NEW YORK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     beta-catenin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human axin gene
                  122 cagtgctccccatgtacgaaggcaggatcct 152
                                                                                                                                                                                                       Local Similarity
                                                                                                                                                           N
                                                                           agaaggcgagtgacgaatttgcctgcggagcagtttttgaggagatctgggacgacgaga 121
                                                                                                                                       tgaccctgggccacttcaaggagcagctcagcaaaaagggaaattacaggtattatttca
                                                                                                                         tcaccctgggccagttcaaggagctgctgaccaaaaagggcagctacagatactacttca 2588
                                                          agaaagtgagcgacgagtttgactgtggggtggtgtttgaggaggttcgagaggacgagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1999-120510/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful for detecting, diagnosing and treating cancer
                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                      57.98;
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                                                                                                                                                                                       0;
                                                                                                                                                                                                      Score 88.6; DB 20
Pred. No. 1.1e-19;
                                                                                                                                                                                         Mismatches
2679
                                                                                                                                                                                                                    DB 20;
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                                                                                                                                                                Matches
                                                                                                                                                                                Query Match
Best Local
                                                                                                       2806
                                         2866 agaaagtgagtgatgagtttgactgtggtgtggtatttgaggaagtacgggaggatgagc 2925
                                                                                                                                                                                                                                       Sequence 3761 BP; 890 A; 1012 C; 1088 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; Figure 9A-9B; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Newly isolated nucleic acid encoding "axis inhibition" (Axin) - useful for detecting, diagnosing and treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gastrointestinal cancer;
diagnosis; treatment; the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murine axin gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Axin; cancer; breast cancer; colorectal cancer;
122 cagtgctccccatgtacgaaggcaggatcct 152
                                                            62 agaaggcgagtgacgaatttgcctgcggagcagtttttgaggagatctggggacgacgaga 121
                                                                                                                   2 tgaccctgggccacttcaaggagcagctcagcaaaaagggaaattacaggtattatttca
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                                                                                                    tcaccctgggccagttcaaggagctgctaaccaagaaggggagctacagatactacttta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1999-120510/10
                                                                                                                                                                108;
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                                                                                                                                                                Conservative
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/product= Axin
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                                                                                                                                                                           53.7%;
71.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             er; esophageal cancer; carcinoma; melanoma; therapy; thyroid carcinoma; tumorigenesis;
                                                                                                                                                               0;
                                                                                                                                                                             Score 82.2; DB 20;
Pred. No. 1.5e-17;
                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                       771 T; 0
                                                                                                                                                                43;
                                                                                                                                                                                                                                       other;
                                                                                                                                                                Indels
                                                                                                                                                                                       Length 3761;
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Best Local Similarity
Matches 69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                  The region encoding the VH region is used to construct a recombinant antibody with a lambda light chain. The antibody recognises an antigenic determinant on the outside core in LPS of P. aeruginosa. See also Q12840.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human antibody gene and corresp. recombinant plasmid or virus - useful in mass -prodn. of human anti Pseudomonas aeruginosa LPS outside core antibody.
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P-PSDB; R13182.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             012839 standard; DNA; 925 BP.
                Q36133 standard; DNA; 657
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 925 BP; 186 A; 231 C; 270 G; 237 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 2; 16pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JP03151876-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monoclonal antibody; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-OCT-1991 (first entry)
                                                                                                   728
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                                                                                                                                                                    gcaactgaacagcctgaaatctgaggacacggctctgtattactgtgtgagagaggaata 667
                                                                                                                                                                                                                                                               ggagcagctcagcaaaaagggaaattacaggtattatttcaagaaggcgagtgacgaatt 80
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                                                                                                   aggtaagat 736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89JP-0291981.
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/note- "Claim 3"
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                                                                                                                                                                                                                                                                                                                                21.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q36133
              C41830 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 657 BP; 150 A; 150 C; 193 G; 164 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 5; Fig 8; 27pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JUN-1991;
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                                                                                                                                                                      594 tgcctatggcctggggtcttttgatatctggggccaagggacaatggtcaccgtctcttc
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                                                                                                                                                                                      tgcctgcggagcagtttttgaggagatctgggacgacgagacagtgctccccatgtacga 140
                                                                                                                                                                                                                                       gcaactgaacagcctgaaatctgaggacacggctctgtattactgtgtgagaggaata 593
                                                                                                                                                                                                                                                             ggagcagctcagcaaaaagggaaattacaggtattatttcaagaaggcgagtgacgaatt 80
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/number= Intron
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/number= Exon
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mapping; gene expression control;  I transduction pathway;  termination sequence; ss.	in its	s.	s.
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22-SEP-1999
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                                                                       C33133 standard;
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                                                                                                                                                                                                                                                                                                    59;
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Similarity 54.6%;
59; Conservative
 (first entry)
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99US-0151065.
99US-0151066.
99US-0151066.
99US-0151303.
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23-MAR 1999
25-MAR 1999
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08-APR 1999
16-APR 1999
23-APR 1999
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27-MAY 1999
11-MAY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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21-JUN-1999; 22-JUN-1999; 23-JUN-1999;

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30-AUG-1999;
31-AUG-1999;
01-SEP-1999;
07-SEP-1999;
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15-SEP-1999;
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                       18-OCT-2000 (first entry)
                                                                                                     7-SEP-1999;
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                                                                                                                                                                            Similarity 54.0
                                                                                                                                                                                                             9908-0151080
9908-0151080
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UN-1999 UN-1999 UN-1999 UN-1999	UN-19		JUN-19	UN-19	JUN-19	JUN-19	JUN-19	JUN-19	JUN-19	JUN-19	JUN-19	-JUN-19	AY-19	MAY - 19		MAY-19		MAY-19	MAY-19	MAY-19	MAY - 19	MAY-19	MAY - 19		ফ্ফ		APR-19		APR-19		APR-19		MAR-19		MAR-19		FEB-20	SEP-2000	EP1033405-	Arabidops	potte	idisa ein i
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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                                            Arabidopsis thaliana DNA fragment SEQ
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                         Hybridisation assay; genetic mapping; gene expression protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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990S-0146388.

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                                             Arabidopsis thaliana
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RESULT 15
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Best Local Similarity 54.6%;
Matches 59; Conservative
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108-OCT-1999
113-OCT-1999
                                                                               Gene signature; messenger RNA; mRNA; relative abundance; frequency, human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
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13-OCT-1999;
14-OCT-1999;
14-OCT-1999;
          11-NOV-1994;
                            01-JUN-1995
                                                               Homo sapiens
                                                                                                                    Human gene signature HUMGS01117.
                                                                                                                                                           T19983;
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                                              WO9514772-A1
                                                                                                                                      17-JUL-1996 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                          A single-stranded DNA (or its complementary strand or the corresp. C double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of thuman genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-C untranslated sequence is unique to a particular mRNA, species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
                                                                                                                                                                                                                                                                    Query Match 19.1%;
Best Local Similarity 57.8%;
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                         Sequence 340 BP; 82 A; 87 C; 95 G; 75 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 528; 2245pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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(OKUB/) OKUBO K.
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                                                                                                                          66 ggcgagtgacgaatttgcctgcggagcagt 95
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                                                                                                                                                                                                                                                                    ; Score 29.2; DB; Pred. No. 2.2; 0; Mismatches
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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Match
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2: //cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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196.096 Million cell updates/sec
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          BB
       US-08-261-110A-3
US-08-261-110A-1
US-09-040-984-45
US-09-058-257-1
US-09-258-371-1
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Matches 48; Conserv
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	16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.2	16.3	16.3	16.3	16.3	16.3	16.3	16.6	16.6
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ALIGNMENTS	US-08-379-452-43	US-08-735-609-1'	US-08-735-609-1	US-09-245-497-4	US-09-244-752-4	US-09-315-372-4	US-08-735-609-4	US-08-735-609-4	US-08-860-635A-20	US-08-677-734A-8	US-08-669-161A-29	US-08-651-999A-6	5449756-3	5198359-3	5449756-10	US-08-358-627F-22	US-08-724-394A-22	US-08-724-394A-21
	Sequence 43, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 4, Appli	Sequence 20, Appl	Sequence 8, Appli	Sequence 29, Appl	Sequence 6, Appli	Patent No. 5449756	Patent No. 5198359	Patent No. 5449756	Sequence 22, Appl	Sequence 22, Appl	Sequence 21, Appl				

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; MOLECULE TYPE: US-08-261-110A-3
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APPLICANT: CERUTI, HERLBERTO
TITLE OF INVENTION: cDNA ENCODING A
TITLE OF INVENTION: EUKARYOTES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS: ADDRESSEE: NIXON, HARGRAVE, DEVANS
STREET: CLINTON SQUARE, P.O. BOX 1
CITY: ROCHESTER
STATE: NEW YORK
COUNTRY: USA
COMMUTERS BEADLASIE FORM:
                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/261,110A FILING DATE: 16-JUN-1994 CLASSIFICATION: 536 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/938,332 FILING DATE: 28-AUG-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                    TELEFAX: (716) 263-1600 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                             NAME: TIMIAN, SUSAN J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 199
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1167 base pairs
                                         TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: lin
                                                                                  nucleic acid
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Score 27.6; Pred. No. 2. Mismatches

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Sequence 45, Application US/09040984
Patent No. 6210883
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GENERAL
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APPLICANT: JAGEND
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                                                                                                                    1232
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1:0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: TIMIAN, SIGAN J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 28-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                     73 gacgaatttgcctgcggagcag 94
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Local Similarity '58.5%;
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: ROCHESTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP STREET: CLINTON SQUARE, P.O. BOX 1051
                                                                                                                                                                                                                                                                                                                                                                                                                        CENGTH:
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28-AUG-1992
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                                                                                                                                                                                                                                                   Score 27.6; DB Pred. No. 2.6; 0; Mismatches
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                                                                                                                                                                                                                                                                                  DB 1;
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US-08-776-265-2/c
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                                                                                                                                                                                               Sequence 2, Application Patent No. 6001631 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
                                                              CORRESPONDENCE ADDRESS:
                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 18-MAR-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: COMPOUNDS AND TITLE OF INVENTION: OF LUNG CANCER
                                                                                                                         APPLICANT:
                                                                                                                                       APPLICANT:
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                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                  258
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                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                            138 GTAATGCT 131
                                                                                                                                                                                                                                                                                                                                       121 acagtgct 128
                                                                                                                                                                                                                                                                                                                                                                       198 GACAAGCAAAGCTTCAAATTTGCCTGCGGACTTCGGTTTGAACTGCACGGGCATGTTGAT 139
                                                                                                                                                                                                                                                                                                                                                                                        61 aagaaggcgagtgacgaatttgcctgcggagcagtttttgaggagatctggggacgacgag 120
                 STREET:
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les 65; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: STATE 6300 Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ttgaccctgggccacttcaaggagcagctcagcaaaaagggaaattacaggtattatttc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 206-282-6031
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Washington
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               E: Finnegan, Henderson, Farabow,
E: Dunner, L.L.P.
1300 I. Street, N.W., Suite 700
                                                                                                                         FERRERO,
                                                                                                                                                                                 BLANCHE,
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No. 6001631el Topoisomerase IV, Corre
Nucleotide Sequences and Uses Thereof
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Pred. No. 2.5;
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

20005-3315 D.C.

COUNTRY:

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Best Local Similarity
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COMPUTER: IBM PC COMPACIBLE
OPERATING SYSTEM: PC-ONS/MS-POS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/776,265
FILING DATE: 24-CAN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Elnaudi, Catol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 32,220
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (202) 408-4444
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: DNA SEQUENCE ENCODING A TUMOR TITLE OF INVENTION: SUPPRESSOR GENE NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: GARKAVTSEV, Igor APPLICANT: RIABOWOL, Karl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/569,721
FILING DATE: 08-DEC-1995
                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                           ADDRESSEE: Burns, Doane, Swecker & Mathis STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
LIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 cacttcaaggagcagctcagcaaaaagggaaattacaggtattatttcaagaaggcgagt 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 gacga 77
                                                             CLASSIFICATION:
                                                                                    FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                   APPLICATION NUMBER: US/09/258,257
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US-09-258-257-1
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Best Local Similarity
Matches 47; Conserv
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SEQUENCE CHARACTERISTICS:
                                                                                 TELEFAX: 415-854-8275 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/258,371
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: MOO1, Leslie A.
REGISTRATION NUMBER: 37,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 415-854-7400
                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Garkavtsev, Ig
APPLICANT: Riabowol, Karl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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CITY: Alexandria
                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1902 base pairs TYPE: nucleic acid STRANDEDNESS: single
              STRANDEDNESS:
                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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REFERENCE/DOCKET NUMBER: 028722-128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                ENGTH:
                       nucleic acid
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                                               1902 base pairs
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linear
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              double
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57.3%;
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                                                                                                                                                                    37,047
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Pred. No. 10;
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US-08-569-721A-1
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                                                                   Best Local Similarity Matches 47; Conserv
                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                         TELEFAX: (650) 854-827
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MOOI, LESLIE A.
REGISTRATION UNMBER: 37,047
REFERENCE/DOCKET NUMBER: 0287
TELECOMMUNICATION INFORMATION:
1132 CATGGCCAATTAAAAAAAATTGTTCATAAAGTAATAATATTACTTGTATTAAAATAAAAA 1073
                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,72.
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                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: GARKAVTSEV, IGOT
APPLICANT: RIABOWOL, Karl
TITLE OF INVENTION: DNA SEQUENCE ENCODING A TUMOR
TITLE OF INVENTION: SUPPRESSOR GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                              STRANDEDNESS:
TOPOLOGY: 11
                  6 cctgggccacttcaaggagcagctcagcaaaaagggaaattacaggtattatttcaagaa 65
                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United States ZIP: 22313-1404
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CITY: Alexandria
STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 ggcgagtgacgaatttgcctgc 87
                                                                                                                                                                                                                                                                            ENGTH:
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                                                                                                                                                                                                                                                         nucleic acid
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                                                                                                                                                                                                                                                                          1902 base pairs
                                                                   Conservative
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57.3%;
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57.3%;
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                                                              Score 26; DB 3; Length 1902; Pred. No. 10; 0; Mismatches 35; Indels
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RESULT 9
US-09-499-082-1/c
; Sequence 1, Application US/09499082
; Patent No. 6143522
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                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                 Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
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                                                                                                                                          1132 CATGGCCAATTAAAAAAATTGTTCATAAAGTAATAATATTACTTGTATTAAAATAAAA 1073
                                                                                  1072 AGCTAATGAAATATTTTCCTTC 1051
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-7400
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
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APPLICATION NUMBER:
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APPLICANT: Riabowol, Karl
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CORRESPONDENCE ADDRESS:
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                                                                                                     66 ggcgagtgacgaatttgcctgc 87
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LOCATION: 109..741
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TOPOLOGY: li
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57.3%;
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Pred. No. 10;
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GENERAL INFORMATION:

APPLICANT:

Garkavtsev,

Igor

Helbing, Caren C. Riabowol, Karl Johnston, Randall N.

CORRESPONDENCE ADDRESS:

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; LOCATION:
US-09-499-082-1
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US-09-258-371-9/c
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GENERAL INFORMATION:
APPLICANT: Garkavtsev,
APPLICANT: Riabowol, K
TITLE OF INVENTION: DN
TITLE OF INVENTION: SU
                                                                                   Sequence 9, Application US/09258371 Patent No. 5986078
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                           Matches
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NAME: MOO1, Les11e A.
REGISTRATION UNMBER: 37,047
REFERENCE/DOCKET NUMBER: 0287
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-854-7400
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                                                                                                                                                                                          1072
                                                                                                                                                                                                                                                         1132 CATGGCCAATTAAAAAAAATTGTTCATAAAGTAATATTACTTGTATTAAAAATAAAAA 1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/499,082
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APPLICATION NUMBER: US 08/569721
FILING DATE: 08-DEC-1995
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/828,15 FILING DATE: 27-MAR-1997 APPLICATION NUMBER: US 08/751230
                                                                                                                                                                                                      66 ggcgagtgacgaatttgcctgc 87
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CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                   6 cctgggccacttcaaggagcagctcagcaaaaagggaaattacaggtattatttcaagaa 65
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109..741
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Leslie A.
7749ER: 37,047
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57.3%;
 DNA SEQUENCE ENCODING THE TUMOR SUPPRESSOR GENE ING1
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Pred. No.
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US-09-258-371-9
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                                                                                                                                                                                                                                                                   Sequence 9, Application US/08751230 Patent No. 6117633
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Best Local Similarity
                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                        APPLICANT: Garkavtse
APPLICANT: Riabowol,
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                          ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                     1231 AGCTAATGAAATATTTTCCTTC 1210
                                                                                                                                                                                                                                                                                                                                                                                                                                  1291 CATGGCCAATTAAAAAAATTGTTCATAAAGTAATAATATTACTTGTATTAAAAATAAAAA 1232
                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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NAME: Mooi, Leslie A.
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
COMPUTER: IBM PC OPERATING SYSTEM:
                                                              COUNTRY: USA
ZIP: 22313-1404
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CITY: Alexandria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
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57.3%;
compatible
PC-DOS/MS-DOS
                                                                                                                                                                                           DNA SEQUENCE ENCODING THE TUMOR SUPPRESSOR GENE ING1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08/751,230
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Pred. No. 11;
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PRIOR APPLICATION DATA:

US 08/569721

CLASSIFICATION: FILING DATE: APPLICATION NUMBER:

15-NOV-1996

US/08/751,230

CURRENT APPLICATION DATA:

PatentIn Release #1.0, Version #1.30

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Best Local Similarity
Watches 47; Conserve
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US-08-751-230-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/09499082 Patent No. 6143522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-854-8275 INFORMATION FOR SEQ ID NO:
PRIOR APPLICATION NUMBER: US/08/828,158
APPLICATION NUMBER: US/08/828,158
FILING DATE: 27-MAR-1997
APPLICATION NUMBER: US 08/751230
FILING DATE: 15-NOV-1996
                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1:0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1231 AGCTAATGAAATATTTTCCTTC 1210
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                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Helbing, Caren APPLICANT: Riabowol, Karl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1291 CATGGCCAATTAAAAAAATTGTTCATAAAGTAATAATATTACTTGTATTAAAATAAAAA 1232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 08-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Garkavtsev, Igor
TITLE OF INVENTION: METHODS OF MODULATING APOPTOSIS
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 ggcgagtgacgaatttgcctgc 87
                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Mooi, Leslie A. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 0 FILING DATE: 08-DEC-1995
                                                                                                            FILING DATE:
                                                                                                                            APPLICATION NUMBER: US/09/499,082
                                                                                                                                                                                                                                                                                                     CITY: Alexandria
                                                                                                                                                                                                                                                                                                                         STREET:
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57.3%;
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Pred. No.
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                                                                                                                                                               Version #1.30
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QΥ
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TYPE: DNA
CORGANIZM: Pseudomonas aeruginosa
US-08-846-762-1
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                                                                                                                                                                                                                                                                                                               SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08846762A Patent No. 5994072
                                                                                                                                                                      Matches
                                                                                                                                                                                    Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lam, Joseph S.
APPLICANT: Burrows, Lori
APPLICANT: Charter, Deborah
APPLICANT: de Kievit, Teresa
TITLE OF INVENTION: No. 5994072el Proteins Involved in the Synthesis and Assembly
TITLE OF INVENTION: of O-Antigen in Pseudomonas Aeruginosa
                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/08/846,762A
CURRENT FILING DATE: 1997-04-30
NUMBER OF SEQ ID NOS: 100
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                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 6580-089
                                                                                                          20093
                                              20033
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ATTORNEY/AGENT INFORMATION:
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                121
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LOCATION:
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                                             ACCAGGGAACGCGGCACCACCGCCGGCGGGGAGCGGTACCAGTAGACCAGCAACGACAGG 19974
                                                              TGGCGCATGGCCAGACGCAAGCCGCCGATCAGCAGCATGCTCAACCACCAGTAGTTGAAC
                                                                                                                               ttgaccctgggccacttcaaggagcagctcagcaaaaagggaaattacaggtattatttc 60
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                                                                                                                                                                      62;
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Mooi, winher: 37,047
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57.3%;
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                                                                                                                                                                      0; Mismatches
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Pred. No. 11;
                                                                                                                                                                                    Score 26; DB
Pred. No. 28;
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                                                                                                                                                                                                      DB 2;
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19973 AC 19972

US-08-469-412A-3/c

Sequence 3, Application US/08469412A Patent No. 5856125

ENERAL INFORMATION:

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RESULT 15
US-09-021-715-3/c
; Sequence 3, Application US/09021715
; Patent No. 6194547
; GENERAL INFORMATION:
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Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,412A
FILING DATE: 05-JUN-1995
                                                                                                                                                                               2240 TGCCCATGGGCCAGTCCTAGGAGCAGCTGGGGATGAAGGGGTTGGACCGGT 2190
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: GAITELT-WAGKOWSKI, EU
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: 123..698
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        OLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 576-0200 °
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UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 94111-3834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sgouras, Dionyssios N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blair, Donald G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beal Jr., Gregory J. Athanasiou, Meropi A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fisher, Robert J.
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                                                                                                                                                                                                                                                     Conservative
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                                Mayrothalassitis, George J.
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Fisher, Robert
                  Blair, Donald G
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                                                                                                                                                                                                                                                                  16.6%;
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                                                                                                                                                                                                                                                                    Score 25.4;
Pred. No. 18;
                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                     16;
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US-09-021-715-3
Search completed: June Job time: 19755 sec
                                                                                                                                                                 Matches
                                                                                                                                                                                Query Match
Best Local
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/021,715
FILING DATE: 10-Feb-198
CLASSIFICATION: - CUBANOWND-
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sgouras, Dionyssios N.
TITLE OF INVENTION: The ERF Genetic Locus and Its Products
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA
                                                                                                                                                                 l Similarity
35; Conserv
                                                                                                                                                                                                                                                                                               (AERF) CDNA"
                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 2432 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Garrett-Wackowski, Eugenia REGISTRATION NUMBER: 37,330 REFERENCE/DOCKET NUMBER: 015280-229000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 123..698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
                                                                                                                                                                 Conservative
                 7,
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                 2001, 00:26:52
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                                                                                                                                                                              Score 25.4;
Pred. No. 18;
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                                                                                                                                                                 Mismatches
                                                                                                                                                                                                 DB 4;
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                                                                                                                                                                 16;
                                                                                                                                                                                                 Length 2432;
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
                                            June 6, 2001, 23:00:49; Search time 3054.04 Seconds (without alignments) 437.657 Million cell updates/sec
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Gapop 10.0 , Gapext 1.0
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153
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gb_est3:*
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gb_est7:*
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gb_est21:*

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em_estro11:*
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em\_estpl9:\*
em\_estpl10:\* em\_estpl8:\* em\_estpl1:\*

em\_estom1:\*

em\_estro4:\*
em\_estro5:\*

em\_estro16:\*

gb\_est45:\*

em\_estin1:\* em\_esthum28:\* em\_esthum26:\*
em\_esthum27:\* em\_esthum21:\*
em\_esthum22:\* em\_esthum19:\* em\_esthum16:\*
em\_esthum17:\*

em\_esthum20:\*

em\_esthum15:\*

em\_esthum24:\*

gb\_est55:\*
gb\_est56:\*
gb\_est57:\*

gb\_est51:\*
gb\_est52:\*

gb\_est53:\*
gb\_est54:\*

gb\_est48:\* gb\_est49:\*

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Result
No.
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                                                                                                                                                                                                              Score
   121
116.8
116.8
188.2
88.2
87.6
83.8
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Match
   79.1
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gb_gss2::*
gb_gss3::*
gb_gss3::*
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gb_gss6::*
gb_gss6::*
gb_gss6::*
gb_gss10::*
gb_gss11::*
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em_gss_rod3:*
em_gss_rod4:*
em_gss_rod5:*
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em_gss_vrt2:*
   548
5495
1070
427
319
601
4601
503
503
516
5216
5216
5216
5216
 7 AA446378
139 BE755017
138 BE68565
165 BE315156
149 BF521997
156 R75687
165 BE314898
140 BE808273
111 AM140896
143 BF076028
3 AA170717
165 BE333754
1 AA022403
4 AA259709
3 AA153185
143 BF039925
144 BF039925
145 BF889872
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AA446378 Zw58b07.r
BE755017 208720 MA
BE668565 158407 MA
BE315156 601140956
BF521997 UI-R-Y0-a
R75687 Y121d06.r1
BE314898 601140035
BE808273 213437 MA
AM140896 EST220830
BF076794 226536 MA
BF076028 225414 MA
AA17017 ms70a09.r
BE333754 us27f06.y
AA028403 mi21f04.r
AA153185 ms6540.r
AA153185 ms65410.r
AA153185 ms65410.r
AA153185 ms62410.r
AA153185 ms62410.r
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138: 139: 140: 141: 142: 142: 144:

gb\_est65:\*
gb\_est76:\*
gb\_est76:\*
gb\_est77:\*
gb\_est78:\*
gb\_est78:\*
gb\_est80:\*

gb\_est58:\*
gb\_est59:\*
gb\_est60:\*
gb\_est61:\*
gb\_est62:\*
gb\_est63:\*

gb\_est64:\*

gb\_est82:\*
gb\_est83:\*
gb\_est84:\*

9b\_est85:\*
9b\_est86:\*
9b\_est88:\*
9b\_est89:\*
9b\_est99:\*
9b\_est90:\*

9b\_est101:\*
9b\_est102:\*
9b\_est103:\*
9b\_est105:\*
9b\_est69:\*
9b\_est69:\*
9b\_est70:\*
9b\_est71:\*
9b\_est7

em\_gss\_other:\*

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RESULT
AA446378
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                                                                                                                                                                                                                                                                                                                                  SOURCE
ORGANISM
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JOURNAL
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67
67
57
                                                                                                                                                                                                   Schellenberg, K., Steptoe, M., Tan, F., Theising, T., Waterston, R. and Wilson, R.
WashU-Merck EST Project 1997
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                    zw58b07.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
IMAGE.774229 5', mRNA sequence.
                                                                                                                                                                                                                                                                                             сикагуота; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 548)
                                                                                                                           Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 490.
                                                                                                                                                                                                                                                                           Hillier, L., Allen, M., Bowles, L., Dubuque, T., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra,
                                                                                                                                                                                                                                                                                                                                                                            AA446378
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Fax: 314 286 1810
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/note-"Yector: P77T3D-Pac (Pharmacia) with a modified /note-"Yector: P7TT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from pooled 8-9 week (total) fetus material with a Not I - oligo(dT) primer [5'
                                                   /clone="IMAGE:774229"
/clone_11b="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                                           /lab_host-"DH10B"
                                                                                                                 ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           548 bp
                                                                                                                                                                                                                                                                  ., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Le,N., Lennon,G., Marra,M., Martin,J., Moore,B.
Steptoe,M., Tan,F., Theising,B., White,Y., Wylie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA355700
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AV671166
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T07178
BF137964
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BF789612
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CNS04RUJ
AZ315171
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AV671166 AV671166
BF118962 601755316
T07178 EST05067 Fe
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AA355700 EST64142
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AW445734 82895 MAR
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BE647747 UI-M-BH1-
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AA699261 HL08054.5
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BE290973 601084133
BE882875 601509279
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AL228087 Tetraodon
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AL304372 Tetraodon
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AW445343 81418 MAR
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1M0032J16
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KEYWORDS
SOURCE
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BE755017
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 BASE COUNT
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
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                                                                                                                                                                                    Seq
                                                                                                                                                                                                                                                                                                                               USDA, ARS, US Meat Animal PO Box 166, Clay Center, N Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                            Design and use of four pooled tissue normalized cDNA libraries for EST discovery in cattle Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 495)
Smith, T.P.L., Casas, E., Stone, R.T.,
Bennett, G.A., Fahrenkrug, S.C., Freki, W.W. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE755017
208720 MARC
                                                                                                                                                                                                      BACKWARD: GTTTTCCCAGTCACGACG
Plate: 56 row: K column: 1
                                                                                                                                                                                                                                                                                   Email: smith@email.marc.usda.gov
Single pass sequencing. Bases ca
v0.980904.e. Vector identified b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COW
                                                                                                                                                                                                                                                    PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                               Contact: Smith TPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota;
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                                                                                                                                                                                                                                       FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                     te: 56 row: K column: 12 primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                    -minmatch 12 options.
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 103
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 ρ
              /note-"Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the and Eco RI sites of the modified pTTT3 vector. Libra went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. a 121 c 170 g 116 t
                                                                           /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                        /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
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Eutheria; Cetartiodactyla; Ruminantia; Pecora;
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2BOV B
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Pred. No. 5.8e-28;
164 g
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                                                                                                                                                                                                                                                                                    called and alt_trimmed with phred by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R.T., Heaton,M.P., Grosse,W.M.,
Freking,B.A., Rohrer,G.A., Laegreid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 548;
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BE668565
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    41
                                                                         Local
              2 tgaccctgggccacttcaaggagcagctcagcaaaaagggaaattacaggtattatttca 61
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TGACCTTGGGCCACTTTAAGGAGCAGCTCAGCAAAAAGGGGAAACTACCGGTATTACTTCA 100
                                                           130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGTCTTGCCCATGTACGAGGGCCGCATCCTG 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130;
                                                                                                                                                                                                                                                                                               BACKWARD: GTTTTCCCAGTCACGACG
Plate: 60 row: O column: 14
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                           EST discovery in cattle (1900) (Inpublished (2000) (Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE668565
158407 M
                                                                                                                                                                                                                                                                                                                                                                  Single pass sequencing. Bases call v0.980904.e. Vector identified by and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                       PCR PRimers
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                                                                                                                                                                                                                                                                                                                             BACKWARD:
                                                                                                                                                                                                                                                                                                                                         FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Design and use of four pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE668565.1 GI:10029156
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                                                         Conservative
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                                                                                                                                                                                              /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 4BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                         Library made from pooled tissue from day 20 and day 40 embryos."
                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                     76.3%;
85.5%;
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                                                     Score 116.8; DB 130
Pred. No. 1.2e-26;
0; Mismatches 22;
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Pred. No. 1.2e-26;
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                                                                                  DB 138;
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                                                        Indels
                                                                                  Length 546;
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             487
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Best Local
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                                                                                                                                                                                                 367 TCACCCTGGGCCAGTTCAAGGAGCTGCTGACCAAAAAGGGCAGCTACAGATACTACTTCA 426
                                                                                                                                                                                                                                                                                                   Local Similarity 74.2
nes 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161 TGGTCTTGCCCATGTACGAGGGCCGCATCCTG 192
                                                                                                                                                                                                                         2 tgaccctgggccacttcaaggagcagctcagcaaaaagggaaattacaggtattatttca 61
                                  cagtgctccccatgtacgaaggcaggatcct 152
                                                                                                                               agaaggcgagtgacgaatttgcctgcggagcagtttttgaggagatctgggacgacgaga 121
                                                                                               AGAAAGTGAGCGACCAGTTTGACTGTGGGGTGGTGTTTGAGGAGGTTCGAGAGGACGAGG
CCGTCCTGCCCGTCTTTGAGGAGAAGATCAT 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cagtgctccccatgtacgaaggcaggatcctg 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: Robert_Strausberg@nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM109 row: o column: 14
High quality sequence stop: 673.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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BE315156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            289
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-*Organ: ovary; Vector: POTB7; Site_1: xhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." a 310 c 316 g 155 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:3140965"
/clone_lib="NHH_MGC_9"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                        57.9%;
74.2%;
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                                                                                                                                                                                                                                                                                                                          Score 88.6; DB 165; Pred. No. 1.3e-17;
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AUTHORS
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1 ttgaccctgggccacttcaaggagcagctcagcaaaaagggaaaattacaggtattatttc 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: msoares@blue.weeg.uiowa.edu
CDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (info@lmage.llnl.gov). IMAGE ID= 1791410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     451 Eckstein Medical Research Building Towa City, IA 52242, Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Res. 6 (9), 791-806 (1996) 97044477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two appr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus.
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                                                                                                                                                                                                                                               118
                                                                                                                                                                                                                                                                                 //lab.host-"pHIOB (Life Technologies)"
//lab.host-"pHIOB (Life Technologies)"
//lab.host-"pHIOB (Life Technologies)"
//lab.host-"pHIOB (Life Technologies)"
//lab.host-"pHIOB (Life Technologies) with a modified
//lab.host-"pHIOB (Life Technologies) with a modified
//lab.host-"pHIOB (Life Technologies) with a modified
polylinker; Site_l: Not I; Site_l: Eco RI; The UI-R-YO
library is a subtracted library derived from an
individually-tagged normalized whole-eye (minus the lens),
library; The driver for the subtraction consisted of a
pool of all previous libraries (UI-R-AO, UI-R-AI, UI-R-EO)
UI-R-EI, UI-R-CO, and UI-R-CI). The tag is a string-of
3-5 nucleotides present between the Not I site and the
oligo-dT track which allows identification of the library
of origin of a clone within the mixture. The subtracted
library (UI-R-YO) was constructed as follows: PCR
amplified cDNA inserts from previous library clones from
which 3' ESTs had been derived were used as a driver in a
hybridization with the normalized whole-eye library in
the form of single-stranded circles. The remaining
single-stranded circles (subtracted library) was purified
by hydroxyapatite column chromatography, converted to
double-stranded circles and electroporated into DHIOB
bacteria (Life Technologies) to generate the UI-R-YO
library. This procedure has been previously described
(Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
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                                                                                                       57.6%;
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Pred. No. 1.
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                                                                                   Mismatches
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1.4e-17;
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agaaggcgagtgacgaatttgcctgcggagcagtttttgaggagatctgggacgacgaga 121

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 aagaaggcgagtgacgaatttgcctgcggagca
 36
AAGAAGGCGAGTGACGAATTTGCCTGTGGAGCA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
Insert Size: 971
High quality sequence stops: 198
Source: IMACE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 971 Std Error: 0.00
Seq primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 319)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                         Similarity
                                                                      Conservative
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                                                                                                                                                                                                               double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pB773 vector (Pharmacia). Library went through one round of normalization to a Cot - 230. Library constructed by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
/clone="IMAGE:158891"
                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Soares breast 2NbHBst"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="GDB:572946"
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                                                                                         57.3%;
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                                                                CCGTCCTGCCCGTCTTTGAGG
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                                                                                                                                          AGAAAGTGAGCGACGAGTTTGACTGTGGGGTGTTTTGAGGAGGTTCGAGAGGACGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Connedistribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM93 row: e column: 09 High quality sequence stop: 600.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 601)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                    127
                                                                                                                                                                                                                                                                                                                                                                                                                 /tissuc_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: ovary; Vector: pOTB7; Site_1: xhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
27 a 189 c 194 g 91 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone="IMAGE:3049328"
/clone_lib="NIH_MGC_9"
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                                                                                                                                                                                                                                                                                                                         55.6%;
75.2%;
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                                                                                                                                                                                                                                                                                                    Score 85; DB 165;
Pred. No. 1.5e-16;
0; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                            Length 601;
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                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                    Gaps
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VERSION
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                                                                                                                                                                                                                                            cagtgctccccatgtacgaaggcaggatcct 152
                                                                                                                                                                                                                                                                                                                         agaaggcgagtgacgaatttgcctgcggagcagtttttgaggagatctggggacgacgaga 121
                                                                                                                                                                                                                   CTGTGCTGCCCGTCTTCGAGGAGAAGATCAT 297
                                                                                                                                                                                                                                                                                                AGAAAGTGAGCGACGAGTTCGAGTGCGGCGTGGTGTTCGAAGAGGTGCGTGAGGACACGG 266
                                                                                                                                                                                                                                                                                                                                                                           TCACCCTGGGCCAGTTCAAGGAGCTGCTGACCAAGAAGGGCAACTACAGGTTCTACTTCA 206
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sequence.
AW140896
AW140896.1
EST.
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EST290830 P
RGIAS43 5'
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Plate: 68 row: 0 column: 3
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WSDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _{
m W} W. and Keele, J.W. Design and use of four pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith, T.P.L., Casas, E., Stone, R.T., Bennett, G.A., Fahrenkrug, S.C., Frek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith, T.P.L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              adrenal, and endometrium."
133 c 166 g 74 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pCMV SPORT6; Site_1: xba1; Site_2: xho1; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal and endometrium."
                                                                                         487\ \text{bp} mRNA EST 30-OCT-Normalized rat embryo, Bento Soares Rattus sp.
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                                                                         end similar to GSK-3beta interacting protein rAxin,
                GI:6160589
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72.2%;
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Pred. No. 3.5e-16;
0; Mismatches 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                CCATCCTGCCTGTCTTTGAAGAAAAGATCAT 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCACCCTGGGCCAGTTCAAGGAGCTGCTAACCAAGAAGGGGAGCTACAGATACTACTATA 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGAAAGTGAGTGACGAGTTTGACTGTGGTGTGGTATTTGAGGAAATACGGGAAGATGAGG 442
                                                                                                                                                                                                                                                                                                                  BF076794
226536 MARC :
BF076794
 USDA,
PO Bo
                                  EST discovery in cattle Unpublished (2000) Contact: Smith TPL
                                                                                        1 (bases 1 to 503)
Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M.,
Bennett, G.A., Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Laegreid,
W.W. and Keele, J.W.
Design and use of four pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: (301)-838-0208

Email: nhlee@tigr.org

For clone availability, additional sequence and expression information related to this EST please check the TIGR Rat Gene Index (http://www.tigr.org/tdb/rgi/rgi.html). To order a clone contact the ATCC (http://www.atcc.org/atcc.html).

Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1998)
Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville,
Tel: (301)-838-3529
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                                                                                                                                                                                                                                         Bos taurus
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Mammalia; Eutheria;
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ARS, US Meat Animal Research Center 166, Clay Center, NE 68933-0166, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Rattus sp."
/db_xref="taxon:10118"
/db_nref="taxon:10118"
/clone="RoTANS43"
/clone=lib="Normalized rat embryo, Bento Soares"
/dev_stage="embryo 8, 12, 18 dpc"
/dev_stage="embryo 8, 12, 18 dpc"
/notce="Vector: pT773Pac; Site_1: EcoRI; Site_2: NotI"
125 c 136 g 97 t
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72.2%;
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Rodentia;
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Pred. No. 3.5e-16;
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Sciurognathi; Muridae; Murinae;
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                                                                                                     USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Single pass sequencing. Bases called and alt_trimmed v0.980904.e. Vector identified by cross_match with the and _minmatch 12 options.
                                Single pass sequencing. Bases ov 0.980904.e. Vector identified and -minmatch 12 options.
                                                                                                                                                                             Contact: Smith TPL
                                                                                                                                                                                              Design and use of four pooled tissue normalized EST discovery in cattle Unpublished (2000)
                                                                                                                                                                                                                                                 1 (bases 1 to 562)
Smith, T.P.L., Casas, E., Stone, R.T.,
Bennett, G.A., Fahrenkrug, S.C., Frek,
W.W. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea
                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus
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BF076028
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Plate: 87 row: N column: 19
Seq primer: ATTTAGGTGACACTATAG.
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FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                            Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: smith@email.marc.usda.gov
                                                                                      Email: smith@email.marc.usda.gov
FORWARD: AGGAAACAGCTATGACCAT
                  PCR PRimers
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a 146 c 185 g 74 t
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/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
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/lab_host="DH10B"
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2BOV Bos
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72.2%;
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Pred. No. 3.5e-16;
0; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA
                                                  called and alt_trimmed by cross_match with the
                                                                                                                                                                                                                                                                  R.T., Heaton,M.P.,
Freking,B.A., Roh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5', mRNA sequence.
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                                                                                                                                                                                                                                                                    P., Grosse, W.M.,
Rohrer, G.A., Laegreid
                                                    with the
                                                                                                                                                                                                                                    cDNA libraries
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VERSION
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 109;
                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191 AGAAAGTGAGCGACGAGTTCGAGTGCGGCGTGGTGTTCGAAGAGGTGCGTGAGGACACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 TCACCCTGGGCCAGTTCAAGGAGCTGCTGACCAAGAAGGGCAACTACAGGTTCTACTTCA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 agaaggcgagtgacgaatttgcctgcggagcagtttttgaggagatctgggacgacgaga 121
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                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                       WashIngton University School of MedicineP
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                      Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                              Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubu
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ms70a09.rl Soares mouse 5', mRNA sequence.
                                                                                                                                                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                          The WashU-HHMI Mouse EST Project
                                                                                                                                       MGI:37771
                                                                                                                                                                                                                                                                                                                   Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                 Waterston, R.
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Plate: 85 row: D column: 1
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                                                                            primer: -28M13 rev2 from Amersham
h quality sequence stop: 428.
Location/Qualifiers
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/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
              /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."

171 c 201 g 90 t
/db_xref="taxon:10090"
                                       ∕organism="Mus
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72.2%;
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Pred. No. 3.6e-16
0; Mismatches 4
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SOURCE
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KEYWORDS
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BE333754
                                                                  FEATURES
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Best Local Similarity
                                                   source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108;
                                                               Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE333754 476 bp mRNA EST 14-JUL-2000 us27f06.yl Soares_NMEBA_branchial_arch Mus musculus cDNA clone IMAGE.3168323 5' similar to TR:O15169 O15169 AXIN; mRNA sequence.
                                                                                                                                             CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Washington University Genome Sequencing Clone distribution: NCI-CGAP clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/image/html/iresources.shtml
                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                  MGI:1063783
                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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                                                                                                                                                                                                                                             cDNA Library Preparation: M. Bento Soares, Ph.D.,
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/clone="IMAGE:3168323"
                                /organism="Mus musculus"
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/lab_host="DH10B"
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71.5%;
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                                                                                                                                                                                               Sequencing Center
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                                                                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
Murinae; Mus.
                                                                                                                                                                                                                                               Fatima Bonaldo
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/clone\_lib="Soares\_NMEBA\_branchial\_arch"

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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGTCTTGCCTGTCTTTGAAGAAAAGATCAT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cagtgctccccatgtacgaaggcaggatcct 152

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108;
                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA028403 516 bp mRNA EST 16-AUG-1996 m121f04.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:464191 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 516)
                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA028403.1
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                                                                                                                                                                                                                        primer: -28M13 rev2 from Amersham
                                                                                                                                                                                        quality sequence stop: 493.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90
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102 c
                         /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:464191"
clone_lib="Soares mouse embryo NbME13.5 14.5"
                                                                                                                                                              ocation/Qualifiers
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71.5%;
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Pred. No. 1.
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1.1e-15;
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KEYWORDS
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AA259709
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ORIGIN
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       333 TCACCCTGGGCCAGTTCAAGGAGCTGCTAACCAAGAAGGGGAGCTACAGATACTACTTTA 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 agaaggcgagtgacgaatttgcctgcggagcagtttttgaggagatctggggacgacgaga 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 tgaccctgggccacttcaaggagcagctcagcaaaaagggaaattacaggtattatttca 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCGTCTTGCCTGTCTTTGAAGAAAAGATCAT 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGAAAGTGAGTGATGAGTTTGACTGTGGTGTGGTATTTGAGGAAGTACGGGAGGATGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 526)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMAGE:733481 5', mRNA sequence.
AA259709
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                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1996)
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                                                                                                                                                                                                              primer: -28ml3 rev2 ET from Amersham
                                                                                                                        quality sequence stop: 485
Location/Qualifiers
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/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/lab_h
/organism="Mus musculus'
/strain="C57BL/6J"
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Pred. No. 1.1e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     St. Louis, MO
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/db\_xref="taxon:10090"

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Query Match 53.7
Best Local Similarity 71.5
Matches 108; Conservative
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232 CCGTCTTGCCTGTCTTTGAAGAAAGATCAT 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="fetus"
//dev_stage="12.5dpc total fetus"
//dev_stage="12.5dp
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/clone_lib="Soares mouse 3NME12 5"
/sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.7%;
71.5%;
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Pred. No. 1.1e-15;
0; Mismatches 43; Indels
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BASE COUNT

Search completed: June 6, 2001, 23:00:52 Job time: 15536 sec

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